


GenCore version 5.1.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2003, 04:07:47 ; Search time 6559 Seconds
(without alignments)
4543.570 Million cell updates/sec

Title: US-09-697-089-2
Perfect score: 1024
Sequence: 1 MNFIKDNKRALIQRMGTRVI.....WQFDDDDLSVITGAFKLVT A 1024

Scoring table: 
Ygapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4106490

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	822	80.3	3355	9	AK095467 Homo sapi
5	822	80.3	3581	9	AF376061 Homo sapi
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8	589	57.5	160583	2	AC010968 Homo sapi
9	559	54.6	138909	9	CNS01DS3
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14	206	20.1	618	6	AX318176 Sequence
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21	87	8.5	261	6	AX318172 Sequence
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23	36	3.5	165	6	AX318178 Sequence
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25	11	1.1	83866	2	AC131423
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ALIGNMENTS

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VERSION AY032589.1 GI:13899172
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 3133)
Geddes, B.J., Wang, L., Huang, W.-J., Lavelle, M., Manji, G.A.,
Brown, M., Jurman, M., Morganstern, J., Merriam, S., Glucksmann, A.,
Distefano, P.S. and Bertin, J.
Human CARD12 is a novel CED4/Apaf-1 family member that induces
apoptosis
JOURNAL Biochem. Biophys. Res. Commun. 284 (1), 77-82 (2001)
MEDLINE 21268963
PUBMED 11374873
REFERENCE 2 (bases 1 to 3133)
AUTHORS Bertin, J.
TITLE Direct Submission
JOURNAL Submitted (15-APR-2001) Neurobiology, Millennium Pharmaceuticals
Inc., 640 Memorial Drive, Cambridge, MA 02139, USA
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ORIGIN

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x AY032589 (1-3133)

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 REFERENCE 1 (bases 1 to 3219)

AUTHORS

Poyet, J.-L., Srinivasula, S.M., Thani, M., Razmara, M.,
 Fernandes-Alnemri, T. and Alnemri, E.S.
 Identification of Ipaf, a human caspase-1-activating protein
 related to Apaf-1
 J. Biol. Chem. 276 (30), 28309-28313 (2001)
 21359454
 MEDLINE
 11390368
 PUBMED
 2 (bases 1 to 3219)
 Poyet, J.-L., Srinivasula, S.M., Fernandes-Alnemri, T. and
 Alnemri, E.S.
 Direct Submission
 Submitted (16-MAY-2001) Microbiology and Immunology, Thomas
 Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107,
 USA

FEATURES

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 Query Match: 90.14% Indels: 2
 DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x AY035391 (1-3219)

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 Qy 21 LysGlnIleThrAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
 Db 205 AAGCAATCACAGATGACCTATTGTATGGAATGCTTGAATCCGGAAGATAAATC 264
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Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IPAK Plate: 50 Row: a Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.

FEATURES

Location/Qualifiers

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DEFINITION to Homo sapiens ICE-protease activating factor mRNA.
ACCESSION AK095467
VERSION AK095467.1 GI:21754727
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens CD34+ Cells cDNA to mRNA, clone_lib:D9OST2
clone:D9OST2003791.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
1
Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaïra,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahara,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project

JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 3355)
AUTHORS	Isogai, T. and Yamamoto, J.
TITLE	Direct Submission
JOURNAL	Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI team); 2-6-7
COMMENT	Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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Percent Similarity:	99.61% Conservative: 0
Best Local Similarity:	99.61% Mismatches: 2
Query Match:	80.27% Indels: 4
DB:	9 Gaps: 0
US-09-697-089-2 (1-1024) x AK095467 (1-3355)	
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Db 382	ATTTGCTGCGAAGAGTGGAGCAGATGCTCTAGAGGATCAATTCACATGATTTTGAAA 441
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Qy 81	PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
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Qy 141	ArgLysAspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
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misc_feature
/note="Region: caspase recruitment domain"

BASE COUNT 1033 a 781 c 843 g 924 t
ORIGIN

Alignment Scores:

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Score: 822.00 Matches: 1022
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Best Local Similarity: 99.61% Mismatches: 2
Query Match: 80.27% Indels: 4
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x AF376061 (1-3581)

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AUTHORS	1		
TITLE	Read, J.C., Pio, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H., Oliveira, V.A., Hayashi, H. and Pawlowski, K.		
JOURNAL	Card domain containing polypeptides, encoding nucleic acids, and methods of use		
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REFERENCE 1 (bases 1 to 3396)
AUTHORS Damiano,J.S., Stehlik,C., Pio,F., Godzik,A. and Reed,J.C.
TITLE Clan, a novel human ced-4-like gene
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JOURNAL Genomics 75 (1-3), 77-83 (2001)
MEDLINE 21365712
PUBMED 11472070
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AUTHORS Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
Research, The Burnham Institute, 10901 North Torrey Pines Road, La
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AUTHORS Hazan, J., Fonknechten, N., Mavel, D., Paternotte, C., Samson, D.,
Artiguenave, F., Davoine, C.S., Cruaud, C., Durr, A., Wincker, P.,
Brottier, P., Cattolico, L., Barbe, V., Burgunder, J.M.,
Prud'Homme, J.F., Brice, A., Fontaine, B., Heilig, R. and
Weissenbach, J.
TITLE Spastin, a novel AAA protein, is altered in the most frequent form
of autosomal dominant spastic paraplegia
JOURNAL Nat. Genet. (1999) In press
REFERENCE 2 (bases 1 to 138909)
AUTHORS Genoscope.
DIRECT SUBMISSION
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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1 (bases 1 to 1355)
Auffray,C., Ansoorge,W., Ballabio,A., Estivill,X., Gibson,K.,
Lehrach,H., Poustka,A. and Lundberg,J.
The European IMAGE consortium for integrated Molecular analysis of
human gene transcripts
Unpublished
2 (bases 1 to 1355)
Pluvinet,R., Estivill,X., Escarceller,M. and Sumoy,L.
Direct Submission
Submitted (15-JUL-2000) Dept. Genetica Molecular, Institut de
Recerca Oncologica (IRO), Hospital Duran i Reynals, Av. Gran Via
s/n Km 2.7 L'Hospitalet de Llobregat, 08907 Barcelona, Catalunya,
SPAIN. Tel: ++34-93-260-7775 Fax: ++34-93-260-7776 WWW site:
http://www.iro.es e-mail enquiries: lsumoy@iro.es
EURO-IMAGE Consortium Contact: Auffray C
CNRS UPR 420 - Genetique Moleculaire et Biologie du Developpement
IFR 1221 - Rue Guy Moquet 19, Batiment G - BP 8
```

94801 Villejuif Cedex, FRANCE
Tel: ++33-1-49 58 34 98
Fax: ++33-1-49 58 35 09
e-mail: auffray@inbio.gen.fr
Distributors:
This clone is available royalty-free through IMAGE Consortium
IMPORTANT: This sequence represents the full insert of this IMAGE
cDNA clone. No attempt has been made to verify whether this
corresponds to the full-length of the original mRNA from which it
was derived.

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ACCESSION AY027788

VERSION AY027788.1 GI:14324114

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE

AUTHORS Damiano, J.S., Stehlik, C., Pio, F., Godzik, A. and Reed, J.C.

TITLE Clan, a novel human ced-4-like gene

JOURNAL Genomics 75 (1-3), 77-83 (2001)

MEDLINE 21365712

PUBMED 11472070

REFERENCE 2 (bases 1 to 1395)

AUTHORS Stehlik, C., Damiano, J.S., Pio, F., Godzik, A. and Reed, J.C.

TITLE Direct Submission

JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death Research, The Burnham Institute, 10901 North Torrey Pines Road, La Jolla, CA 92037, USA

FEATURES

source Location/Qualifiers

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Qy 894 GlySerLeuSerSerLeuLysHisLeuGluGluValProGlnLeuValLysLeuGly 913

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Db 1321 GTTATTACAGGTGCTTTTAACTAGTAAGTCT 1353

RESULT 13

AX318174

LOCUS AX318174 891 bp DNA linear PAT 14-DEC-2001

DEFINITION Sequence 179 from Patent WO0190156.

ACCESSION AX318174

VERSION AX318174.1 GI:17900865

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Reed, J.C., Pio, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H.,

Oliveira,V.A., Hayashi,H. and Pawlowski,K.
Card domain containing polypeptides, encoding nucleic acids, and
methods of use
Patent: WO 0190156-A 179 29-NOV-2001;
The Burnham Institute (US)
Location/Qualifiers
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BASE COUNT 237 a 228 c 217 g 209 t
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Query Match: 22.66% Indels: 2
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x AX318174 (1-891)

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RESULT 14
AX318176 AX318176 618 bp DNA linear PAT 14-DEC-2001
LOCUS Sequence 181 from Patent WO0190156.
ACCESSION AX318176
VERSION AX318176.1 GI:17900867
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 181 29-NOV-2001;
The Burnham Institute (US)
FEATURES
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BASE COUNT 194 a 113 c 148 g 163 t
ORIGIN

Alignment Scores:
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Score: 206.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.12% Indels: 0
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x AX318176 (1-618)

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QY 780 AlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThr 799
Db 61 GCTATAAACTAGCTGAAGGCTGAAAAACCTGAAGAAGATGTTTATTTATTTCATTGACC 120
QY 800 HisLeuSerAspIleGlyGlyMetAspTyrIleValLysSerLeuSerGluPro 819

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2003, 03:11:25 ; Search time 486 Seconds
(without alignments)
4744.951 Million cell updates/sec

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Searched: 2185239 seqs, 1125999159 residues

Word size: 1
Total number of hits satisfying chosen parameters: 4368727

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1024	100.0	3133	22	AAS03945	Human caspase recr
2	922	90.0	3213	22	AAH78219	Nucleotide sequenc
3	827	80.8	3615	22	AAS03946	Human caspase recr
4	721	70.4	3396	22	ABK22731	Human CDNA encodin
5	721	70.4	3545	22	AAH98254	Murine EST-derived
6	663	64.7	2215	22	AAH78218	Nucleotide sequenc
7	425	41.5	2950	22	AAH99581	Human protein enco
8	271	26.5	1395	24	ABK22732	Human CDNA encodin
9	232	22.7	891	24	ABK22766	Human CDNA encodin
10	206	20.1	618	24	ABK22767	Human CDNA encodin
c 11	180	17.6	2735	22	AAH34171	Human colon cancer
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13	150	14.6	608	22	AAS26160	Human CDNA encodin
14	97	9.5	522	22	AAS26575	Human CDNA encodin
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16	87	8.5	261	24	ABK22765	Human CDNA encodin
17	80	7.8	421	22	ABA45612	Human breast cell
18	80	7.8	421	22	ABA56119	Human foetal liver
19	80	7.8	421	22	ABA25770	Probe #4236 for ge
20	80	7.8	421	22	AAK04305	Human brain expres
21	80	7.8	421	22	AAK29801	Human bone marrow
22	80	7.8	421	22	AAI14389	Probe #4322 for ge
23	80	7.8	421	22	AAI35764	Probe #4450 used t
24	80	7.8	421	22	AAI04213	Probe #4204 used t
25	73	7.1	220	22	ABSO4362	Human genome-deriv
26	73	7.1	220	22	ABA50734	Human breast cell
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28	73	7.1	220	22	ABA35668	Probe #14134 for g
29	73	7.1	220	22	AAK17044	Human brain expres
30	73	7.1	220	22	AAK42828	Human bone marrow
31	73	7.1	220	22	AAI23590	Probe #13523 for g
32	73	7.1	220	22	AAI48904	Probe #17590 used
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35	36	3.5	165	24	ABK22768	Human CDNA encodin
c 36	19	1.9	60	24	ABN40447	Human spliced tran
c 37	9	0.9	29	24	ABK22753	Human CLAN A PCR p
38	9	0.9	33	24	ABL58191	Human retinoblasto
c 39	9	0.9	848	21	AAC54488	Arabidopsis thalia
c 40	9	0.9	850	21	AAC54274	Arabidopsis thalia
c 41	9	0.9	896	22	AAH94390	Human foetal cDNA,
c 42	9	0.9	1382	21	AAZ36643	Human tumour rejec
c 43	9	0.9	1854	21	AAC39548	Arabidopsis thalia
c 44	9	0.9	1956	22	AAI58192	Human polynucleoti
c 45	9	0.9	2167	21	AAZ36644	Human tumour rejec

ALIGNMENTS

RESULT 1
AAS03945
ID AAS03945 standard; cDNA; 3133 BP.
XX
AC AAS03945;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human caspase recruitment domain 12 (CARD-12) cDNA.
XX
KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;
KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;
KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;
KW aplastic anaemia; myocardial infarction; inflammatory disorder;
KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;
KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;
KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ss;

KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;
XX excitotoxic brain damage; liver disease.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 36..3110
FT /*tag= a
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XX W0200130971-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US29643.
XX
XX 27-OCT-1999; 99US-0161822.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Bertin J, Robison KE;
XX
XX WPI: 2001-308628/32.
XX P-PSDB: AAU02880.
XX
XX Isolated caspase recruitment domain-12 polypeptide and nucleic acids
XX encoding them, useful for treating and diagnosing disorders associated
XX with abnormal apoptosis such as cancer, arthritis and Alzheimer's
XX disease -
XX
XX Claim 2; Fig 1; 93pp; English.
XX
XX The sequence represents a cDNA which encodes the human caspase
XX recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a
XX number of proteins that transmit signals that activate apoptosis and
XX inflammatory pathways in response to stress and other stimuli. Therefore,
XX CARD-12 and its corresponding nucleic acid may be used in treatment and
XX diagnosis of patients suffering from disorders associated with an
XX abnormal level (an increase or a decrease) of apoptotic cell death or
XX abnormal activity of stress-related pathways. The disorders include
XX cancer, viral infections (e.g. caused by poxviruses, adenoviruses),
XX autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),
XX neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral
XX sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial
XX infarction, stroke), inflammatory and immune system disorders (e.g.
XX Crohn's disease, insulin-dependent diabetes, contact dermatitis,
XX psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,
XX lepromatous leprosy), ischaemic and hypoxic brain injury, kidney
XX ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial
XX meningitis and liver disease.

XX SQ Sequence 3133 BP; 903 A; 691 C; 729 G; 810 T; 0 other;

Alignment Scores:

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Percent Similarity:	100.00%	Conservative:	0
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US-09-697-089-2 (1-1024) x AAS03945 (1-3133)

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Qy	101	LeuAlaGlnAspLeuLysAspLeuTrpHisThrProSerPheLeuAsnPheTrpProLeu	120
Db	336	TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACATTTTAT	395
Qy	121	GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp	140
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Qy	161	LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln	180
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Qy	221	LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg	240
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Qy	341	ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr	360
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Db 1582 GACATTACATCCCATTTATAGCAGCCCTCTCCGGTACACCTGTGGGTCTATCTGTGAAGCC 1641
QY |||||||
Db 1642 ACCAGGGCTGTTATGAAGCAGCTCGCAGCAGTGTATCAACAGCGCTGCTTCTCGGACTT 1701
QY |||||||
QY 522 SerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThrThr 541
Db 1702 TCCATCGCCCAAGAGGCTCTCTGGACACAGGAATCTTTGCCAAGTGTGAAAACACCACT 1761
QY |||||||
QY 542 GluGlnGluIleLeuLysAlaIleAsnSerPheValGluCysGlyIleHisLeu 561
Db 1762 GAGCAAGAAATTCGAAGGCCATAAACAATCAATTCCTTTGTAGAGTGTGCCATCCATTTA 1821
QY |||||||
QY 562 TyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPheGlnGly 581
Db 1822 TATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAGGT 1881
QY |||||||
QY 582 LysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGluHis 601
Db 1882 AAAAGCTTATATATCAACTCAGGGAACATCCCGGATTACTTATTGACATCTTTGAACAT 1941
QY |||||||
QY 602 LeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAlaMet 621
Db 1942 TTGCCCAATTTGCAAGTCCCTGGACTTCATTAAGTGGACTTTTATGGGGAGGTATG 2001
QY |||||||
QY 622 AlaSerTrpGluLysAlaGluAspThrGlyGlyIleHisMetGluAlaProGlu 641
Db 2002 GCTTCATGGGAAAAGGCTCGAAGACACAGGTGGAAATCCACATGGAAGAGGCCCCAGAA 2061
QY |||||||
QY 642 ThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThr 661
Db 2062 ACCTACATTTCCAGCAGGCTGTATCTTTGTTCTCAACTGGAGCAGCAATTCAGGACT 2121
QY |||||||
QY 662 LeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr-TyrLeuG1 681
Db 2122 CTGGAGTCCACACTCGGGATTTCAAGAGTTGAATAAGCAAGATATCAG-ATATCTGGG 2180
QY |||||||
QY 681 yLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAl 701
Db 2181 GAAATATTTCAGCTCTGCCCACAGGCTCAGGCTGCAATATAAGAGATGCTGGTGTGGC 2240
QY |||||||
QY 701 aGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAl 721
Db 2241 TGGAAAGCTTCAGTTGGTCTCAGCACCTGTGAAGAACATTTATTTCTCATGCTGGAAGC 2300
QY |||||||
QY 721 aSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThrLe 741
Db 2301 CAGTCCCTCCACCATAGAGATGAGAGGCACATCATCATCTGTGAACAAACCTGAAACCTT 2360
QY |||||||
QY 741 uSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAs 761
Db 2361 GAGTATTCATGACCTACAGAATCAACGGCTGCCGGTGGTCTGTGACTGACAGCTGGGTAA 2420
QY |||||||
QY 761 nLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaI1 781
Db 2421 CTTGAAGAACCTTACAAAGCTCATATGGATTAACATAAAGATCAATGAGAAGATGCTAT 2480
QY |||||||
QY 781 eLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLe 801
QY |||||||

Db 2481 AAAACTAGCTGAAGGCCTGAAAAACCTGAAGAAGATGTGTTTATTTCATTTGACCCACTT 2540
QY |||||||
QY 801 uSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAs 821
Db 2541 GTCTGACATTTGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCGAAGTGAACCTTGGA 2600
QY |||||||
QY 821 pLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAl 841
Db 2601 CCTTGAAGAAATTCATTAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2660
QY |||||||
QY 841 aGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuG1 861
Db 2661 TCAGAAATCTTCAAAATTTGGTCAAACTGAGCATTTCTGATTTATCAGAAAAATTACCTGGA 2720
QY |||||||
QY 861 uLysAspGlyAsnGluAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGluGlnLe 881
Db 2721 AAAAGATGGAATGAAGCTCTTCATGAACATGATGCAGAGATGAAGCTGTAGAACAGCT 2780
QY |||||||
QY 881 uThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 901
Db 2781 CACCGCACTGATGCTGCCCTGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTGTTGAA 2840
QY |||||||
QY 901 sHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAs 921
Db 2841 ACATTTGGAGGAGGTCCCAAACTGCTCAAGCTTGGGTTGAAAAACTGGAGACTCACAGA 2900
QY |||||||
QY 921 pThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnG1 941
Db 2901 TACAGAGATTAGAAATTTTAGGTGCATTTTGTGAAAGAAACCTCTGAAAAAATTTCCAGCA 2960
QY |||||||
QY 941 nLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPh 961
Db 2961 GTTGAAATTTGGCGGAAATCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATT 3020
QY |||||||
QY 961 eGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAspPr 981
Db 3021 TCAGAAATCTTAAGCAATTAGTGTGTTTGTGACTTACTAAAGAAATTTCTACCTGATCC 3080
QY |||||||
QY 981 oAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAlaAr 1001
Db 3081 AGCATTTAGTCAGAAACCTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCTAG 3140
QY |||||||
QY 1001 gLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLysLe 1021
Db 3141 GCTTGTGGTGGCAATTTGATGATGATCTCAGTGTATTACAGGTGCTTTTAAACT 3200
QY |||||||
QY 1021 uValThrAla 1024
Db 3201 AGTAACTGCT 3210
RESULT 3
AAS03946
ID AAS03946 standard; DNA; 3615 BP.
AC AAS03946;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human caspase recruitment domain 12 (CARD-12) genomic DNA.
XX
KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;
KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
KW systemic lupus erythematosus; arthritis; neurologic disorder; stroke;
KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;
KW aplastic anaemia; myocardial infarction; inflammatory disorder;
KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;
KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;
KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ds;
KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;
KW excitotoxic brain damage; liver disease.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
 FT 1..3615
 FT /*tag= a
 FT /product= "Human CARD-12"
 XX
 PN WO200130971-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-US29643.
 XX
 PR 27-OCT-1999; 99US-0161822.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Bertin J, Robison KE;
 XX
 DR WPI: 2001-308628/32.
 DR P-PSDB: AAU02881.
 XX
 PT Isolated caspase recruitment domain-12 polypeptide and nucleic acids
 PT encoding them, useful for treating and diagnosing disorders associated
 PT with abnormal apoptosis such as cancer, arthritis and Alzheimer's
 PT disease -
 XX
 PS Disclosure; Fig 2; 93pp; English.
 XX
 CC The sequence represents a genomic DNA which encodes the human caspase
 CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a
 CC number of proteins that transmit signals that activate apoptosis and
 CC inflammatory pathways in response to stress and other stimuli. Therefore,
 CC CARD-12 and its corresponding nucleic acid may be used in treatment and
 CC diagnosis of patients suffering from disorders associated with an
 CC abnormal level (an increase or a decrease) of apoptotic cell death or
 CC abnormal activity of stress-related pathways. The disorders include
 CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses),
 CC autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),
 CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral
 CC sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial
 CC infarction, stroke), inflammatory and immune system disorders (e.g.
 CC Crohn's disease, insulin-dependent diabetes, contact dermatitis,
 CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,
 CC lepromatous leprosy), ischaemic and hypoxic brain injury, kidney
 CC ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial
 CC meningitis and liver disease.
 XX
 SQ Sequence 3615 BP; 1041 A; 811 C; 845 G; 918 T; 0 other;

Alignment Scores:
 Pred. No.: 0 Length: 3615
 Score: 827.00 Matches: 927
 Percent Similarity: 99.78% Conservative: 0
 Best Local Similarity: 99.78% Mismatches: 1
 Query Match: 80.76% Indels: 2
 DB: 22 Gaps: 0

US-09-697-089-2 (1-1024) x AAS03946 (1-3615)

Qy 89 LeuPheHisGlnThrSerGluCysAspLeuAlaGlnAspLeuLysAspLeu 108
 Db 736 CTTTTTCATCAGACATCAGAGGAGACTTGGACGATTGGCTCAGGATTTAAAGGACTTG 795
 Qy 109 TyrHisThrProSerPheLeuAsnPhetYrProLeuGlyGluAspIleAspIlePhe 128
 Db 796 TACCATACCCCATCTTTCGAACTTTATCCCTTGGTGAGATATGACATATTATTTT 855
 Qy 129 AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHisHisArg 148
 Db 856 AACTTGAAGACACCTTCACAGAACCCTGCTGCTGGAGGAGGACCACCATCACCGC 915
 Qy 149 ValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlu 168
 Db 916 GTGAGCAGCTGACCCCTGAATGGCTCCTCGAGGCTCTTCAGAGCCCTTCATCATTTGAA 975

QY 169 GlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySer 188
 DB 976 GGGGAATCTGGCAAGGCAAGTCCACTCTCTGTCAGGGAATTCGCAATGCTGGGGCTCC 1035
 QY 189 GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla 208
 DB 1036 GGAAGTGCAGGCTCTGACCAAGTTCAAAATTCGCTCTCTCCCTCCTCAGCAGGCCC 1095
 QY 209 GlnGlyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThrIleArg 228
 DB 1096 CAGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCGATATACCTGCACAATCAGG 1155
 QY 229 LysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAsp 248
 DB 1156 AAGCAGACATTCATGGCCATGCTGCTGAAGCTGGGCGAGAGGTCTCTTCTCTTGTAT 1215
 QY 249 GlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuLysGluAsn 268
 DB 1216 GGTACAAATGAATTCAGCCCCAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAAC 1275
 QY 269 HisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArg 288
 DB 1276 CACGCTTCAAGAACATGGTCATCGTCACCACTACCACTGAGTGCCTGAGGCACATACGG 1335
 QY 289 GlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu 308
 DB 1336 CAGTTTGGTCCCTGACTGCTGAGTGGGGATATGACAGAAACACGCGCCAGGCTCTC 1395
 QY 309 IleArgGlnValLeuLysGluLeuAlaGluGlyLeuLeuGlnIleGlnLysSer 328
 DB 1396 ATCCGAGAAGTGCCTGATCAAGGAGCTTGCCTCAAGGCTTGTGCTCCAAATTCAGAAATCC 1455
 QY 329 ArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCysAlaIleGln 348
 DB 1456 AGTGTCTGAGGAATCTCATGAAGACCCCTCTCTTTGTGTATCATCTTGTGCATCCAG 1515
 QY 349 MetGlyGluSerGluPheHisSerHisThrThrThrLeuPheHisThrPheTyrAsp 368
 DB 1516 ATGGGTGAAAGTGAGTTCCTCACTCTCACACACAAACACGCTGTTCATCATCTCTATGAT 1575
 QY 369 LeuLeuIleGlnLysAsnLysHisLysHisGlyValAlaAlaSerAspPheIleArg 388
 DB 1576 CTGTGTATCAGAAAAACAAACACAAATAAAGGTGTGCTGCAAGTACTTCATTCCTCGG 1635
 QY 389 SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAspPhe 408
 DB 1636 AGCTGGACCACCTGTGGAGACCTAGCTCTGGAGGCTGTGTCTCCACACAGTTTGATTTC 1695
 QY 409 GluLeuGlnAspValSerSerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCys 428
 DB 1696 GAACCTGCAGGATGTGTCCAGCGTGAATGAGGATGCTGCTGCACAACTGGGCTCTCTGT 1755
 QY 429 LysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGlu 448
 DB 1756 AAATATACAGCTCAAGAGTTTCAAGCCAAAGTATAAAATCTTTTCAAAAGTCAATTCAGAG 1815
 QY 449 TyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGluProGluGluValThr 468
 DB 1816 TACACAGCAGCAGACACTCAGCAGTTTATGTACGCTCTCATGAGCAGGAGGAGTGACC 1875
 QY 469 LysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerThrTyrSer 488
 DB 1876 AAGGGGAATGTTTACTTTCAGAAAAATGTTTCCATTTTCGGACATTTACATCCACTATAGC 1935
 QY 489 SerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLysHis 508
 DB 1936 AGCCTGCTCCGGTACACTGTGGGTCTATCTGTGGAAGCCACCAGGCGTGTATGAAGCAC 1995
 QY 509 LeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAlaLysArgProLeu 528
 DB 1996 CTCGACAGCTGTATCAACACGCGCTGCTCTTCGGACTTTTCCATTCGCAAGAGGCGCTCTC 2055

QY 529 TrpArgGlnGluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAla 548
|||||
Db 2056 TGGAGACAGGAATCTTTGGCAAGTGTGAAAACACACCACCTGAGCAAGAAATCTGAAAGCC 2115
QY 549 IleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLys 568
|||||
Db 2116 ATAACATCAATTCCTTTAGAGTGTGCATCCATTTATATCAAGAGAGTACATCCAAA 2175
QY 569 SerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlySerLeuTyrIleAsnSer 588
|||||
Db 2176 TCAGCCTCGAGCCAGAAATTTGAAGCTTTCTTCAAGGTAAAGCTTATATCAACTCA 2235
QY 589 GlyAsnIleProAspTyrLeuPheAspPhePheGluHisLeuProAsnCysAlaSerAla 608
|||||
Db 2236 GGGAACTCCCGATTACTTTATTGACTTCTTTGAACATTTGCCCAATTTGCAAGTGC 2295
QY 609 LeuAspPheIleLysLeuAspPheTyrGlyAlaMetAlaSerTrpGluLysAlaAla 628
|||||
Db 2296 CTGGACTTCATTAACCTGGACTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTGCA 2355
QY 629 GluAspThrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSerArgAla 648
|||||
Db 2356 GAAGACACAGGTGAATCCACATGGAAGAGGCCCAAGAACCTTACATCCCAGCAGGGCT 2415
QY 649 ValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuArgAsp 668
|||||
Db 2416 GTATCTTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGCTCACACTCCGGGAT 2475
QY 669 PheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePheSerSerAlaTh 688
|||||
Db 2476 TTTCAGCAAGTTGAATAAGCAAGATATCAG-ATATCTGGGAAATAATTTCAGCTCTGCCAC 2534
QY 688 rSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuValLe 708
|||||
Db 2535 AGCCTCAGCTGCGAAATAAAGAGATGCTGTGTGGGTGAAGCTCAGTTTGTCTCT 2594
QY 708 uSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAs 728
|||||
Db 2595 CAGCACCTGTAAGAACATTTATCTCTCATGTGTGGAAGCCAGCTCCCTCACCATAGAAGA 2654
QY 728 pGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAs 748
|||||
Db 2655 TCAGAGGCCACATCACATCTGTAAACAACTGAAACCTTGAGTATTTCATGACCTACAGAA 2714
QY 748 nGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLe 768
|||||
Db 2715 TCACCGCTGCGGGTGGTCTGACTGACAGCTTGGTAACTTGAAGAACCTTACAAAGCT 2774
QY 768 uIleMetAspAsnIleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLy 788
|||||
Db 2775 CATAATGGATAACATAAAGATGAATGAAGAAGATGCTATAAAACTAGCTGAAGGCTGAA 2834
QY 788 sasnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGlyWe 808
|||||
Db 2835 AAACCTGAAGAAGATGTGTTTATTTTCATTTGACCCACTTGTCTGACATTTGGAGAGGAAT 2894
QY 808 tAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuVa 828
|||||
Db 2895 GGATACATAGTCAAGTCTCTGCAAGTGAACCCCTGTGACCTTGAAGAAATTCAAATAGT 2954
QY 828 lSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuVa 848
|||||
Db 2955 CTCCTGCTGCTGTCTGCAAAATGCAGTGAATAATCTAGCTCAGAAATCTTCACAAATTTGCT 3014
QY 848 lLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLe 868
|||||
Db 3015 CAAACTGACCATTTCTGATTTATCAAAAAATTTACCTGGAAAAAGATGGAATGAAGCTCT 3074
QY 868 uHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProThr 888
|||||
Db 3075 TCATGAACATGATCGACAGATGAAGCTGTAGAACAGCTCACCGCACTGATGCTGCCGCG 3134
QY 888 pGlyCysAspValGlnGlySerLeuSerLeuLysHisLeuGluValProGln 908

Db 3135 GGGCTGTGACGTGCAAGGCAGCCTGAGAGCCTGTTGAAACATTTTGGAGAGGTCCCCACA 3194
QY 908 nLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGl 928
|||||
Db 3195 ACTCGTCAAGCTTGGGTTGAAAAACTGGAGACTCACAGATACAGAGATTAGAAATTTTAGG 3254
QY 928 yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnAr 948
|||||
Db 3255 TGCATTTTTTTGGAAGAACCCCTCTGAAAAACTTCCAGCAGTTGAATTTGGCGGGAATCG 3314
QY 948 gValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuVa 968
|||||
Db 3315 TGTGAGCAGTGTGATGGTGGCTTGCCTTCATGGGTGATTGTGAGAAATCTTAAAGCAATAGT 3374
QY 968 lPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSe 988
|||||
Db 3375 GTTTTTTGACTTTAGTACTAAAGAATTTCTACCTGATCCAGCATTTAGTCAGAAAACTTAG 3434
QY 988 rGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAs 1008
|||||
Db 3435 CCAAGTGTTATCCAGTTAACTTTCTGCAAGAAAGCTAGGCTTGTGGTGGAATTTGA 3494
QY 1008 pAspAspAspLeuSerValIleThr 1016
|||||
Db 3495 TCATGATGATCTCAGTGTATTATACA 3519
RESULT 4
ABK22731
ID ABK22731 standard; cDNA; 3396 BP.
XX
AC ABK22731;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human cDNA encoding CLAN A.
XX
KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
XX
OS Homo sapiens.
XX
PN WO200190156-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US17158.
XX
PR 24-MAY-2000; 2000US-0579240.
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275980P.
PR 23-MAY-2001; 2001US-0864921.
XX
PA (BURN-) BURNHAM INST.
XX
PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX
DR WPI; 2002-083086/11.
XX
PT P-PSDB; AAU80861.
PT New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke

XX Claim 1; Page 166-171; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)

CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain

CC from it, and the polynucleotides encoding them. Also included are a

CC recombinant vector comprising the polynucleotide, recombinant cells

CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian

CC and insect cells) and an anti-CARD antibody. The CARD-containing

CC polypeptide and CARD-encoding nucleic acid are useful for treating a

CC pathology characterised by abnormal cell proliferation (e.g. cancer),

CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In

CC particular, the polypeptide and nucleic acid are useful for treating

CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth

CC muscle cell proliferation in arteries following balloon angioplasty

CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,

CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,

CC graft-versus-host disease, stroke, myocardial infarction, heart failure,

CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's

CC disease) or immunodeficiency associated disease (e.g. human

CC immunodeficiency virus (HIV) infection). The nucleic acids are useful

CC in a variety of diagnostic applications. The present sequence is a

CC cDNA encoding a CARD domain containing protein.

SQ Sequence 3396 BP; 992 A; 737 C; 793 G; 874 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	3396
Score:	721.00	Matches:	1021
Percent Similarity:	99.42%	Conservative:	0
Best Local Similarity:	99.42%	Mismatches:	3
Query Match:	70.41%	Indels:	6
DB:	24	Gaps:	0

US-09-697-089-2 (1-1024) x ABK22731 (1-3396)

QY 1 MetAsnPhelLeuLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20

DB 277 ATGAATTTTCATAAAGGACAATAGCGAGCCCTTATTCAAAGATGGGAATGACTGTATA 336

QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIle 40

DB 337 AAGCAAAATCACAGATGACCTATTGTATGGAATGTCATCGAATCGGAGAAAGTAACATC 396

QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60

DB 397 ATTGCTCGGAGAGGTGGACAGGATGCTGCTAGAGGATCATTCACATGATTTTGAA 456

QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80

DB 457 AAGGTTTCAGAGTCTGTAACTCTTTCTTAAATCCCTTAAGGAGTGAACATCTCTTA 516

QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAsp 100

DB 517 TTTCAGGACTTGAATGGACAAGTCTTTTCATCAGACATCAGAGGAGACTTGGACCAT 576

QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120

DB 577 TTGGCTCAGGATTTAAGACTTGTACCATCCCATCTTTCTTGAACCTTTATCCCTCT 636

QY 121 GlyGluAspIleAspIlePheAsnLeuLysSerThrPheThrGluProVal-LeuTr 140

DB 637 GGTGAAGATATTGACATATTATTTTAACTTGAAGACACCTTCACAGAACCATTAT -CCTGTG 695

QY 140 PargLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAl 160

DB 696 GAGGAAGACCAACACCATCACCGCGTGAGCAGCTGACCTGATGCGCTCTCGACGC 755

QY 160 aLeuGlnSerProCysIleIleGluGlySerGlyLysGlyLysSerThrLeuLeuGln 180

DB 756 TCTTCAGAGCCCTGCATCATTCATTGAAGGGGAATCTGGCAAGGCAAGTCCATCTGCTGCA 815

QY 180 nArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVa 200

DB 816 GCGCATTCGCCATGCTCTGGGGCTCGGAAAGTGCAGAGCTCTGACCAAGTTCAAAATTCGT 875

QY 200 lPhePheLeuArgLeuSerArgAlaGlnGlyClyLeuPheGluThrLeuCysAspGlnIe 220

DB 876 CTTCTTCTCCGTCTCAGCAGGGCCAGGGTGGAGCTTTTGAACCCCTCTGTGATCAACT 935

QY 220 uLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuAr 240

DB 936 CTTGGATATACCTGCACAATCAGGAAGCAGACATTCATGCCATGCTGCTGAAGCTGG 995

QY 240 gGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProG 260

DB 996 GCAGAGGGTCTCTTTCTCTTCTGATGGCTACAATGAATTAAGCCGCCAGACTGCCAGA 1055

QY 260 uIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrTh 280

DB 1056 AATCGAAGCCCTGTATTAAGGAAACCCCGCTTCAAGAACATGGTCATCGTCACCACTAC 1115

QY 280 rThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMe 300

DB 1116 CACTGAGTGCCTGAGGCACATACGCGACTTGGTCCCTGACTGCTGAGTGGGGGATAT 1175

QY 300 tThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGlu 320

DB 1176 GACAGAAGACAGCGCCAGGCTCTCATCCGAGAAGTCTGATCAAGAGACTTGCTGAAGG 1235

QY 320 yLeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPh 340

DB 1236 CTTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGTAATCTCATGAAGACCCCTCTCT 1295

QY 340 eValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnTh 360

DB 1296 TGTGGTCACTACTGTGCAATCCAGATGGTGAAGTGGATGCCACTCTCACACACAAC 1355

QY 360 rThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysLysG 380

DB 1356 AACGCTGTTCATACCTTCTATGATCTCTGTATACAGAAAAACAACAACAATAAAGG 1415

QY 380 yValAlaAlaSerAspPheIleArgSerLeuAspHisCys-GlyAspLeuAlaLeuGlu 400

DB 1416 TGTGGCTCAAGTACTTTCATTCGGAGCTGGACCAACCG-TGGAGACCTAGCTCTGGAGG 1474

QY 400 lyValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspV 420

DB 1475 GTGTGTTCTCCACAAGTTTGTATTCGAACTGCAGAGTGTGTCCAGCGTGAATGAGGATG 1534

QY 420 alLeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrL 440

DB 1535 TCCTGCTGACAACCTGGGCTCTCTCTGTAATATACAGCTCAAAAGGTTCAAGCCAAAGTATA 1594

QY 440 yspPhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuT 460

DB 1595 AATTCTTTTCAAGTCAATTCAGGAGTACACAGCAGGAGAGACTTCAGCAGCTTTATTGA 1654

QY 460 hrSerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerI 480

DB 1655 CGTCTCATGACCCAGAGGAGGTGACCAAGGGGAATGGTTACTTGCAGAAATATGGTTTCCA 1714

QY 480 leSerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValG 500

DB 1715 TTTCCGACATTTACATCCACTTATAGCAGCTGCTCCGCTACACCTGTGGTCTCATCTGTGG 1774

QY 500 luAlaThrArgAlaValaMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuG 520

DB 1775 AAGCCACAGGGCTGTATGAAGCACCCTCGCAGCAGTGTATCAACACGCGCTCGCTTCG 1834

QY 520 lyLeuSerIleAlaLysArgProLeuTrpArgGlnGlnSerLeuGlnSerValLysAsnT 540

DB 1835 GACTTTCCATCGCCCAAGAGGCTCTCTCGAGACAGGAATCTTTGCAAAAGTGTGAAAAACA 1894

QY 540 hrThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleH 560

Db 1895 CCAGTGGAGCAAGAAATCTCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCC 1954
Qy 560 isLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheG 580
Db 1955 ATTTATATCAAGAGTACATCCAATCAGCCCTGAGCCAGAAATTTGAAGCTTTCTTTC 2014
Qy 580 InGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheG 600
Db 2015 AAGGTAAAGCTTATATCAACTCAGGGAACATCCCGATTAATTTGACTTCTTTG 2074
Qy 600 luHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyA 620
Db 2075 AACATTTGCCAAATTTGTCAAGTGCCTCGGACTTCATTAACATGGACTTTTATGGGGGAG 2134
Qy 620 laMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaP 640
Db 2135 CTATGGCTTCATGGAAAGGCTGCAGAGACACAGGTGGAAATCCACATGGAAGAGGCC 2194
Qy 640 roGluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheA 660
Db 2195 CAGAAACCTACATTCAGCAGCGGCTGTATCTTTCTTCAACTGGAAGCAGGAATTC 2254
Qy 660 rgThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr-Tyr 679
Db 2255 GGACTCTGGAGGTCACATCCCGGATTTTCAGCAAGTTCAATAAGCAAGATATCAG-ATAT 2313
Qy 680 LeuGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGly 699
Db 2314 CTGGGAAATATTCAGCTCTGCCACAAGCTCAGGCTGCAATTAAGAGATGCTCGT 2373
Qy 700 ValAlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetVal 719
Db 2374 GTGGCTGAAGCCTCAGTTTGTCTCTCAGCACCTGTAAGAACATTTATCTCTCATGTG 2433
Qy 720 GluAlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLys 739
Db 2434 GAAGCCAGTCCCTCCACCATAGAAGATGAGAGGCACATCACATCTGTAAACAACCTGAAA 2493
Qy 740 ThrLeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeu 759
Db 2494 ACCITGATTAATCATGACCTACAGAATCAACGGCTGCCGGTGGTCTGACTGACAGCTTG 2553
Qy 760 GlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAsp 779
Db 2554 GGTAACCTTGAAGAACCTTACAAAGCTCATATGGATACATAAAGATCAATGAAGAAGAT 2613
Qy 780 AlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThr 799
Db 2614 GCTATAAACCTAGCTGAAGGCTGAAAAACCTGAAAGAGATGTGTTTATTTTCATTTGACC 2673
Qy 800 HisLeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluPro 819
Db 2674 CACTGTCTGACATGGAGAGGAATGATATACATAGTCAAGTCTCTCTCAAGTGAACCC 2733
Qy 820 CysAspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIle 839
Db 2734 TGTGACCTTGAAGAAATTCATTTAGTCTCTCTCTCTGCTGCAAAATGCAGTGAATAATC 2793
Qy 840 LeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyr 859
Db 2794 CTAGCTCAGAATCTTCACAAATTTGGTCAAACTGAGCATCTTGAATTTATCAGAAATATAC 2853
Qy 860 LeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlu 879
Db 2854 CTGGAAAAAGATGGAATGAAGCTCTTCATGAATCATGCACAGATGAAGCTGTAGAA 2913
Qy 880 GlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeu 899
Db 2914 CAGCTCACCGCAGCTATGCTGCCCTGGGGCTGTGAGCTGCAAGGCAGCCTGAGCAGCCTG 2973
Qy 900 LeuLysHisLeuGluGluValIleProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeu 919
Db 2974 TTGAACATTTGGAGGAGGTCCCACTCGTCAAGCTTGGGTTGAAATACTGGAGACTC 3033

Qy 920 ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe 939
Db 3034 ACAGATACAGAGATTAGAAATTTTAGTGCAATTTTGGAAAGAACCTCTGAAAACATTC 3093
Qy 940 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGly 959
Db 3094 CAGCAGTTGAATTTGGCGGAAATCGTGTGACAGCTGATGGATGGCTTCATGGGT 3153
Qy 960 ValPheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuPro 979
Db 3154 CTATTTGAGAATCTTAAGCAATTTAGTGTTTTGTACTTTAGTACTAAAAGAATTTTACCT 3213
Qy 980 AspProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGlu 999
Db 3214 GATCCAGCATTAGTCAGAAACTTAGCCAAAGTGTATCCAGTTAACTTTCTGCAAGAA 3273
Qy 1000 AlaArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPhe 1019
Db 3274 GCTAGGCTTGTGGGTGCAATTTTGATGATGATGATCTCAGTGTATTACAGGTGCTTTT 3333
Qy 1020 LysLeuValThrAla 1024
Db 3334 AAACCTAGTAACGTCT 3348
RESULT 5
AAH98254
ID AAH98254 standard; cDNA; 3545 BP.
XX
AC AAH98254;
XX
DT 12-OCT-2001 (first entry)
XX
DE Murine EST-derived coding sequence SEQ ID NO: 111.
XX
Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX Mus musculus.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
DR P-PSDB; AAM23595.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
FS Claim 1; Page 250-251; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA

CC of the invention.

XX Sequence 3545 BP; 1038 A; 755 C; 816 G; 936 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	3545
Score:	721.00	Matches:	1021
Percent Similarity:	99.42%	Conservative:	0
Best Local Similarity:	99.42%	Mismatches:	3
Query Match:	70.41%	Indels:	6
DB:	22	Gaps:	0

US-09-697-089-2 (1-1024) x AAH98254 (1-3545)

QY	1	MetAsnPheIleLysAspAsnSerAtqAlaLeuIleGlnArgMetGlyMetThrValIle	20
DB	232	ATGAATTTCAATAAGGACAATAGCCGAGCCCTTATTCAAAGAATGGAAATGACTGTATA	291
QY	21	LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle	40
DB	292	AAGCAATCACAGATGACCTATTGTATGAATGTTCTGAATCGGAAGAAGTAACATC	351
QY	41	IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLys	60
DB	352	ATTTGCTCGCAGAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA	411
QY	61	LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu	80
DB	412	AAGGTTTCAGAGTCCGTGAACCTTTCTTTAAATFCCCTTAAGGAGTGGAACTATCCFCTA	471
QY	81	PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp	100
DB	472	TTTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGAGAT	531
QY	101	LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu	120
DB	532	TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTT	591
QY	121	GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp	140
DB	592	GGTGAAGATATTGCATATTATTTTAACTTGAAGAAGCCCTTCAGAACCTGTCTGTGG	651
QY	141	ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla	160
DB	652	AGGAAGACCAACACCATCATCCCGTGGAGCAGTGAACCTGAATGGCCCTCTCCAGGCT	711
QY	161	LeuGlnSerProCysIleIleGluGlyGluSerGlyLysSerThrLeuLeuGln	180
DB	712	CTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG	771
QY	181	ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheVal	200
DB	772	CGCATTCGCATGCTGTGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAATTCGTC	831
QY	201	PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu	220
DB	832	TTCTTCTCCGCTCTCAGCAGGGCCAGGTGGACTTTTAAAAACCCCTCTGTGATCAACT	891
QY	221	LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg	240
DB	892	CTGGATATACCTGCACAATCAGAGACACATTCATGGCCATGCTGTGAAGCTGCGG	951
QY	241	GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu	260
DB	952	CAGAGGGTCTTTTCTTCTTGATGGCTACAATGAATTCAGCCCCCAAGACTGCCAGAA	1011
QY	261	IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr	280
DB	1012	ATCGAGCCCTGTAAAGGAAAAACCCGCTTCAAGAACATGGTTCATPGTCACCACTACC	1071
QY	281	ThrGluCysLeuArgHisIleArgGlnPheGlyValaLeuThrAlaGluValGlyAspMet	300
DB	1072	ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATG	1131

QY	301	ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly	320
DB	1132	ACAGAGACAGCGCCAGGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGTGAAGGC	1191
QY	321	LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe	340
DB	1192	TTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTT	1251
QY	341	ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr	360
DB	1252	GTGGTCATCACTTGTGCAATCCAGATGGGTCAAGTCCAGTCCACTCTCACACAAACA	1311
QY	361	ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly	380
DB	1312	ACGCTGTTCATACCTTCTATGATCTGTGTATACAGAAAACAACAACAATAAAGGT	1371
QY	381	ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAsp-LeuAlaLeuGlu	400
DB	1372	GTGGCTGCAAGTGACTTCATTCGGAGCTGGACCACCTGTGGATA-CCTAGCTCTGGAGG	1430
QY	400	YValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVa	420
DB	1431	TGTGTTCTCCACAAAGTTTGAATTCGAACCTGCAGGATGTCTCCAGCGTGAATGAGGATG	1490
QY	420	LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLy	440
DB	1491	CTGTCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGATAAA	1550
QY	440	sPhePheHisLysSerPheGlnGluTyrThrAlaGlyArgGluSerSerLeuLeuTh	460
DB	1551	ATTCTTTCACAAGTCATTCAGGAGTACACAGCAGGAGCAAGACTCAGCAGTTTATTGAC	1610
QY	460	rSerHisGluProGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIl	480
DB	1611	GTCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGTTACTTGCAGAAAAATGGTTCCAT	1670
QY	480	eSerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGl	500
DB	1671	TTCGGACATTACATCCACTTATAGCAGCTGCTCCGTACACCTGTGGGTCTCTGTGGA	1730
QY	500	uAlaThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuGl	520
DB	1731	AGGCACAGGCGCTGTATGAAGCACCTCGCAGCAGTGTATCAACACAGCGCTCCCTTCGG	1790
QY	520	yLeuSerIleAlaLysArgProLeuTrpArgGlnGlnSerLeuGlnSerValLysAsnTh	540
DB	1791	ACTTTCATCGCAAGAGGCTCTCTGGAGACAGGAATCTTGCAAAAGTGTGAAAAACAC	1850
QY	540	rThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleH1	560
DB	1851	CACGTGAGCAAGAAATTCGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGSCATCCA	1910
QY	560	sLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPheGl	580
DB	1911	TTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCAAGAAATTTGAAAGCTTTCTTCA	1970
QY	580	nGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGl	600
DB	1971	AGGTAAAGCTTATATATCAACTCAGGGAACATCCCGCATTACTTATTTGACTTCTTTGA	2030
QY	600	uHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAsp-PheTyrGlyGlyA	620
DB	2031	ACATTTGCCCAATTTGTCAAGTGTCTGAGACTTCATTAACCTGGG-CTTTTATGGGGGAG	2089
QY	620	laMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlap	640
DB	2090	CTATGGCTTTCATGGGAAAAAGCTGCAGAGACACAGGTGGAAATCCACATGGAAGAGCCC	2149
QY	640	roGluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheA	660
DB	2150	CAGAAACCTACATTCACGAGGCGTGTCTTTGTTCTTCAACTGGGAAGCAGGAATTCA	2209

XX Sequence 2215 BP; 621 A; 522 C; 519 G; 553 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	2215
Score:	663.00	Matches:	737
Percent Similarity:	99.73%	Conservative:	0
Best Local Similarity:	99.73%	Mismatches:	1
Query Match:	64.75%	Indels:	2
DB:	22	Gaps:	0

US-09-697-089-2 (1-1024) x AAH78218 (1-2215)

Qy 15 MetGlyMetThrValIleLeuLysGlnIleThrAspLeuPheValTrpAsnValLeuAsn 34
Db 1 ATGGGAAGTACCTGTTATTAAGCAATACAGATGACCTATTGTATGAATGTTCTGAAT 60

Qy 35 ArgGluGluValAsnIleLeuCysGluLysValGluGlnAspAlaAlaArgGlyIle 54
Db 61 CGCGAAGAAGTAAACATCATTTGCTGCGAGAAGGTGGAGCAGGATGCTGTAGAGGATC 120

Qy 55 IleHisMetIleLeuLysLysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLys 74
Db 121 APTCAGATGATTTTGAAAGAGGTTTCAGAGTCCCTGTAACCTCTTTCTTAAATCCCTTAAG 180

Qy 75 GluTrpAsnTyrProLeuPheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSer 94
Db 181 GAGTGGAACTATCTCTATTTCAGGACTTGAATGGCAAGATCTTTTCATCAGACATCA 240

Qy 95 GluGlyAspLeuAspLeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPhe 114
Db 241 GAAGGAGACTTTGGAGATTTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTT 300

Qy 115 LeuAsnPheTyrProLeuGlyGluAspIleAspIlePheAsnLeuLysSerThrPhe 134
Db 301 CTGAACCTTTATCCCTTGGTGAAGATATTGACATATTATTTAACTTGAAGACACCTTC 360

Qy 135 ThrGluProValLeuTrpArgLysAspGlnHisHisArgValGluGlnLeuThrLeu 154
Db 361 ACAGAACTCTCTGTGGGAAGGACCAACACCATCACCGTGGAGCAGCTGACCCCTG 420

Qy 155 AsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGlyGluSerGlyLysGly 174
Db 421 AATGCCCTCTCGCAGGCTTTTCAGAGCCCTGCAATCATTAAGGGGAATCTGGCAAGGC 480

Qy 175 LysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeu 194
Db 481 AAGTCCACTCTGCTGCAGGAATGCCATGCTCTGGGGCTCCGGAAAGTGAAGGCTCTG 540

Qy 195 ThrLysPheLysPheValPhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGlu 214
Db 541 ACCAAGTTCAATTCGTCTCTTCCTCGCTCTCAGCAGGGCCAGGGTGGACTTTTGA 600

Qy 215 ThrLeuCysAspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAla 234
Db 601 ACCCTCTGTATCAACTCCTGGATATACCTGGCAATCAGAAAGCAGACATTCATGGCC 660

Qy 235 MetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLys 254
Db 661 ATGCTGTGTGAGCTCGGCAGAGGGTCTTTCTCTCTGTGATGCTACAAATGAATCAAG 720

Qy 255 ProGlnAsnCysProGluIleGluAlaLeuLysGluAsnHisArgPheLysAsnMet 274
Db 721 CCCCAGAACTGCCAGAAATCGAAGCCCTGTATAAGGAAAAACACCCCGCTTCAAGAACATG 780

Qy 275 ValIleValThrThrThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThr 294
Db 781 GTCAATGTCACACTTACCACTGAGTGCCTGAGGCACATACGCGCAGTTTGGTGCCTGACT 840

Qy 295 AlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIle 314
Db 841 GCTGAGGTGGGGATATCAGAGAGACACAGCGCCCGAGGCTCTCATCCGAGAAAGTCTGATC 900

Qy 315 LysGluLeuAlaIaGluGlyLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeu 334
Db 901 AAGGAGCTTGTGAGGCTTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTC 960

Qy 335 MetLysThrProLeuPheValIleThrCysAlaIleGlnMetGlyGluSerGluPhe 354
Db 961 ATGAAGACCCCTCTCTTGTGTGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTC 1020

Qy 355 HisSerHisThrGlnThrThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsn 374
Db 1021 CACTCTCACACACAAACACGCTGTTCATACCTTCTATGATCTGTTATCAGAAAAAC 1080

Qy 375 LysHisLysHisLysGlyValAlaAlaSerAspPheIleArgSerLeuAspHisCysGly 394
Db 1081 AAACACAAACATAAAGGTGTGGCTGCAAGTGACTTCAATTCGGAGCCTGGACCACCTGTGA 1140

Qy 395 AspLeuAlaLeuGluGlyValPheSerHisLysPheAspPheGluLeuGlnAspValSer 414
Db 1141 GACCTAGCTCTGGAGGGTGTCTCTCCACAAAGTTGATTTCCGAACCTCAGGATGTGTC 1200

Qy 415 SerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArg 434
Db 1201 AGCGTGAATGAGGATGCTCTGCAAACTGGGCTCTCTGTAAATATACAGCTCAAGG 1260

Qy 435 PheLysProLysTyrLysPhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArg 454
Db 1261 TTCAGCCAAAGTATAAATCTTTCACAAAGTCATTCAGGAGTACACAGCAGGAGGAAGA 1320

Qy 455 LeuSerSerLeuLeuThrSerHisGluProGluGluValThrLysGlyAsnGlyTyrLeu 474
Db 1321 CTCAGCAGTTTATTGACGTCTCATGAGCAGAGGAGGTGACCAAGGGGAATGGTTACTTG 1380

Qy 475 GlnLysMetValSerIleSerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThr 494
Db 1381 CAGAAAATGGTTTCCATTTTCGACATATACATCCATTAACAGCCTCTCGGTACACC 1440

Qy 495 CysGlySerSerValGluAlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGln 514
Db 1441 TGTGGTCTCATCTGTGGAAGCCACCAGGCTGTATTATGAAGACCTCGCAGCAGTGTATCAA 1500

Qy 515 HisGlyCysLeuLeuGlyLeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeu 534
Db 1501 CACGGCTCCCTCTCGGACTTTCCATCGCAAGAGGCTCTCTGGAGACAGAAATCTTTG 1560

Qy 535 GlnSerValLysAsnThrThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPhe 554
Db 1561 CAAGTGTGAAAAACACACCTGAGCAGAAATCTCGAAGCCATAAACATCAATTCCTTT 1620

Qy 555 ValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGlu 574
Db 1621 GTAGAGTGTGCATCCATTTATATCAAGAGAGTACATCCAAATCAGCCCTCAGCCAGAA 1680

Qy 575 PheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyr 594
Db 1681 TTTGAAGCTTCTTCAAGGTAAAGCTTATATCAACTCAGGGAACATCCCCGATTAC 1740

Qy 595 LeuPheAspPhePheGluHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeu 614
Db 1741 TTAATTCATCTCTTGAACATTTGCCCAATTTGCAAGTGCCTGGACTTCATTAACATG 1800

Qy 615 AspPheTyrGlyGlyAlaMetAlaSerTrpGluLysAlaIaGluAspThrGlyGlyIle 634
Db 1801 GACTTTTATGGGGAGCTATGGCTTCATGGGAAAAAGGTGCAAGACACAGGTGGAATC 1860

Qy 635 HisMetGluAlaProGluThrTyrIleProSerArgAlaValSerLeuPhePheAsn 654
Db 1861 CACATGGAAGAGGCCCCAGAAACCTACATCCCAGAGGCTGTATCTTTTCTTCAAC 1920

Qy 655 TrpLysGlnGluPheArgThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLys 674
Db 1921 TGGAGCAGGAATTCAGGACTCTGGAGGTACACTCCGGGATTCAGCAAGTTGAATAAG 1980

Qy 675 GlnAspIleThr-TyrLeuGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIle 694

Db 1981 CAAGATATCAG-ATATCTGGGAAATATTTCAGCTCGCCACCAAGCTCAGGCTGCAAT 2039
QY 694 eLysArgCysAlaGlyValAlaGlySerLeuSerLeuValLeuSerThrCysLysAsn11 714
Db 2040 AAAGACATGTGTGGTGGTGGGAGAGCTCAGTTGGTCCCTGAGCACCTGTGAAGAACAT 2099
QY 714 eTyrSerLeuMetValGluAlaSerProLeuThrIleGluAspGluArgHisIleThrSe 734
Db 2100 TTATTTCTCTGTGTGGAGCCAGTCCCTCACCATAGAAGATGAGAGGCACATCACATC 2159
QY 734 rValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAnGlnArgLeuPro 752
Db 2160 TGTAAACAAACCTGAAACCTTGAGTATTTCATGACCTACAGAAATCAACGGCTGCG 2214

RESULT 7

AAH99581
ID AAH99581 standard; cDNA; 2950 BP.

AC AAH99581;

XX 16-OCT-2001 (first entry)

DE Human protein encoding cDNA sequence SEQ ID NO:416.

XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; virucide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianemic; anaemia;
KW antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.

XX Homo sapiens.

OS WO200153455-A2.

XX 26-JUL-2001.

XX 22-DEC-2000; 2000WO-US35017.

XX 23-DEC-1999; 99US-0471275.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI: 2001-457603/49.

DR P-PSDB; AAM25640.

XX Isolated human polynucleotides encoding polypeptides, useful for the
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -

PS Claim 1; Page 511-512; 1217pp; English.

XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianemic; antiaggregant; haemostatic; vulnerary;
CC antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;

CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.

XX
SQ Sequence 2950 BP; 915 A; 592 C; 628 G; 815 T; 0 other;

Alignment Scores: 0 Length: 2950
Pred. No.: 0 Matches: 625
Score: 425.00
Percent Similarity: 99.36% Conservative: 0
Best Local Similarity: 99.36% Mismatches: 2
Query Match: 41.50% Indels: 4
DB: 22 Gaps: 0

US-09-697-089-2 (1-1024) x AAH99581 (1-2950)

QY 398 LeuGluGlyValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsn 417
Db 47 CTGGAGGGGTGTCTCCCAAGTTGATTTCGAACTCAGATGTGTCAGCGTGAAT 106
QY 418 GluAspValLeuLeuThrThrGlyLeuLeuLysLysTyrThrAlaGlnArgPheLysPro 437
Db 107 GAGGATGCTCTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCA 166
QY 438 LysTyrLysPhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSer 457
Db 167 AAGTATAAATCTTTTTCACAAAGTCATTCAGGAGTACACAGCAGGAGAAAGACTCAGCAGT 226
QY 458 LeuLeuThrSerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMet 477
Db 227 TTATTGACGCTCATGAGCCAGAGGAGGTGACCAAGGGAAATGGTTACTTCGAGAAAATG 286
QY 478 ValSerIleSerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySer 497
Db 287 GTTTCATTCGACATTCATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTCA 346
QY 498 SerValGluAlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCys 517
Db 347 TCTGTGGAAGCCACCAGGGCTGTATTGAAGCACCTCGCAGCAGTGTATCAACACGGCTGC 406
QY 518 LeuLeuGlyLeuSerIleAlaLysArgProLeuTyrArgGlnGlnSerLeuGlnSerVal 537
Db 407 CTCTCGGACTTTCATCGCCAGAGGCGCTCTCTGGAGACAGAAATCTTTGGAAGTGTG 466
QY 538 LysAsnThrThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCys 557
Db 467 AAAACACCACTGAGCAAGAAATTCGAAAGCCATAAACAATCAATTCCTTGTAGAGTGT 526
QY 558 GlyIleHisLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAla 577
Db 527 GGCATCCATTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCT 586
QY 578 PhePheGlnClyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAsp 597
Db 587 TTCCTTCAAGGTAAGAAAGCTTATATATCAACTCAGGGGAACATCCCCCATTTATTGTAC 646
QY 598 PhePheGluHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAsp-PheTy 617
Db 647 TTCCTTGAACATTTGCCCAATTTGTGCAAGTGTCTGGACTTCATTAACACTGGG-CTTTTA 705
QY 617 rGlyGlyAlaMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetG1 637
Db 706 TGGGGGAGCTATGGCTTCATGGGAAAAGGCTGCAGAAAGACACAGGTGGAATCCACATGGA 765

CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.

XX SQ Sequence 1395 BP; 436 A; 248 C; 327 G; 384 T; 0 other;

Alignment Scores:

Pred. No.: 1.88e-254 Length: 1395
Score: 271.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.46% Indels: 0
DB: 24 Gaps: 0

US-09-697-089-2 (1-1024) x ABK22732 (1-1395)

Qy 754 GlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIle 773
Db 541 GGTCTGACTGACAGCTTGGTAACTTGAAGAACCTTACAAAGCTCATAATGGATAACATA 600
Qy 774 LysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysMet 793
Db 601 AAGATGAATGAAGAGATGCTATAAACTAGCTGAAGGCCCTGAAAGAACTGAAGAAGATG 660
Qy 794 CysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMetAspTyrIleValLys 813
Db 661 TGTATTATTCATTGACCCACTGTCTGACATTTGAGAGGGAATGGATTATAGTCAAG 720
Qy 814 SerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuValSerCysLeuSer 833
Db 721 TCTCTGTCAAGTGAACCTGTGACCTTGAAGAAATTCATAGTCTCTGCTGTGCT 780
Qy 834 AlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeu 853
Db 781 GCAATGACGTGAAATCCTAGCTCAGAACTTTCACAAATTTGGTCAAACTGAGCATTCCT 840
Qy 854 AspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAsp 873
Db 841 GATTTATCAGAAATACCTGGAAAAAGATGGAATGAAGCTTTCATGAAGTATGCAC 900
Qy 874 ArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTyrGlyCysAspValGln 893
Db 901 AGGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCGCTGGGCTGTGACGTGCAA 960
Qy 894 GlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeuValLysLeuGly 913
Db 961 GCGAGCCTGACGAGCTGTTGAACATTTGGAGGAGGTCCCACTCGTCAAGCTTGGG 1020
Qy 914 LeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLys 933
Db 1021 TTGAAAAACTGGAGACTCACAGATACAGAGATTAGAATTTTAGTGCATTTTGGAAAG 1080
Qy 934 AsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGly 953
Db 1081 AACCTCTGAAAAAATCTCCAGCAGTTGAATTTGGCGGAAATCTGTGAGCAGTGATGGA 1140
Qy 954 TrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPhePheAspPheSer 973
Db 1141 TGGCTTGCTTCATGGGTGATTTTGAGAACTTTAGCAATTAGTGTTTTGGACTTTAGT 1200
Qy 974 ThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnValLeuSerLys 993
Db 1201 ACTAAAGAATTTTACCTGATCCAGCATTAGTCAGAAACTTAGCCAGAGTGTATCCCAAG 1260
Qy 994 LeuThrPheLeuGlnGlnAlaArgLeuValGlyTrpGlnPheAspAspAspLeuSer 1013
Db 1261 TTAACCTTTCTGCAAGAGCTAGGCTTGTGGGTGGCAATTTGATGATGATGATCTCAGT 1320
Qy 1014 ValIleThrGlyAlaPheLysLeuValThrAla 1024
Db 1321 GTTATTACAGGTGCTTTTAAACTAGTAACTGCT 1353

RESULT 9

ABK22766

ID ABK22766 standard; cDNA; 891 BP.

XX AC ABK22766;

XX DT 26-MAR-2002 (first entry)

XX DE Human cDNA encoding CLAN NACHT.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.

XX OS Homo sapiens.

XX PN WO200190156-A2.

XX XX 29-NOV-2001.

XX XX 24-MAY-2001; 2001WO-US17158.

XX XX 24-MAY-2000; 2000US-0579240.

XX XX 10-OCT-2000; 2000US-0686347.

XX XX 14-MAR-2001; 2001US-275980P.

XX XX 23-MAY-2001; 2001US-0864921.

XX XX (BURN-) BURNHAM INST.

XX PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

XX PI Oliveira VAM, Hayashi H, Pawlowski K;

XX DR WPT; 2002-083086/11.

XX DR P-PSDB; AAU80872.

XX XX New caspase recruitment domain (CARD)-containing polypeptides and
XX encoding nucleic acids, useful for treating abnormal cell proliferation
XX or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
XX arthritis or stroke

XX PS Claim 1; Page 200-201; 216pp; English.

XX CC The invention relates to an isolated caspase recruitment domain (CARD)
XX -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
XX from it, and the polynucleotides encoding them. Also included are a
XX recombinant vector comprising the polynucleotide, recombinant cells
XX containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
XX and insect cells) and an anti-CARD antibody. The CARD-containing
XX polypeptide and CARD-encoding nucleic acid are useful for treating a
XX pathology characterised by abnormal cell proliferation (e.g. cancer),
XX abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
XX particular, the polypeptide and nucleic acid are useful for treating
XX keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
XX muscle cell proliferation in arteries following balloon angioplasty
XX (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
XX allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
XX graft-versus-host disease, stroke, myocardial infarction, heart failure,
XX neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
XX disease) or immunodeficiency associated disease (e.g. human
XX immunodeficiency virus (HIV) infection). The nucleic acids are useful
XX in a variety of diagnostic applications. The present sequence is a
XX cDNA encoding a CARD domain containing protein.

SQ Sequence 891 BP; 237 A; 228 C; 217 G; 209 T; 0 other;

Alignment Scores:

```
Pred. No.: 1.5e-216 Length: 891
Score: 232.00 Matches: 296
Percent Similarity: 99.33% Conservative: 0
Best Local Similarity: 99.33% Mismatches: 1
Query Match: 22.66% Indels: 2
DB: 24 Gaps: 0

US-09-697-089-2 (1-1024) x ABK22766 (1-891)
Qy 161 LeuGlnSerProCysIleIleGluGlySerGlyLysGlyLysSerThrLeuLeuGln 180
Db 1 CTTTCAGAGCCCTGCATCATGTGAAGGGATCTGGCAAGGCAAGTCCATCTGCTGCAG 60
Qy 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheVal 200
Db 61 CGCATTCGCATCTGCTGGGCTCGGAAAGTCAAGGCTCTGACCAAGTTCAAATTCGTC 120
Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 220
Db 121 TTCTTCCTCCGCTCTCAGCAGGGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACT 180
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240
Db 181 CTGATATACCTGGCACAATCAGGAACGACATTCATGGCCATGCTCTGAAGCTCGG 240
Qy 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
Db 241 CAGAGGGTCTCTTTCCCTCTCTGATGGCTACAAATGAATCAAGCCCAAGAACTGCCAGAA 300
Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280
Db 301 ATCGAAGCCCTGTAAAGAGAAACCCAGCTTCAAGAACATGCTCATCGTCAACCACTAAC 360
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyValAlaLeuThrAlaGluValGlyAspMet 300
Db 361 ACTGAGTGCCTGAGGCACATACGGCAGTTGGTGGCCCTGACTGCTGAGGTGGGGGATG 420
Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
Db 421 ACAGAACACAGCGCCAGGCTCTCATCCGAGAAAGTGTGTATCAAGGAGCTGCTGAAGGC 480
Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
Db 481 TTGTGTCTCAAAATTCAGAAATCAGAGTGTCTGAGGAATCTCATGAGACCCCTCTCTTT 540
Qy 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
Db 541 GTGCTCATCACTGTGCAATCCAGTGGTGAAGTGAGTTCACCTCTCACACAAACA 600
Qy 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysLysGly 380
Db 601 ACGCTGTTCCATACCTTCTATGATCTGTTCATACAGAAAAACAAACAAACATAAAGGT 660
Qy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCys-GlyAspLeuAlaLeuGlu 400
Db 661 GTGGCTCAAGTACATTCGAGGCTGGACCCG-TGGAGACCTAGCTCTGGAGGG 719
Qy 400 YValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVa 420
Db 720 TGTGTTCTCCCAAGTTGATTCGAACATGCAAGTGTCTCAGCGTGAATGAGATGT 779
Qy 420 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyr 440
Db 780 CCGTCTCACAACCTGGGCTCTCTGTAATATACAGCTCAAAAGTTCAAGCCAAAGTATAA 839
Qy 440 sPhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSer 457
Db 840 ATTCTTTTCAAGTCAATTCAGGAGTACACAGCAGGACGAGGACGAGCTCAGCAGT 891

RESULT 10
ABK22767
ID ABK22767 standard; cDNA; 618 BP.
XX
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AC ABK22767;
XX 26-MAR-2002 (first entry)
XX Human cDNA encoding CLAN LRR.
DE
XX
XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
XX
XX Homo sapiens.
OS
XX
XX WO200190156-A2.
PN
XX
XX 29-NOV-2001.
PD
XX
XX 24-MAY-2001; 2001WO-US17158.
PF
XX
XX 24-MAY-2000; 2000US-0579240.
PR
XX 10-OCT-2000; 2000US-0686347.
PR
XX 14-MAR-2001; 2001US-275980P.
PR
XX 23-MAY-2001; 2001US-0864921.
XX
XX (BURN-) BURNHAM INST.
PA
XX
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX
XX WPI; 2002-083086/11.
DR P-PSDB; AAU08073.
DR
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -
XX
XX Claim 1; Page 202-203; 216pp: English.
XX
XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.
XX
XX Sequence 618 BP; 194 A; 113 C; 148 G; 163 T; 0 other;
SQ
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Alignment Scores:
Pred. No.: 2,61e-191 Length: 618
Score: 206.00 Matches: 206
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 20.12% Indels: 0
DB: 24 Gaps: 0
US-09-697-089-2 (1-1024) x ABK22767 (1-618)
QY 760 GlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAsp 779
Dd 1 GGTAACTTGAAGAACCTTACAAAGCTCATAATGGATAACATAAGATGAATGAAGAAGAT 60
QY 780 AlaIleLysLeuAlaGluLysLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThr 799
Dd 61 GCTATAAACTAGCTGAAGCCCTGAAAAACCTGAAGAAGATGTTTATTTTCATTGGACC 120
QY 800 HisLeuSerAspIleGluGlyMetAspTyrIleValLysSerLeuSerSerGluPro 819
Dd 121 CACTTCTCGACATGGACAGGGAATGGATTACATAGTCAAGTCTCTGTCAGTGAACCC 180
QY 820 CysAspLeuGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIle 839
Dd 181 TGTGACCTTGAAGAAATTCATTTAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 840 LeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyr 859
Dd 241 CTAGCTCAGAAUCTTCAAAATTTGGTCAAACTGAGCATCTTGGATTATCAGAAATTAAC 300
QY 860 LeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlu 879
Dd 301 CTGGAAGAAAGATGGAATGAAGCTCTTCATGAACGTGACAGGATGAACGTGTAGAA 360
QY 880 GlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerLeu 899
Dd 361 CAGCTCACCAGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 900 LeuLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeu 919
Dd 421 TTGAAACATTTGGAGGAGGTCCACAACTCGTCAAGCTTTGGGTGGAACACTGGAGACTC 480
QY 920 ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe 939
Dd 481 ACAGATACAGAGATTAGATTTTAGTGTCATTTTGGGAAGAACCCCTCTGAAAAACTTC 540
QY 940 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGly 959
Dd 541 CAGCAGTTGAATTTGGCGGAAATCGTGTGACGAGTGTGATGGCTTGCCTTCATGGGT 600
QY 960 ValPheGluAsnLeuLys 965
Dd 601 GTATTTGAGAACTTTAAG 618
RESULT 11
AAH34171/c
ID AAH34171 standard; cdNA; 2735 BP.
AC AAH34171;
XX
DT 03-SEP-2001 (first entry)
DE Human colon cancer antigen encoding cdNA SEQ ID NO:1253.
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
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PA (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX WPI; 2001-235357/24.
DR P-PSDB; AAG74766.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers -
PS Claim 1; Page 3017; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate p
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing P.
CC Inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAH77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 2735 BP; 791 A; 555 C; 512 G; 876 T; 1 other;

Alignment Scores:
Pred. No.: 2,67e-165 Length: 2735
Score: 180.00 Matches: 180
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QY 865 AsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeu 884
Dd 2667 AATGAAGCTCTTCATGAACGTGACAGGATGAAGCTGCTAGAACAGCTCACCCGACTG 2608
QY 885 MetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLysHisLeuGlu 904
Dd 2607 ATGTCGCCCTGGGCTGTGACGTGCAAGCAGCCTGAGCAGCTTGTGTAACATTTGGAG 2548
QY 905 GluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIle 924
Dd 2547 GAGGTCCCACTCGTCAAGCTTGGTTGAAAAAATGGAGACTCACAGATACAGAGATT 2488
QY 925 ArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeu 944
Dd 2487 AGAATTTTAGGTGCATTTTGTGAAAGAACCCCTCTCAAAACCTCCAGCAGTTGAATTTG 2428
QY 945 AlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetClyValPheGluAsnLeu 964
Dd 2427 GCGGGAAATCGTGTGACAGTGTGATGATGCTTGCCTTCATGGGTGATTTGAGAAATCTT 2368
QY 965 LysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuVal 984
Dd 2367 AAGCAATTAGTGTGTTTTCGACTTTAGTACTAAGAAATTTCTACCTGATCCAGCATTAGTC 2308
QY 985 ArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGly 1004
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PF			PR	29-SEP-2000;	2000US-0236370.
XX	31-JAN-2000;	2000US-0179065.	PR	02-OCT-2000;	2000US-0236802.
PR	04-FEB-2000;	2000US-0180628.	PR	02-OCT-2000;	2000US-0237037.
PR	24-FEB-2000;	2000US-0184664.	PR	02-OCT-2000;	2000US-0237038.
PR	02-MAR-2000;	2000US-0186350.	PR	02-OCT-2000;	2000US-0237039.
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PR	17-MAR-2000;	2000US-0190076.	PR	13-OCT-2000;	2000US-0239935.
PR	18-APR-2000;	2000US-0198123.	PR	13-OCT-2000;	2000US-0239937.
PR	19-MAY-2000;	2000US-0205515.	PR	20-OCT-2000;	2000US-0240960.
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PR	22-AUG-2000;	2000US-0227182.	PR	17-NOV-2000;	2000US-0249209.
PR	23-AUG-2000;	2000US-0227009.	PR	17-NOV-2000;	2000US-0249210.
PR	30-AUG-2000;	2000US-0228924.	PR	17-NOV-2000;	2000US-0249211.
PR	01-SEP-2000;	2000US-0229287.	PR	17-NOV-2000;	2000US-0249212.
PR	01-SEP-2000;	2000US-0229343.	PR	17-NOV-2000;	2000US-0249213.
PR	01-SEP-2000;	2000US-0229344.	PR	17-NOV-2000;	2000US-0249214.
PR	01-SEP-2000;	2000US-0229345.	PR	17-NOV-2000;	2000US-0249215.
PR	05-SEP-2000;	2000US-0229509.	PR	17-NOV-2000;	2000US-0249216.
PR	05-SEP-2000;	2000US-0229513.	PR	17-NOV-2000;	2000US-0249217.
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PR	06-SEP-2000;	2000US-0230438.	PR	17-NOV-2000;	2000US-0249244.
PR	08-SEP-2000;	2000US-0231242.	PR	17-NOV-2000;	2000US-0249245.
PR	08-SEP-2000;	2000US-0231243.	PR	17-NOV-2000;	2000US-0249264.
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PR	08-SEP-2000;	2000US-0231414.	PR	17-NOV-2000;	2000US-0249299.
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PR	14-SEP-2000;	2000US-0232397.	PR	05-DEC-2000;	2000US-0251030.
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PR	14-SEP-2000;	2000US-0233065.	PR	08-DEC-2000;	2000US-0251989.
PR	21-SEP-2000;	2000US-0234223.	PR	08-DEC-2000;	2000US-0251990.
PR	21-SEP-2000;	2000US-0234274.	PR	11-DEC-2000;	2000US-0254097.
PR	25-SEP-2000;	2000US-0234997.	PR	05-JAN-2001;	2001US-0259678.
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PR	26-SEP-2000;	2000US-0235484.	XX		
PR	27-SEP-2000;	2000US-0235834.	XX		
PR	27-SEP-2000;	2000US-0235836.	XX		
PR	29-SEP-2000;	2000US-0236327.	XX		
PR	29-SEP-2000;	2000US-0236367.	XX		
PR	29-SEP-2000;	2000US-0236368.	XX		
			PA	(HUMA-) HUMAN GENOME SCI INC.	
			XX		
			XX		
			PI	Rosen CA, Barash SC, Ruben SM;	
			XX		
			DR	WPI; 2001-488783/53.	
			DR	P-PSDB; AAU16173.	

XX New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -

PS Claim 1: SEQ ID No 339; 980pp: English.

XX The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. Antibodies to the proteins can also
CC be used in alleviating symptoms associated with the disorders and in
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angioneurosis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence encodes a novel secreted protein of the invention.

Alignment Scores:
Pred. No.: 1-26e-136 Length: 608
Score: 150.00 Matches: 150
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.65% Indels: 0
DB: 22 Gaps: 0

US-09-697-089-2 (1-1024) x AAS26160 (1-608)

QY 499 ValGluAlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeu 518
DB 88 GTGAAGCCACACAGGGCTGTATTGAAGCACCTCGACAGCTGTATCAACACGGCTGCCTT 147
QY 519 LeuGlyLeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLys 538
DB 148 CTCGGACTTTCCATCGCCAAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAAA 207
QY 539 AsnThrThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGly 558
DB 208 AACACCACTGAGCAAGAAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGC 267
QY 559 IleHisLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhe 578
DB 268 ATCCATTTATATCAAGAGAGTACATCAAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTC 327
QY 579 PheGlnGlySerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhe 598
DB 328 TTTCAAGGTAAAGCTTATATATCACTCAGGGAACATCCCGATTACTTATTGACTTC 387
QY 599 PheGluHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGly 618
DB 388 TTTGAACATTGGCCCAATTGTGAAGTGTCTGGACTTCATTAACCTGGACTTTATGGG 447
QY 619 GlyAlaMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGlu 638
DB 448 GGAGCTATGGCTTCATGGGAAAGGCTGCAAGACACACAGGCGGAATCCATCGAAGAG 507
QY 639 AlaProGluThrTyrIleProSerArgAla 648
DB 508 GCCCCAGAAACCTACATTCACGAGGGCT 537

RESULT 14

AAS26575

ID AAS26575 standard; cDNA; 522 BP.

XX AC

XX AAS26575;

XX AC

XX 07-NOV-2001 (first entry)

XX DT

XX Human cDNA encoding a novel secreted protein, Seq ID 754.

XX DE

XX XX

XX Human; immunosuppressive; antiarthritic; ss; antirheumatic;

XX KW cytotatic; cardiac; vasotropic; cerebroprotective; nootropic;

XX KW neuroprotective; antibacterial; virucide; fungicide; opthalmological;

XX KW vulnery; secreted protein; rheumatoid arthritis;

XX KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;

XX KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;

XX KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;

XX KW corneal infection; wound healing; epithelial cell proliferation;

XX KW skin ageing; food additive; preservative; antiproliferative.

XX OS Homo sapiens.

XX XX

XX WO20015322-A2.

XX PN

XX 02-AUG-2001.

XX XX

XX 17-JAN-2001; 2001WO-US01341.

XX XX

XX 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214886.

XX PR 30-JUN-2000; 2000US-0215135.

XX PR 07-JUL-2000; 2000US-0216647.

XX PR 07-JUL-2000; 2000US-0216880.

XX PR 11-JUL-2000; 2000US-0217487.

XX PR 11-JUL-2000; 2000US-0217496.

XX PR 14-JUL-2000; 2000US-0218290.

XX PR 26-JUL-2000; 2000US-0220963.

XX PR 26-JUL-2000; 2000US-0220964.

XX PR 14-AUG-2000; 2000US-0224518.

XX PR 14-AUG-2000; 2000US-0224519.

XX PR 14-AUG-2000; 2000US-0225213.

XX PR 14-AUG-2000; 2000US-0225214.

XX PR 14-AUG-2000; 2000US-0225266.

XX PR 14-AUG-2000; 2000US-0225267.

XX PR 14-AUG-2000; 2000US-0225268.

XX PR 14-AUG-2000; 2000US-0225270.

XX PR 14-AUG-2000; 2000US-0225447.

XX PR 14-AUG-2000; 2000US-0225757.

XX PR 14-AUG-2000; 2000US-0225758.

XX PR 14-AUG-2000; 2000US-0225759.

XX PR 18-AUG-2000; 2000US-0226279.

XX PR 22-AUG-2000; 2000US-0226681.

XX PR 22-AUG-2000; 2000US-0226868.

XX PR 23-AUG-2000; 2000US-0227009.

XX PR 30-AUG-2000; 2000US-0228924.

XX PR 01-SEP-2000; 2000US-0229287.

XX PR 01-SEP-2000; 2000US-0229343.

XX PR 01-SEP-2000; 2000US-0229344.

XX PR 01-SEP-2000; 2000US-0229345.

XX PR 05-SEP-2000; 2000US-0229509.

XX PR 05-SEP-2000; 2000US-0229513.

XX PR 06-SEP-2000; 2000US-0230437.

XX PR 06-SEP-2000; 2000US-0230438.

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PR	08-SEP-2000;	2000US-0232081.	PR	01-DEC-2000;	2000US-0250160.
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PR	21-SEP-2000;	2000US-0234223.	PR	08-DEC-2000;	2000US-0251990.
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PR	26-SEP-2000;	2000US-0235484.	PA	(HUMA-) HUMAN GENOME SCI INC.	
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PR	27-SEP-2000;	2000US-0235836.	PI	Rosen CA, Barash SC, Ruben SM;	
PR	29-SEP-2000;	2000US-0236327.	XX		
PR	29-SEP-2000;	2000US-0236367.	DR	WPI; 2001-488783/53.	
PR	29-SEP-2000;	2000US-0236368.	DR	P-PSDB; AAU16588.	
PR	29-SEP-2000;	2000US-0236369.	XX		
PR	29-SEP-2000;	2000US-0236370.	PT	New nucleic acid molecules encoding 461 human secreted proteins for	
PR	29-SEP-2000;	2000US-0236370.	PT	diagnosing, preventing, treating or ameliorating medical conditions and	
PR	02-OCT-2000;	2000US-0236802.	PT	used as food additives or preservatives -	
PR	02-OCT-2000;	2000US-0237037.	XX		
PR	02-OCT-2000;	2000US-0237038.	XX		
PR	02-OCT-2000;	2000US-0237039.	PS	Claim 1; SEQ ID No 754; 980pp; English.	
PR	02-OCT-2000;	2000US-0237040.	XX		
PR	13-OCT-2000;	2000US-0239935.	CC	The invention relates to isolated nucleic acid molecules and their	
PR	13-OCT-2000;	2000US-0239937.	CC	encoded secreted proteins. The nucleic acids and proteins are used to	
PR	20-OCT-2000;	2000US-0240960.	CC	prevent, treat or ameliorate a medical condition in e.g. humans, mice,	
PR	20-OCT-2000;	2000US-0241221.	CC	rabbits, goats, horses, cats, dogs, chickens or sheep. They	
PR	20-OCT-2000;	2000US-0241785.	CC	are also used in diagnosing a pathological condition or susceptibility	
PR	20-OCT-2000;	2000US-0241786.	CC	to a pathological condition. Antibodies to the proteins can also	
PR	20-OCT-2000;	2000US-0241787.	CC	be used in alleviating symptoms associated with the disorders and in	
PR	20-OCT-2000;	2000US-0241808.	CC	diagnostic immunoassays e.g. radioimmunoassays or enzyme linked	
PR	20-OCT-2000;	2000US-0241809.	CC	immunosorbant assays (ELISA). Disorders which are diagnosed or treated	
PR	20-OCT-2000;	2000US-0241826.	CC	include autoimmune diseases e.g. rheumatoid arthritis,	
PR	01-NOV-2000;	2000US-0244617.	CC	hyperproliferative disorders e.g. neoplasms of the breast or liver,	
PR	08-NOV-2000;	2000US-0246474.	CC	cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders	
PR	08-NOV-2000;	2000US-0246475.	CC	e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.	
PR	08-NOV-2000;	2000US-0246476.	CC	Alzheimer's disease, infections caused by bacteria, viruses and fungi	
PR	08-NOV-2000;	2000US-0246477.	CC	and ocular disorders e.g. corneal infection, and many other	
PR	08-NOV-2000;	2000US-0246478.	CC	disorders listed in the specification. The polypeptides can also	
PR	08-NOV-2000;	2000US-0246523.	CC	be used to aid wound healing and epithelial cell proliferation, to	
PR	08-NOV-2000;	2000US-0246524.	CC	prevent skin aging due to sunburn, to maintain organs before	
PR	08-NOV-2000;	2000US-0246525.	CC	transplantation, for supporting cell culture of primary tissues, to	
PR	08-NOV-2000;	2000US-0246526.	CC	regenerate tissues and in chemotaxis. The polypeptides can also be used	
PR	08-NOV-2000;	2000US-0246527.	CC	as a food additive or preservative to increase or decrease storage	
PR	08-NOV-2000;	2000US-0246528.	CC	capabilities, fat content, lipid, protein, carbohydrate, vitamins,	
PR	08-NOV-2000;	2000US-0246532.	CC	minerals, cofactors and other nutritional components. The present	
PR	08-NOV-2000;	2000US-0246609.	CC	sequence encodes a novel secreted protein of the invention.	
PR	08-NOV-2000;	2000US-0246610.			
PR	08-NOV-2000;	2000US-0246611.			
PR	08-NOV-2000;	2000US-0246613.			
PR	17-NOV-2000;	2000US-0249207.			
PR	17-NOV-2000;	2000US-0249208.			
PR	17-NOV-2000;	2000US-0249209.			
PR	17-NOV-2000;	2000US-0249210.			
PR	17-NOV-2000;	2000US-0249211.			
PR	17-NOV-2000;	2000US-0249212.			
PR	17-NOV-2000;	2000US-0249213.			
PR	17-NOV-2000;	2000US-0249214.			
PR	17-NOV-2000;	2000US-0249215.			
PR	17-NOV-2000;	2000US-0249216.			
PR	17-NOV-2000;	2000US-0249217.			
PR	17-NOV-2000;	2000US-0249218.			
PR	17-NOV-2000;	2000US-0249244.			

Alignment Scores:

Pred. No.:	6.26e-85	Length:	522
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.47%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2 (1-1024) x AAS26575 (1-522)

Qy	80	LeuPheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAsp	99
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Qy	100	AspLeuAlaGlnAspLeuLysAspLeuTyHisThrProSerPheLeuAsnPhenTyPro	119

Db 63 GATTGGCTCAGGATTTAAAGGACTGTACCATACCCCATCTTTCTGAACCTTTATCCC 122
Qy 120 LeuGlyGluAspIleAspIlePheAsnLeuLysSerThrPheThrGluProValLeu 139
Db 123 CTGTGTGAAGATATGACATATTTTAACTTGAAGACCTTCACAGACCTGCTCTG 182
Qy 140 TrpArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGln 159
Db 183 TGGAGGAAGGACCAACACCATCACCGCTGGAGCAGCTGACCTGAATGGCTCTCTGCAG 242
Qy 160 AlaLeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSer 176
Db 243 GCTCTTCAGAGCCCTGCATCATTTGAAGGGAATCTGGCAAGGCAAGTCC 293

RESULT 15

ABK22733

ID ABK22733 standard; cDNA; 578 BP.

AC ABK22733;

XX DT 26-MAR-2002 (first entry)

XX DE Human cDNA encoding CLAN C.

XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.

XX OS Homo sapiens.

XX PN WO200190156-A2.

XX XX 29-NOV-2001.

XX PD 24-MAY-2001; 2001WO-US17158.

XX PF 24-MAY-2000; 2000US-0579240.

XX PR 10-OCT-2000; 2000US-0686347.

XX PR 14-MAR-2001; 2001US-275980P.

XX PR 23-MAY-2001; 2001US-0864921.

XX XX (BURN-) BURNHAM INST.

XX XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

PI Oliveira VAM, Hayashi H, Pawlowski K;

XX WPI; 2002-083086/11.

DR P-PSDB; AAU80863.

XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke

XX Claim 1; Page 177; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In

CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.

XX SQ Sequence 578 BP; 172 A; 106 C; 143 G; 157 T; 0 other;

Alignment Scores:

Pred. No.: 4.48e-77 Length: 578
Score: 89.00 Matches: 89
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.69% Indels: 0
DB: 24 Gaps: 0

US-09-697-089-2 (1-1024) x ABK22733 (1-578)

Qy 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20

Db 277 ATGAATTTTCATAAAGGACAATAGCGAGCCCTTATTCAAAGAATGGAATGACTGTATA 336

Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIle 40

Db 337 AAGCAAAATCACAGATGACCTATTTGTATGGAATGTCGCGAAGAAGTAAACATC 396

Qy 41 IleCysCysGluLysValGluGlnAspAlaLaArgGlyIleIleHisMetIleLeuLys 60

Db 397 ATTTGCTCGAGAGGTGGACGAGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 456

Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80

Db 457 AAGGGTTCAGAGTCTCTTAAGCTCTTTCTAAATCCCTTAAGGAGTGAACATCTCTCTA 516

Qy 81 PheGlnAspLeuAsnGlyGlnSerLeu 89

Db 517 TTTCAGGACTTGAATGGACAAGTCTT 543

Search completed: January 31, 2003, 04:26:58

Job time : 528 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2003, 04:09:41 ; Search time 3285 Seconds
(without alignments)
5048.456 Million cell updates/sec

Title: US-09-697-089-2
Perfect score: 1024
Sequence: 1 MNFIKNSRALIQRMGMTVI.....WQFDDDDLSVITGAFKLWTA 1024

Scoring table:
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 1
Total number of hits satisfying chosen parameters: 32308016

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame_plus_p2n.model -DEV=xlh
-Q/cyn2_l1/USPto_spool/US09697089/runat_29012003_091154_13480/app_query.fasta_1.1223
-DB=EST -QFMT=fastap -SUFFIX=olip2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZ=500 -MINLEN=2000000000
-USER=US09697089 -ACGN_1_1_2475 -runat_29012003_091154_13480 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_RUNTIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hc.*
9: gb_estl.*
10: gb_est2.*
11: gb_hc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	183	17.9	552	17	AQ309404	AQ309404 CITBI-E1-
C 2	156	15.2	480	10	AV719179	AV719179 AV719179
C 3	121	11.8	741	13	BI824482	BI824482 603038854
C 4	116	11.3	748	13	BI908869	BI908869 603066455
C 5	114	11.1	364	9	AI263294	AI263294 qx57b01.x
C 6	74	7.2	261	10	AW337918	AW337918 he12h11.x
C 7	60	5.9	371	10	AV656315	AV656315 AV656315
C 8	56	5.5	553	17	AQ320928	AQ320928 RPI111-93
C 9	55	5.4	476	12	BG210375	BG210375 RST29913
C 10	48	4.7	630	17	AQ112439	AQ112439 CIT-HSP-2
C 11	45	4.4	509	10	AW418826	AW418826 ha21e11.x
C 12	35	3.4	470	17	AQ624020	AQ624020 HS-5378.B
C 13	34	3.3	650	10	BB627584	BB627584 BB627584
C 14	33	3.2	219	17	AQ283886	AQ283886 RPI111-78
C 15	32	3.1	412	14	H25984	H25984 YL56907.r1
C 16	30	2.9	499	9	AI023795	AI023795 ox08d03.x
C 17	23	2.2	518	17	BH348412	BH348412 CH230-42F
C 18	23	2.2	602	17	AZ360053	AZ360053 LM0103H11
C 19	21	2.1	697	17	BH293386	BH293386 CH230-44G
C 20	18	1.8	635	17	B58691	B58691 CIT-HSP-201
C 21	18	1.8	840	12	BF207840	BF207840 601862546
C 22	15	1.5	775	13	BI854236	BI854236 603381263
C 23	14	1.4	619	17	BH267158	BH267158 CH230-19B
C 24	14	1.4	675	10	BB108531	BB108531 BB108531
C 25	14	1.4	817	17	BH358172	BH358172 CH230-18E
C 26	13	1.3	719	14	BQ204082	BQ204082 UI-R-DNI-
C 27	11	1.1	251	12	BF903662	BF903662 IL2-MT018
C 28	10	1.0	221	10	BB593094	BB593094 BB593094
C 29	10	1.0	275	10	BB575989	BB575989 BB575989
C 30	10	1.0	389	10	AW401018	AW401018 Landigest
C 31	10	1.0	446	9	AI222422	AI222422 qh04f06.x
C 32	10	1.0	865	12	BF185320	BF185320 601844132
C 33	10	1.0	1765	17	AG068034	AG068034 Pan trogl
C 34	9	0.9	54	10	AW307272	AW307272 sf54h07.y
C 35	9	0.9	187	9	AU166132	AU166132 AU166132
C 36	9	0.9	217	10	AW326139	AW326139 18288.MAR
C 37	9	0.9	237	14	BQ458950	BQ458950 HA02M04r
C 38	9	0.9	237	14	BQ656632	BQ656632 HA02M04r
C 39	9	0.9	240	9	AJ460952	AJ460952 AJ460952
C 40	9	0.9	240	9	AJ461386	AJ461386 AJ461386
C 41	9	0.9	245	10	AW458474	AW458474 sh09f07.y
C 42	9	0.9	248	13	BM101090	BM101090 EBP101.SQ
C 43	9	0.9	251	13	BM374011	BM374011 EBP101.SQ
C 44	9	0.9	285	14	BQ761907	BQ761907 EBP101.SQ
C 45	9	0.9	294	10	BB330264	BB330264 BB330264

ALIGNMENTS

RESULT 1
AQ309404/c
LOCUS CITBI-E1-2528J13.TF CITBI-E1 Homo sapiens genomic clone 2528J13,
DEFINITION DNA sequence.
ACCESSION AQ309404
VERSION AQ309404.1 GI:4041438
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and

Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other GSSs: CITBI-E1-2528J13.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2528J13"
/clone_lib="CITBI-E1"
/sex="male"
/cell_type="sperm"
/notes="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 144 a 121 c 130 g 157 t
ORIGIN

Alignment Scores:
Pred. No.: 7.61e-178 Length: 552
Score: 183.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 17.87% Indels: 0
DB: 17 Gaps: 0

US-09-697-089-2 (1-1024) x AQ309404 (1-552)

Qy 477 MetValSerIleSerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGly 496
|||||
Db 550 ATGTTTCCATTTCGGACATTACATCCACTATAGCAGCTGCTCCCGGTACACCTGTGGG 491
Qy 497 SerSerValGluAlaThrArgAlaValMetIleHisLeuAlaValTyrGlnHisGly 516
|||||
Db 490 TCATCTGTGGAAGCCACAGCGCTGTATGAAGCACCTCGCAGCAGTGATCAACACGCG 431
Qy 517 CysLeuLeuGlyLeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSer 536
|||||
Db 430 TGCCTTCTCGGACTTTCATCGCCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGT 371
Qy 537 ValLysAsnThrThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGlu 556
|||||
Db 370 GTGAARAACACCATCTGAGCAGAAGTTCTGAAGCCATAACATCAATCTCTTGTAGAG 311
Qy 557 CysGlyIleHisLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGlu 576
|||||
Db 310 TGTGGCATCCATTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAGAAATTTGAA 251
Qy 577 AlaPheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPhe 596
|||||
Db 250 GCTTTCTTCAAGTAAAGCTTATATCAACTCAAGTCAAGTCTTCAATTAACATGACTTT 191
Qy 597 AspPheGluHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPhe 616
|||||
Db 190 GACTTCTTTGAACATTTGCCCAATGTGCAAGTCTCTGGACTTCATTAACATGACTTT 131
Qy 617 TyrGlyGlyAlaMetAlaSerTrpGluLysAlaIleGluAspThrGlyGlyIleHisMet 636
|||||
Db 130 TATGGGGAGCTATGGCTTCATGGAAAGGCTCAGACAGACAGGTGGATCCACATG 71
Qy 637 GluGluAlaProGluThrThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLys 656
|||||

Db 70 GAAGAGCCCCAGAAACCTACATTCCAGGAGGCTGATCTTGTCTTCACTGGAAG 11
Qy 657 GlnGluPhe 659
|||||
Db 10 CAGGAATTC 2
RESULT 2
AV719179/c 480 bp mRNA linear EST 16-OCT-2000
LOCUS AV719179 GLC Homo sapiens cDNA clone GLCEQA10 5', mRNA sequence.
DEFINITION AV719179
ACCESSION AV719179
VERSION AV719179.1 GI:10816331
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
Qian, B., Wu, T., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.,
Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zeng, L.,
Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang
Y., Gu, Y., Chen, Z. and Han, Z.
Homo sapiens cDNA GLC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
1..480
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCEQA10"
/clone_lib="GLC"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 138 a 120 c 85 g 137 t
ORIGIN

Alignment Scores:
Pred. No.: 4.66e-150 Length: 480
Score: 156.00 Matches: 156
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.23% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2 (1-1024) x AV719179 (1-480)

Qy 869 HisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTrp 888
|||||
Db 480 CATGAACGTATGACAGAGTGAACGTGTAGAACAGCTCACCGCAGCTGATGCTCCCTGG 421
Qy 889 GlyCysAspValGlnGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGln 908
|||||
Db 420 GGCTGTGACGTGCAAGCAGCGCTGAGCAGCCTGTTGAACATTTGGAGGAGGTCCCAAC 361
Qy 909 LeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGly 928
|||||
Db 360 CTCGCTCAAGCTTGGGTTTGAAGAACTGGAGACTCACAGATACAGAGATTAGAAATTTAGGT 301
Qy 929 AlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArg 948
|||||
Db 300 GCATTTTTTGAAGAAGAACCCCTCTGAAAAACTTCACGAGCTGAATTTGGCGGGAATCGT 241
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QY 949 ValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuVal 968
    |||
Db 240 GTCAGCAGTGTGGTGGTCTTCATGGGTGTATTTGAGAACTCTTAAGCAATTAGTG 181
QY 969 PhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSer 988
    |||
Db 180 TTTTGTGACTTTAGTACTAAGAATTTCTACCTGATCCAGCATTAGTCAGAAACTTAGC 121
QY 989 GlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAsp 1008
    |||
Db 120 CRAAGTGTATCAAGTAACTTTCTGCAAGAGCTAGGCTGTGGGTGGCAATTGAT 61
QY 1009 AspAspLeuSerValIleThrGlyAlaPheLysLeuValThrala 1024
    |||
Db 60 GATGATGATCTCAGTGTATTATCAGAGAGCTTTTAAACTAGTAACTGCT 13

RESULT 3
BI824482 741 bp mRNA linear EST 04-OCT-2001
LOCUS 603038854F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5179909 5',
DEFINITION mRNA sequence.
ACCESSION BI824482
VERSION BI824482.1 GI:15936032
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 741)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11448 row: k column: 14
High quality sequence start: 3
High quality sequence stop: 705.
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/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
BASE COUNT 233 a 147 c 164 g 197 t
ORIGIN
Alignment Scores:
Pred. No.: 9,71e-114 Length: 741
Score: 121.00 Matches: 147
Percent Similarity: 98.66% Conservative: 0
Best Local Similarity: 98.66% Mismatches: 0
Query Match: 11.82% Indels: 2
Db: 13 Gaps: 0
US-09-697-089-2 (1-1024) x BI824482 (1-741)

```

```

QY 10 AlaLeuIleGlnArgMetGlyMetThrValIleLysGlnIleThrAspAspLeuPheVal 29
    |||
Db 257 GCCCTATTCAAGAAATGGGAATGACTGTATTAAGCAAAATCACAGATGACCTATTGTA 316
QY 30 TrpAsnValLeuAsnArgGluGluValAsnIleIleCysCysGluLysValGluGlnAsp 49
    |||
Db 317 TGGAAATGTTCTCAATCGCGAAGAAGTAACATCATTTGCTGCGAGAAGGTGGCAGGAT 376
QY 50 AlaAlaArgGlyIleIleHisMetIleLeuLysGlySerGluSerCysAsnLeuPhe 69
    |||
Db 377 GCTGCTAGAGGATCATTCACATGATTTTGAAGAGGGTTCAGAGTCTCTTAACTCTTT 436
QY 70 LeuLysSerLeuLysGluTrpAsnTyrProLeuPheGlnAspLeuAsnGlyGlnSerLeu 89
    |||
Db 437 CTTAAATCCCTTAAGAGTGGAACTATCTCTATTTCAGGACTTGAATGGCAAAAGTCTT 496
QY 90 PheHisGlnThrSerGluGlyAspLeuAspAspLeuAlaGlnAspLeu-LysAspLeuTy 109
    |||
Db 497 TTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTTCAAGGACTTGT 556
QY 109 rhisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleAspIlePheAs 129
    |||
Db 557 CCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATGTACATATTTTAA 616
QY 129 nLeuLysSerThrPheThrGluProVal-LeuTrpArgLysAspGlnHisHisArgv 149
    |||
Db 617 CTTGAAAGACACTTCACAGAACCTGTCTCTGTGGAGGAGGACCAACACCATCACC 676
QY 149 algluGlnLeuThrLeuAsnGly 156
    |||
Db 677 TGGAGCAGCTGACCCCTGAATGGG 699

RESULT 4
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LOCUS 603066455F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215669 5',
DEFINITION mRNA sequence.
ACCESSION BI908869
VERSION BI908869.1 GI:16171950
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 748)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11541 row: m column: 14
High quality sequence start: 7
High quality sequence stop: 744.
Features
Location/Qualifiers
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/db_xref="taxon:9606"
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/tissue_type="leukocyte"
/lab_host="DH10B"
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(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon

```

cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

BASE COUNT 236 a 148 c 166 g 198 t
ORIGIN

Alignment Scores:
Pred. No.: 1.41e-108 Length: 748
Score: 116.00 Matches: 136
Percent Similarity: 98.55% Conservative: 0
Best Local Similarity: 98.55% Mismatches: 0
Query Match: 11.33% Indels: 2
DB: 13 Gaps: 0

US-09-697-089-2 (1-1024) x BI08869 (1-748)

Qy 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 252 ATGAATTTTCATAAAGGACAATAGCGGCCCTTATTCAAAGAATGGGAATGACTGTTATA 311
Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIle 40
Db 312 AAGCAAAATCACAGATGACCTATTTGTATGGAATGTTCTGAATCGGAAGATAACATC 371
Qy 41 IleCysGluLysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60
Db 372 ATTTGCTCGAGAGAGGTGGACGAGATGCTGTAGAGGGATCATTCATGATTTTGA 431
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
Db 432 AAGGGTTTCAGAGTCTGTAACTCTTTCTTAATCCCTTAAAGGAGTGAACATATCTCTA 491
Qy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAsp 100
Db 492 TTTGAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAAGGAGACTTGGACGAT 551
Qy 101 LeuAlaGlnAspLeu--LysAspLeuTyrHisThrProSerPheLeuAsnPhetYrProL 120
Db 552 TTGGCTCAGGATTTTACAAGGACCTGTGACCATACCCATCTTTTCTGAACCTTTTATCCCC 611
Qy 120 euGlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGlu 136
Db 612 TTGGTGAAGATATGACATTATTTTAACTTGAAGACCTTCACAGAA 661

RESULT 5
AI263294/c AI263294 364 bp mRNA linear EST 03-FEB-1999
LOCUS qx57b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3',
DEFINITION mRNA sequence.

ACCESSION AI263294
VERSION AI263294.1 GI:3871497

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center

Clone Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbr/image/image.html

Insert Length: 2146 Std Error: 0.00

Seq primer: -400P from Gbco

High quality sequence stop: 364.

FEATURES
source

Location/Qualifiers

1..364
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2005417"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

BASE COUNT 117 a 84 c 55 g 108 t
ORIGIN

Alignment Scores:

Pred. No.: 7.32e-107 Length: 364
Score: 114.00 Matches: 114
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.13% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x AI263294 (1-364)

Qy 911 LysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhe 930
Db 364 AAGCTTGGTGTGAAAACTGGAGACTCACAGATACAGATTAGAAATTTAGGTGCATTT 305
Qy 931 PheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSer 950
Db 304 TTTGGAAAGAACCCCTCGAAAACCTCCAGCAGTTGAATTTGGCGGAAATCGTGTGAGC 245
Qy 951 SerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPhePhe 970
Db 244 AGTGATGATGGCTTGCCTTCATGGGTGATTTGAGAACTCTTAAGCAATAGTGTGTTTT 185
Qy 971 AspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnVal 990
Db 184 GACTTTAGTACTAAAGAATTTCTACCTGATCCAGCATTAGCAGAAAACITAGGCCAAGTG 125
Qy 991 LeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAspAsp 1010
Db 124 TTATCCAAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATTTGATGATGAT 65
Qy 1011 AspLeuSerValIleThrGlyAlaPheLysLeuValThrAla 1024
Db 64 GATCTCAGTGTATTACAGGTGCTTTTAAACTAGTAACCTGCT 23

RESULT 6

AW337918/c

LOCUS

DEFINITION

AW337918

VERSION

AW337918.1

KEYWORDS

SOURCE

ORGANISM

Human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,

Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

AW337918 261 bp mRNA linear EST 31-JAN-2000
LOCUS hei2hl1.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918853 3',
DEFINITION mRNA sequence.

ACCESSION AW337918

VERSION AW337918.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,

Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 201.

FEATURES

source

Location/Qualifiers
1. .261
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2918853"
/clone_lib="NCI-CGAP_CML1"
/tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL rearrangement positive, includes both chronic phase and myeloid blast crisis"
/lab_host="DH10B"

/note="Organ: whole blood; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."

BASE COUNT 86 a 54 c 38 g 83 t

ORIGIN

Alignment Scores:
Pred. No.: 9,33e-66 Length: 261
Score: 74.00 Matches: 74
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.23% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2 (1-1024) x AW337918 (1-261)

QY 951 SerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPhePhe 970

|||||

Db 260 AGTGATGGATGCTTGCCTTCATCGGTGATTTGAGAACTTAAGCAATTAGCTTTTT 201

|||||

QY 971 AspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnVal 990

|||||

Db 200 GACTTTAGTACTAAAGAAATTTACTCTGATCCAGCATATTAGTCAGAAAACCTTAGCCAAAGT 141

|||||

QY 991 LeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAspAsp 1010

|||||

Db 140 TTATCAAGTTAACTTTCTGCAAGAGCTAGCTGTGTGGTGGCAATTTGATGATGAT 81

|||||

QY 1011 AspLeuSerValIleThrGlyAlaPheLysLeuValThrAla 1024

|||||

Db 80 GATCTCAGTGTATTACAGGTGCTTTAAACTAGTAACCTGCT 39

|||||

RESULT 7

AV656315

LOCUS AV656315 371 bp mRNA linear EST 16-JAN-2002

DEFINITION AV656315 GLC Homo sapiens cDNA clone GLCEQA10 3', mRNA sequence.

ACCESSION AV656315

VERSION AV656315.1 GI:9877329

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 371)

Xu.X., Huang.J., Xu.Z., Qian.B., Zhu.Z., Yan.Q., Cai.T., Zhang.X.,

Xiao.H., Qu.J., Liu.F., Huang.Q., Cheng.Z., Li.N., Du.J., Hu.W.,

Shen.K., Lu.G., Fu.G., Zhong.M., Xu.S., Gu.W., Huang.W., Zhao.X.,

Hu.G., Gu.J., Chen.Z. and Han.Z.

Insight into hepatocellular carcinogenesis at transcriptome level

by comparing gene expression profiles of hepatocellular carcinoma

with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

21625106

CONTACT: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex.45)

FEATURES

source

Location/Qualifiers
1. .371
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCEQA10"
/clone_lib="GLC"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 112 a 85 c 91 g 82 t 1 others

ORIGIN

Alignment Scores:
Pred. No.: 3.83e-51 Length: 371
Score: 60.00 Matches: 113
Percent Similarity: 98.26% Conservat: 0
Best Local Similarity: 98.26% Mismatches: 1
Query Match: 5.86% Indels: 2
DB: 10 Gaps: 0

US-09-697-089-2 (1-1024) x AV656315 (1-371)

QY 625 GluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaProGluThrTyrIle 644

|||||

Db 1 GAAAGGCTGCAGAGACACAGGTGGAATCCACATGGAGAGGCCCAACCTACATT 60

|||||

QY 645 ProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArgThrLeuGluVal 664

|||||

Db 61 CCCAGCAGGGCTGATCTTTGTTCTCACTGGAGCAGCAATTCAGGACTCTGGAGGTC 120

|||||

QY 665 ThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePh 684

|||||

Db 121 ACACCTCCGGGATTCAGCAAGTTGAATAAGCAAGATATCAG-ATATCTGGGAAATATT 179

|||||

QY 684 eSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLe 704

|||||

Db 180 CAGCTCTGCCACAGCCCTCAGGCTGCAATAAAGAGATGTCTGGTGGCTGGAGCCCT 239

|||||

QY 704 uSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLe 724

|||||

Db 240 CAGTTTGGTCTCTCAGCACCCTGTAAAGACATTTATCTCTCATGTTGGAGCCAGTCCCT 299

|||||

QY 724 uThrIleGluAspGluArgHisIleThrSerValThrAsnLeu 738

|||||

Db 300 CACCATAAGATGAGAGGCACATCACATCTGTGAACAAACCTG 342

|||||

RESULT 8

AQ320928

LOCUS AQ320928/c 553 bp DNA linear GSS 06-MAY-1999

DEFINITION RPC111-93C9-TV RPC1-11 Homo sapiens genomic clone RPC1-11-93C9, DNA

sequence.

ACCESSION AQ320928

VERSION AQ320928.1 GI:4053662

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 553)

Adams.M.D., Rounsley.S.D., Zhao.S., Bass.S., Linher.K., Golden.K.,

Berry.K., Granger.D., Suh.E., Wible.C., de Jong.P. and Venter.J.C.

Use of human BAC End Sequences for Sequence-Ready Map Building

Unpublished (1998)

Other GSSs: RPC111-93C9.TJ

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850


```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2372c1"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"
BASE COUNT 188 a 126 c 124 g 192 t
ORIGIN
Alignment Scores:
Pred. No.: 1.66e-38 Length: 630
Score: 48.00 Matches: 48
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.69% Indels: 0
DB: 17 Gaps: 0
US-09-697-089-2 (1-1024) x A0112439 (1-630)
QY 784 AlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeuSerAsp 803
|||||
Db 486 GCTGAAGGCTGAACCACTGAAGAGATGTTTATTTCATTGACCACCTGTCTGAC 545
|||||
QY 804 IleGlyGluGlyMetAspTyrIleValLysSerLeuSerGluProCysAspLeuGlu 823
|||||
Db 546 ATTGGAGGGAGTATACATAGTCAAGTCTCTGTCAGTGAACCTGTGACCTTGAA 605
|||||
QY 824 GluIleGlnLeuValSerCysCys 831
|||||
Db 606 GAAATTCAATTAGTCTCCTGCTGC 629
|||||
RESULT 11
AW418826/c 509 bp mRNA linear EST 09-FEB-2000
LOCUS ha21e11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874380 3',
DEFINITION mRNA sequence.
ACCESSION AW418826
VERSION AW418826.1 GI:6946758
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 509)
REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 461.
FEATURES
source
1..509
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2874380"
/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid5 was
```

```
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1323912-1325831, 1471368-1472903 and
1492104-1493255). Subtraction by Bento Soares and M.
Fatima Bonaldo.
BASE COUNT 161 a 99 c 80 g 169 t
ORIGIN
Alignment Scores:
Pred. No.: 1.63e-35 Length: 509
Score: 45.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.39% Indels: 0
DB: 10 Gaps: 0
US-09-697-089-2 (1-1024) x AW418826 (1-509)
QY 980 AspProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGlu 999
|||||
Db 508 GATCCAGCATTAGTCAGAAAACCTTAGCCAGTGTATCCAGTTAACTTTCTGCAAGAA 449
|||||
QY 1000 AlaArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPhe 1019
|||||
Db 448 GCTAGGCTTGTGGTGGAATTTGATGATGATGATCTCAGTGTATTATACAGGTGCTTTT 389
|||||
QY 1020 LysLeuValThrAla 1024
|||||
Db 388 AACTAGTAACCTGCT 374
|||||
RESULT 12
AQ624020 470 bp DNA linear GSS 16-JUN-1999
LOCUS HS_5378_B2_C12_SP6E RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION genomic clone Plate=954 Col=24 Row=F, DNA sequence.
ACCESSION AQ624020
VERSION AQ624020.1 GI:5086412
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 470)
REFERENCE
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 954 row: F column: 24
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 470.
Location/Qualifiers
1..470
/organism="Homo sapiens"
/db_xref="taxon:9606"
```

/clone="Plate=954 Col=24 Row=F"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"

/note="vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRII. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"

BASE COUNT 142 a 101 c 107 g 117 t 3 others
ORIGIN

Alignment Scores:

Pred. No.: 3.09e-25 Length: 470
Score: 35.00 Matches: 35
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.42% Indels: 0
DB: 17 Gaps: 0

US-09-697-089-2 (1-1024) x AQ624020 (1-470)

QY 679 TyrLeuGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAla 698

Db 65 TATCTGGGAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAATAAAGAGATGTGCT 124

QY 699 GlyValAlaGlySerLeuSerLeuValLeuSerThrCysLysAsn 713

Db 125 GGTGTGGCTGGAGCCTCAGTTTGGTCTCTCAGCAGCTGTAGAAC 169

RESULT 13

BB627584

LOCUS

DEFINITION BB627584 RIKEN full-length enriched, adult male urinary bladder Mus

musculus cDNA clone 9530011P19 5', mRNA sequence.

ACCESSION BB627584

VERSION BB627584.1 GI:16465218

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 650)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,Y., Konno,H., Kouda,
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura

S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara

,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

e mouse tissues.

Location/Qualifiers

1. .650

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="9530011P19"

/clone_lib="RIKEN full-length enriched, adult male urinary
bladder"

/sex="male"

/tissue_type="urinary bladder"

/dev_stage="adult"

/lab_host="Dh10B"

/note="Site_1: SalI; Site_2: BamHI; cDNA library was

prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in

RIKEN, Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was

primed with a primer [5'

GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was

prepared by using trehalose thermo-activated reverse

transcriptase and subsequently enriched for full-length by

cap-trapper. cDNA went through one round of normalization

to Rn = 20.0 and subtraction to Rn = 370.0. Second

strand cDNA was prepared with the primer adapter of

sequence [5' GAGAGAGAGATTCGAGTTAAATTAATCCCCCCCCCC

3']. cDNA was cleaved with XhoI and BamHI. Vector: a

modified pBluescript KS(+) after bulk excision from

Lambda FLC I."

BASE COUNT 164 a 174 c 173 g 139 t

ORIGIN

Alignment Scores:

Pred. No.: 4.77e-24 Length: 650

Score: 34.00 Matches: 34

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.32% Indels: 0

DB: 10 Gaps: 0

US-09-697-089-2 (1-1024) x BB627584 (1-650)

QY 255 ProGlnAsnCysProGluIleGluAlaLeuLysGluAsnHisArgPhelyAsnMet 274

Db 380 CCCCAGAACTCCAGAAATTAAGAGGAAACCATCGCTTCAAGAACATG 439

QY 275 ValIleValThrThrThrThrGluCysLeuArgHisIleArg 288

Db 440 GTCATTGTCCACCACCACCGAGTGCTGAGGCATATCAGA 481

RESULT 14

AQ283886

LOCUS

DEFINITION

AQ283886

ACCESION

VERSION

AQ283886.1

GI:3910204

KEYWORDS

GSS.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AQ283886 219 bp DNA linear GSS 27-APR-1999
RPCI11-78E13-TV RPCI-11 Homo sapiens genomic clone RPCI-11-78E13,
DNA sequence.

DEFINITION
AQ283886
ACCESION
VERSION
AQ283886.1
GI:3910204
KEYWORDS
GSS.

SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 219)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@igr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..219
/organism="Homo sapiens"
/db_xref="GDB:7529676"
/db_xref="taxon:9606"
/clone="RPCI-11-78E13"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"
69 a 45 c 46 g 59 t

BASE COUNT
ORIGIN

Alignment Scores:
Pred. No.: 1.53e-23 Length: 219
Score: 33.00 Matches: 33
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.22% Indels: 0
DB: 17 Gaps: 0

US-09-697-089-2 (1-1024) x AQ283886 (1-219)

Qy 701 AlaGlySerLeuSerLeuValIleuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
Db 3 GCTGGAAGCCTTAGTGTGCTCCTCAGCACCTGTGAAGACATTTATCTCATGTGGAA 62

Qy 721 AlaSerProLeuThrIleGluAspClnuAArgHisIleThr 733
Db 63 GCCAGTCCCTGACCATAGAAGATGAGAGGCACATCACA 101

RESULT 15
H25984/c
LOCUS
DEFINITION
y156g07.r1 Soares breast 3NbHBst Homo sapiens cdna clone
IMAGE:162300 5', mRNA sequence.
H25984
H25984
VERSION
H25984.1 GI:895107
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 412)
Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 942
High quality sequence stops: 347
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 942 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 347.
Location/Qualifiers
1..412
/organism="Homo sapiens"
/db_xref="GDB:576544"
/db_xref="taxon:9606"
/clone="IMAGE:162300"
/clone_lib="Soares breast 3NbHBst"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: breast; Vector: p7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGGCGCGCCTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified p7T3 vector (Pharmacia).
Library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M.Fatima
Bonaldo."

BASE COUNT
ORIGIN

Alignment Scores:
Pred. No.: 3.32e-22 Length: 412
Score: 32.00 Matches: 32
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.12% Indels: 0
DB: 14 Gaps: 0

US-09-697-089-2 (1-1024) x H25984 (1-412)

Qy 993 LysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAspAspAspLeu 1012
Db 338 AAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGGGTGGCAATTTGATGATGATCTC 279

Qy 1013 SerValIleThrGlyAlaPheLysLeuValThrAla 1024
Db 278 AGTGTTATTACAGGCGCTTTTAAACTAGTAACTGCT 243

Search completed: January 31, 2003, 07:10:58
Job time : 3294 secs



GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model
Run on: January 31, 2003, 04:22:17 ; Search time 85 Seconds
(without alignments)
3694.553 Million cell updates/sec
Title: US-09-697-089-2
Perfect score: 1024
Sequence: 1 MNFIKNSRALIQRMGTVI.....WQFDDDDLSVITGAFKLWTA 1024

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 441362 seqs, 153338381 residues
Word size: 1
Total number of hits satisfying chosen parameters: 878600
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries

Command line parameters: -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09697089/runat_29012003_091154_13493/app_query.fasta.1.1223
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=olip2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptlo -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09697089 -CGN_1_1_46_@runat_29012003_091154_13493 -NCPU=6 -ICPU=3
-NO_XLIFY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	8	0.8	591	4	US-09-144-367-4
C 2	8	0.8	1220	4	US-09-227-357-54
C 3	8	0.8	1225	1	US-08-286-020-1
C 4	8	0.8	1225	1	US-08-603-919-1
C 5	8	0.8	1839	1	US-08-272-875-1
C 6	8	0.8	1839	1	US-08-272-875-2
C 7	8	0.8	1980	1	US-08-350-741-1
C 8	8	0.8	1980	2	US-08-463-875A-1
C 9	8	0.8	2759	4	US-09-144-367-1
C 10	8	0.8	3236	4	US-08-961-527-222
C 11	8	0.8	3573	4	US-09-353-585-4
C 12	8	0.8	5275	1	US-08-485-588-1

C 13	8	0.8	5275	1	US-08-484-565-1
C 14	8	0.8	5275	2	US-08-480-751-1
C 15	8	0.8	5275	2	US-08-943-986-1
C 16	8	0.8	5275	3	US-08-353-784-1
C 17	8	0.8	5275	3	US-08-484-719B-1
C 18	8	0.8	5275	4	US-08-484-159-1
C 19	8	0.8	6471	4	US-09-353-585-1
C 20	8	0.8	11907	4	US-08-061-376-4
C 21	8	0.8	12752	2	US-08-459-146-1
C 22	8	0.8	12752	2	US-08-459-065-1
C 23	8	0.8	14255	1	US-08-320-559-1
C 24	8	0.8	14255	1	US-08-327-392-1
C 25	8	0.8	14255	1	US-08-306-691B-55
C 26	8	0.8	14255	3	US-08-545-860D-1
C 27	8	0.8	14255	5	PCT-US94-04496-1
C 28	8	0.8	87350	3	US-08-781-891-79
C 29	8	0.8	87543	4	US-09-791-211-3
C 30	7	0.7	34	4	US-08-840-767-29
C 31	7	0.7	110	1	US-08-356-790-2
C 32	7	0.7	219	3	US-07-791-931-2
C 33	7	0.7	246	1	US-08-053-131-154
C 34	7	0.7	246	1	US-08-096-762-154
C 35	7	0.7	246	4	US-09-042-353-69
C 36	7	0.7	246	4	US-08-758-417A-333
C 37	7	0.7	282	4	US-09-042-353-94
C 38	7	0.7	282	4	US-09-042-353-111
C 39	7	0.7	282	4	US-09-042-353-113
C 40	7	0.7	282	4	US-08-758-417A-358
C 41	7	0.7	282	4	US-08-758-417A-375
C 42	7	0.7	282	4	US-08-758-417A-377
C 43	7	0.7	284	4	US-09-042-353-78
C 44	7	0.7	284	4	US-08-758-417A-342
C 45	7	0.7	285	4	US-09-042-353-110

ALIGNMENTS

RESULT 1

US-09-144-367-4/C
; Sequence 4, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 591
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: Other
; LOCATION: (0)...(0)
US-09-144-367-4

Alignment Scores:
Pred. No.: 76.9 Length: 591
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
Gaps: 0
DBs: 4

US-09-697-089-2 (1-1024) x US-09-144-367-4 (1-591)

QY 361 ThrLeuPheHisThrPheTyrAsp 368
|||||

Db 49 ACACTTTCCATACTTTTATGAC 26

US-09-227-357-54

Sequence 54, Application US/09227357

Patent No. 6342581

GENERAL INFORMATION:

APPLICANT: Fischer et al.

TITLE OF INVENTION: 123 Human Secreted Proteins

FILE REFERENCE: P2010P1

CURRENT FILING DATE: 1997-07-08

CURRENT FILING DATE: 1998-01-08

EARLIER APPLICATION NUMBER: PC7/US98/13684

EARLIER FILING DATE: 1998-07-07

EARLIER APPLICATION NUMBER: 60/051,926

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/052,793

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,925

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,929

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/052,803

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/052,732

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,931

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,932

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,916

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,930

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,918

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,920

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/052,733

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/052,795

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,919

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,928

EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/055,722

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,723

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,948

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,949

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,953

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,950

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,947

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,964

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/056,360

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,684

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,984

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,954

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/058,785

EARLIER FILING DATE: 1997-09-12

EARLIER APPLICATION NUMBER: 60/058,664

EARLIER FILING DATE: 1997-09-12

EARLIER APPLICATION NUMBER: 60/058,660

EARLIER FILING DATE: 1997-09-12

EARLIER APPLICATION NUMBER: 60/058,661

EARLIER FILING DATE: 1997-09-12

NUMBER OF SEQ ID NOS: 672

SOFTWARE: Patentin ver. 2.0

SEQ ID NO 54

LENGTH: 1220

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (1197)

OTHER INFORMATION: n equals a,t,g, or c

FEATURE:

NAME/KEY: SITE

LOCATION: (1208)

OTHER INFORMATION: n equals a,t,g, or c

FEATURE:

NAME/KEY: SITE

LOCATION: (1209)

OTHER INFORMATION: n equals a,t,g, or c

US-09-227-357-54

Alignment Scores:

Pred. No.: 156

Score: 8.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 0.78%

DB: 4

Length: 1220

Matches: 8

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-697-089-2 (1-1024) x US-09-227-357-54 (1-1220)

Qy 199 PheValPhePheArgLeuSer 206

Db 253 TTTGTTTTTTCTTGAGACTGAGT 276

RESULT 3

US-08-286-020-1

Sequence 1, Application US/08286020

Patent No. 5539095

GENERAL INFORMATION:

APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela

TITLE OF INVENTION: A Chitinase cDNA Clone From a Disease Resistant American Elm Tree

TITLE OF INVENTION: Elm Tree

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ian C. McLeod

STREET: 2190 Commons Parkway

CITY: Okemos

STATE: Michigan

COUNTRY: USA

ZIP: 48864

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage

COMPUTER: Acer

OPERATING SYSTEM: MS-DOS 5.00

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,020

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Ian C. McLeod

REGISTRATION NUMBER: 20,931

REFERENCE/DOCKET NUMBER: MSU 4.1-207

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5539095e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1225

TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:

ORGANISM: Ulmus Americana
STRAIN: NPS 3-487
INDIVIDUAL ISOLATE: N/A
DEVELOPMENTAL STAGE: N/A
HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: N/A
CELL LINE: N/A
ORGANELLE: N/A
IMMEDIATE SOURCE: N/A
POSITION IN GENOME: N/A
FEATURE:

NAME/KEY: chitinase encoding DNA

LOCATION:

IDENTIFICATION METHOD: sequencing

OTHER INFORMATION: DNA needed for chitinase

OTHER INFORMATION: in elm.

PUBLICATION INFORMATION:

US-08-286-020-1

Alignment Scores:
Pred. No.: 156 Length: 1225
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-286-020-1 (1-1225)

Qy 452 GlyArgLeuSerSerLeuLeu 459

Db 1085 GCGCGTCGTTGTCGTCACCTCTT 1108

RESULT 4

US-08-603-919-1

Sequence 1, Application US/08603919

Patent No. 5728382

GENERAL INFORMATION:

APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela

TITLE OF INVENTION: A Chitinase cDNA Clone From a

TITLE OF INVENTION: Disease Resistant American

TITLE OF INVENTION: Elm Tree

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ian C. McLeod

STREET: 2190 Commons Parkway

CITY: Okemos

STATE: Michigan

COUNTRY: USA

ZIP: 48864

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage

COMPUTER: Acer

OPERATING SYSTEM: MS-DOS 5.00

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/603,919

FILING DATE:

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5728382e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1225

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM: Ulmus Americana

STRAIN: NPS 3-487

INDIVIDUAL ISOLATE: N/A

DEVELOPMENTAL STAGE: N/A

HAPLOTYPE: N/A

TISSUE TYPE: N/A

CELL TYPE: N/A

CELL LINE: N/A

ORGANELLE: N/A

IMMEDIATE SOURCE: N/A

POSITION IN GENOME: N/A

FEATURE:

NAME/KEY: chitinase encoding DNA

LOCATION:

IDENTIFICATION METHOD: sequencing

OTHER INFORMATION: DNA needed for chitinase

OTHER INFORMATION: in elm.

PUBLICATION INFORMATION:

US-08-603-919-1

Alignment Scores:

Pred. No.: 156 Length: 1225
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-603-919-1 (1-1225)

Qy 452 GlyArgLeuSerSerLeuLeu 459

Db 1085 GCGCGTCGTTGTCGTCACCTCTT 1108

RESULT 5

US-08-272-875-1

Sequence 1, Application US/08272875

Patent No. 5487996

GENERAL INFORMATION:

APPLICANT: Takeji SHIBATANI

APPLICANT: Saburo KOMATSUBARA

APPLICANT: Kenji OMORI

APPLICANT: Hiroyuki AKATSUKA

TITLE OF INVENTION: GENE CODING FOR ESTERASE AND NOVEL

TITLE OF INVENTION: MICROORGANISM CONTAINING SAID GENE

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

STREET: P.O. Box 747

CITY: Falls Church

STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/272,875
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/980,516A
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 355440/1991
FILING DATE: 25-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 137502/1992
FILING DATE: 13-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3175P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 241 1300
TELEFAX: 703 241 2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1839 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN: Serratia marcescens Sr41
US-08-272-875-1

Alignment Scores:
Pred. No.: 232 Length: 1839
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-272-875-1 (1-1839)

QY 450 ThrAlaGlyArgLeuSerSer 457
|||||
Db 1094 ACAGCGGGCGAGCTTATCATCG 1117

RESULT 6

US-08-272-875-2
Sequence 2, Application US/08272875
Patent No. 5487996
GENERAL INFORMATION:
APPLICANT: Takeji SHIBATANI
APPLICANT: Saburo KOMATSUBARA
APPLICANT: Kenji OMORI
APPLICANT: Hiroyuki AKATSUKA
TITLE OF INVENTION: GENE CODING FOR ESTERASE AND NOVEL
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: P.O. Box 747
CITY: Falls Church

STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/272,875
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/980,516A
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 355440/1991
FILING DATE: 25-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 137502/1992
FILING DATE: 13-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3175P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 241 1300
TELEFAX: 703 241 2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1839 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN: Serratia marcescens M-1
US-08-272-875-2

Alignment Scores:
Pred. No.: 232 Length: 1839
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-272-875-2 (1-1839)

QY 450 ThrAlaGlyArgLeuSerSer 457
|||||
Db 1094 ACAGCGGGCGAGCTTATCATCG 1117

RESULT 7

US-08-350-741-1/c
Sequence 1, Application US/08350741
Patent No. 5804194
GENERAL INFORMATION:
APPLICANT: DOUGAN G.,
APPLICANT: CHARLES I.G.,
APPLICANT: HORMAECHÉ C.E.,
APPLICANT: JOHNSON K.S.,
APPLICANT: CHATFIELD S.N.
TITLE OF INVENTION: LIVE VACCINES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON and VANDERHYE PC
STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
CITY: ARLINGTON

STATE: VIRGINIA
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,741
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/340,741
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 07/952,737
FILING DATE: 30-NOV-1992
APPLICATION NUMBER: GB 9007194.5
FILING DATE: 30-MAR-1990
APPLICATION NUMBER: PCT/GB91/00484
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-158
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 395..1822
US-08-350-741-1

Alignment Scores:
Pred. No.: 249 Length: 1980
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-350-741-1 (1-1980)
QY 451 AlaGlyArgLeuSerSerLeu 458
Db 1331 GCTGGCGTCGACTTTCATCGCTT 1308

RESULT 8
US-08-463-875A-1/c
Sequence 1, Application US/08463875A
Patent No. 5980907
GENERAL INFORMATION:
APPLICANT: DOUGAN, Gordon
APPLICANT: CHARLES, Ian G.
APPLICANT: HORMAECH, Carlos E.
APPLICANT: JOHNSON, Kevin S.
APPLICANT: CHATFIELD, Steven N.
TITLE OF INVENTION: LIVE VACCINES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON and VANDERHYE PC
STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA

ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,875A
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/340,741
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 07/952,737
FILING DATE: 30-NOV-1992
APPLICATION NUMBER: GB 9007194.5
FILING DATE: 30-MAR-1990
APPLICATION NUMBER: PCT/GB91/00484
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-158
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 395..1822
US-08-463-875A-1

Alignment Scores:
Pred. No.: 249 Length: 1980
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 2 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-463-875A-1 (1-1980)
QY 451 AlaGlyArgLeuSerSerLeu 458
Db 1331 GCTGGCGTCGACTTTCATCGCTT 1308

RESULT 9
US-09-144-367-1/c
Sequence 1, Application US/09144367
Patent No. 6432639
GENERAL INFORMATION:
APPLICANT: Lichte, Jay
APPLICANT: Guido, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/09/144,367
CURRENT FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/058,612
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2759
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: CDS

; LOCATION: (70)...(1581)
; OTHER INFORMATION: Human CYP3A4 cDNA reference sequence
US-09-144-367-1

Alignment Scores:
Pred. No.: 344 Length: 2759
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 4 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-144-367-1 (1-2759)

Qy 361 ThrLeuPheHisThrPheTyAsp 368

Db 283 ACACCTTCCATACCTTTTATGAC 260

RESULT 10

US-08-961-527-222/c
; Sequence 222, Application US/08961527
; Patent No. 6420135

GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 391

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/961,527

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Brookes, A. Anders

; REGISTRATION NUMBER: 36,373

; REFERENCE/DOCKET NUMBER: FB340P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 222:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3236 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-08-961-527-222

Alignment Scores:
Pred. No.: 402 Length: 3236
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 4 Gaps: 0

US-09-697-089-2 (1-1024) x US-08-961-527-222 (1-3236)

Qy 688 ThrSerLeuArgLeuGlnIleIys 695

Db 2083 ACATCTTGAGGTGCACATATAA 2060

RESULT 11

US-09-353-585-4

; Sequence 4, Application US/09353585

; Patent No. 6287865

GENERAL INFORMATION:

; APPLICANT: Dixon, Mark S

; Jones, David A

; Jones, Jonathan DG

; TITLE OF INVENTION: Plant pathogen resistance genes and uses

; thereof

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nixon & Vanderhye PC

; STREET: 8th Floor, 1100 No. 6287865th Glebe Road

; CITY: Arlington

; STATE: Virginia

; COUNTRY: United States of America

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/353,585

; FILING DATE: 15-Jul-1999

; CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q

; 1/68

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/930,277

; FILING DATE: 27-OCT-1997

; APPLICATION NUMBER: PCT/GB96/00785

; FILING DATE: 01-APR-1996

; APPLICATION NUMBER: GB 9506658.5

; FILING DATE: 31-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Ms Mary J Wilson

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 620-69

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3573 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Tomato

; STRAIN: Cf2

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-353-585-4

Alignment Scores:
Pred. No.: 443 Length: 3573
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 4 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-353-585-4 (1-3573)

Qy 758 SerLeuGlyAsnLeuLysAsnLeu 765

Db 980 TCATTGGGAATCTGAAAACTTG 1003

RESULT 12

US-08-485-588-1/c
; Sequence 1, Application US/08485588
; Patent No. 5688938
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,588
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/005
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5275 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 515..3769
; OTHER INFORMATION:
US-08-485-588-1

Alignment Scores: 646 Length: 5275
Pred. No.:

Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 1 Gaps: 0
US-09-697-089-2 (1-1024) x US-08-485-588-1 (1-5275)
QY 331 LeuArGAsnLeuMetLysThrPro 338
|||||
Db 2433 TTGCGGAACCTTGATGACAGCGCC 2410
RESULT 13
US-08-484-565-1/c
; Sequence 1, Application US/08484565
; Patent No. 5763569
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,565
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/006
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5275 base pairs

```

; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5275 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 515..3769
; OTHER INFORMATION:
US-08-480-751-1

Alignment Scores:
Pred. No.: 646
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 0.78%
DB: 2

US-09-697-089-2 (1-1024) x US-08-480-751-1 (1-5275)

Qy 331 LeuAqAsnLeuMetLysThrPro 338
      |||||
Db 2433 TTCCGGAACTTGATGAGACGCC 2410

RESULT 15
US-08-943-986-1/c
; Sequence 1, Application US/08943986
; Patent No. 5962314
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,986
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,565
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117

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Mon Feb 3 14:11:33 2003

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> FILING DATE: 21 October, 1994
> APPLICATION NUMBER: U.S. 08/292,827
> FILING DATE: 23 August, 1994
> APPLICATION NUMBER: U.S. 08/141,248
> FILING DATE: 22 October, 1993
> APPLICATION NUMBER: U.S. 08/009,389
> FILING DATE: 23 February, 1993
> APPLICATION NUMBER: U.S. 08/017,127
> FILING DATE: 12 February, 1993
> APPLICATION NUMBER: U.S. 07/934,161
> FILING DATE: 21 August, 1992
> APPLICATION NUMBER: U.S. 07/834,044
> FILING DATE: 11 February, 1992
> APPLICATION NUMBER: U.S. 07/749,451
> FILING DATE: 23 August, 1991
> ATTORNEY/AGENT INFORMATION:
> NAME: Heber, Sheldon O.
> REGISTRATION NUMBER: 38,179
> REFERENCE/DOCKET NUMBER: 213/006
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: (213) 489-1600
> TELEFAX: (213) 955-0440
> TELEX: 67-3510
> INFORMATION FOR SEQ ID NO: 1:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 5275 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: single
> TOPOLOGY: linear
> MOLECULE TYPE: cDNA to mRNA
> FEATURE:
> NAME/KEY: CDS
> LOCATION: 515..3769
> OTHER INFORMATION:
> US-08-943-986-1

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Alignment Scores:	646	Length:	5275
Pred. No.:	8.00	Matches:	8
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	0.78	Gaps:	0
DB:	2		

US-09-697-089-2 (1-1024) x US-08-943-986-1 (1-5275)

Qy 331 LeuArgAsnLeuMetLysThrPro 338

Db 2433 TTGCGGAACTTGATGAAGACGCC 2410

Search completed: January 31, 2003, 07:12:50
Job time : 106 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2003, 06:19:11 ; Search time 110 Seconds

(without alignments)
4182.247 Million cell updates/sec

Title: US-09-697-089-2

Perfect score: 1024

Sequence: 1 MNFKDNRSLRIQRMGTVI.....WQFDDDLVITGAFKLVT A 1024

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 396772 seqs, 224632407 residues

Word size: 1

Total number of hits satisfying chosen parameters: 792425

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : PublishedApplications_NA:

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1024	100.0	3133	10	US-09-841-739-1
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c	5	827	80.8	3615	10	US-09-841-739-12	Sequence 12, Appl
	6	721	70.4	3396	9	US-09-864-921-96	Sequence 96, Appl
	7	271	26.5	1395	9	US-09-864-921-98	Sequence 98, Appl
	8	232	22.7	891	9	US-09-864-921-179	Sequence 179, Appl
	9	206	20.1	618	9	US-09-864-921-181	Sequence 181, Appl
	10	154	15.0	768	9	US-09-864-921-102	Sequence 102, Appl
	11	150	14.6	608	10	US-09-764-864-339	Sequence 339, Appl
	12	97	9.5	522	10	US-09-764-864-754	Sequence 754, Appl
	13	89	8.7	578	9	US-09-864-921-100	Sequence 100, Appl
	14	87	8.5	261	9	US-09-864-921-177	Sequence 177, Appl
	15	80	7.8	421	10	US-09-864-761-4236	Sequence 4236, Ap
	16	73	7.1	220	10	US-09-864-761-20988	Sequence 20988, A
	17	36	3.5	165	9	US-09-864-921-183	Sequence 183, Appl
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	20	9	0.9	331	10	US-09-878-574-2550	Sequence 2550, Ap
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	23	9	0.9	2631	10	US-09-815-242-3821	Sequence 3821, Ap
	24	9	0.9	2643	10	US-09-815-242-6578	Sequence 6578, Ap
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c	45	8	0.8	606	10	US-09-951-470-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-3

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Score: 1024.00 Matches: 1024
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

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Qy 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLys 60
Db 121 ATTTGCTCGGAAAGGTGGAGCAGATGCTGTAGAGGATCATTCACATGATTTTGAA 180
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Db 2941 CCAGCATTAGTCAGAAACTTAGCCAAAGTGTATCCAAGTTAACTTTCTGCAAGAGCT 3000
QY 1001 ArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
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RESULT 2

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; Sequence 1, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)....(3107)
US-09-841-739-1
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Score: 1024.00 Matches: 1024
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Qy LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
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Qy PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr 460
Db 1356 TTCTTTTCAAGTCAATCCAGAGTATACAGCAGGAGGAGACTCAGCAGTTTATTGACG 1415
Qy SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db 1416 TCTCATGAGCCAGAGGAGGTGACCAGGGGAATGGTTACTTGCAGAAATGGTTTCCATT 1475
Qy SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
Db 1476 TCGGACATTACATCCATTATAGCAGCTGCTCCGGTACACCTGTGGGTCACTGTGGAA 1535
Qy AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520
Db 1536 GCCACAGGGGTGTATCAAGACCTCGCAGCAGTGTATCAACACGGCTGCTTCGGA 1595
Qy LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr 540
Db 1596 CTTTCCATCGCCAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGGTGGAAGAACACC 1655
Qy ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db 1656 ACTGAGCAAGAAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGGGCATCCAT 1715
Qy LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
Db 1716 TTATATCAAGAGGTACATCAAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAA 1775
Qy GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAppPheGlu 600
|||||

Db 1776 GGTAAAAAGCTTATATATCAACTCAGGGAACATCCCGATTACTTATTATTGACTTCTTTGAA 1835
Qy HisLeuProAsnCysAlaSerAlaLeuAuspPheIleLysLeuAuspPheTyrGlyGlyAla 620
Db 1836 CATTTGCCCAATTTGCAAGTGTCTGTGACTTCATTTAACTGGACTTTTATGGGGAGCT 1895
Qy MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640
Db 1896 ATGGCTTCATGGGAAAAAGGCTGCAGAGACACACAGTGAATCCACATGGAAGAGGCCCA 1955
Qy GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660
Db 1956 GAAACCTACATTTCCAGCAGGGCTGTATCTTTGTCTTCACTGGAAGCAGGAATTCAGG 2015
Qy ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
Db 2016 ACTCTGAGGTCACACTCCGGATTTTCAGCAAGTTGAATAAGCAAGATATCAATATCTG 2075
Qy GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
Db 2076 GGGAAATATTTCAGCTCTGCCACAAGCTCAGGCTGCAAAATAAAGAGATGTCTGGTGTG 2135
Qy AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
Db 2136 GCTGGAGGCTCAGTTTGGTCTCAGCACCTGTGAAGAACATTTATTCTCATGGTGAA 2195
Qy AlaSerProLeuThrIleGluAuspGluArgHisIleThrSerValThrAsnLeuLysThr 740
Db 2196 GCCAGTCCCTCACCATTAGAAGATGAGAGGCACATCATCTGTAAACAACTGAAACCC 2255
Qy LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Db 2256 TTGAGTATTTCATGACCTACAGAAATCAACGGCTGCGGGTGTCTGACTGACAGCTTGGT 2315
Qy AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAla 780
Db 2316 AACTTGAAGAACCTTACAAAGCTCATATGGATAACATAAAGATGAATGAAGAAGATGCT 2375
Qy IleLysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHis 800
Db 2376 ATAAACTAGCTGAAGCCTGAAACCTGAAAGAGATGTGTTTATTTCATTGACCCAC 2435
Qy LeuSerAspIleGlyGlyGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
Db 2436 TTGTCTCAGATTGGAGAGGGAATGGATTACATAGTCAAGTCTCTCTCAAGTGAACCTGT 2495
Qy AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
Db 2496 GACCTTGAAGAAATCAATTAGTCTCTCTGCTGCTGTGCAAAATGCAGTGAATACTCTA 2555
Qy AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Db 2556 GCTCAGAACTTTCACAAATTTGGTCAAACTGAGCATCTTGATTATCAGAAAAATACCTG 2615
Qy GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
Db 2616 GAAAAAGATGAAATGAAGCTCTTTCATGACTGATCGACAGGATGAAGCTGTGAACAG 2675
Qy LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
Db 2676 CTCACCCACTGATGTGCTCCCTGGGGCTGTGACGTGAAGGACCCCTGAGCAGGCTGTG 2735
Qy LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920
Db 2736 AAACATTTGGAGGAGGTCACACAACTCGTCAAGCTTGGTTGAAAACTGGAGACTCACA 2795
Qy AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 2796 GATACAGAGATTAGAAATTTTAGTGTCAATTTTGGAAAGAACCCCTCTGAAAAACTTCAG 2855
Qy GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyVal 960
Db 2856 CAGTTGAATTTGGCGGGAAATCGGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGA 2915

Db 2176 TCAGCCCTGAGCCAAAGAAATTGAAAGCTTTCTTCAAGGTAAAGCTTATATATCAACTCA 2235
Qy GlyAsnIleProAspTyrLeuPheAspPheGluHisLeuProAsnCysAlaSerAla 608
Db 2236 GGGAAACATCCCGAATTACTTATTGACTCTTTGAAACATTTGGCCCAATTTGGCAAGTGCC 2295
Qy 609 LeuAspPheIleLeuAspPheTyrGlyAlaMetAlaSerTyrGluLeuAlaAla 628
Db 2296 CTGACTTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTGCA 2355
Qy 629 GluAspThrGlyIleHisMetGluAlaProGluThrTyrIleProSerArgAla 648
Db 2356 GAAGACACAGGTGAATCCACATGAAGAGGCCCCAGAAACCTACATTCACAGAGGCT 2415
Qy 649 ValSerLeuPheAsnTyrLeuGluPheArgThrLeuGluValThrLeuArgAsp 668
Db 2416 GTATCTTTGTTCTCACTGGAACAGAGATTCAGGACTCTGGAGGTCACACTCCGGAT 2475
Qy 669 PheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePheSerSerAlaTh 688
Db 2476 TTCAGCAAGTTGAATAAGCAAGATATCAG-ATATCTGGGGAATAATTTCAGCTCTGCCAC 2534
Qy 688 rSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuValLe 708
Db 2535 AAGCCTCAGGCTGCAATAAAGAGATGTCGTGGTGGAGCCCTCAGTTTGGTCCCT 2594
Qy 708 uSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAs 728
Db 2595 CAGCACCTGTGAAGAACATTTATCTCTCATGGTGGAGCCAGTCCCTCCACATAGAGA 2654
Qy 728 pGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAs 748
Db 2655 TGAGAGGCACATCATCTCTTAACAAACCTGAAACCTTGAGTATTTCATGACCTTACAGAA 2714
Qy 748 nGluArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLe 768
Db 2715 TCAACGGCTGCCGGGTGGTCTGACTGACAGCTTGGGTGAACCTTGGAAGAACCTTACAAAGCT 2774
Qy 768 uIleMetAspAsnIleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLy 788
Db 2775 CATATGGATTAACATAAGATGAATGAAGAGATGCTATAAACTAGCTGNAAGCCCTGAA 2834
Qy 788 sAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGlyLyme 808
Db 2835 AAACCTGAAGAAGATGTGTTATTTCATTTCACCCACTTGTCTGACATTTGGAGAGGAAT 2894
Qy 808 tAspTyrIleValLysSerLeuSerGluProCysAspLeuGluIleGlnLeuVa 828
Db 2895 GGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGTGACCTTGAAGAAATTCAAATTAGT 2954
Qy 828 lSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuVa 848
Db 2955 CTCCTGCTGTCTGCTCAATGACAGTGAATAATCCTAGCTCAGAACTTTCACAAATTTGGT 3014
Qy 848 lLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLe 868
Db 3015 CAAACTGAGCATTTCTGATTATACAGAAATTTACCTGGAAAAAGATGGAATGAAGTCT 3074
Qy 868 uHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTr 888
Db 3075 TCATGAATGATCAGACAGGATGAACGTGTAGAACAGCTCACCCGACTGATGCTGCCCTG 3134
Qy 888 pGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGl 908
Db 3135 GGGCTGTGACGTGAAGGACGCTGAGCAGCTGTTGAAACATTTGGAGAGGTCGCCACA 3194
Qy 908 nLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAspThrGluIleArgIleLeuGl 928
Db 3195 ACTGCTCAAGCTTGGTGTGAAACTGGAGACTCACAGATACAGAGATTAGAAATTTAGG 3254
Qy 928 yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnAr 948

Db 3255 TGCATTTTTTGGAAAGAACCCCTCTGAAAAACTTCCAGCAGTTGAATTTGGCGGGAATPCG 3314
Qy 948 qValSerSerAspGlyTyrLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuVa 968
Db 3315 TGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGTTATTTGAGAAATCTTAAGCAATTAGT 3374
Qy 968 lPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSe 988
Db 3375 GTTTTTTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTAG 3434
Qy 988 rGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTyrGlnPheAs 1008
Db 3435 CCAAGTGTATCCAAAGTTAACTTTTCTCAAGAAAGTAGGCTTGTGGGTGGCAATTGA 3494
Qy 1008 pAspAspLeuSerValIleThr 1016
Db 3495 TGATGATGATCTCACTGTTATTACA 3519
RESULT 4
US-09-841-739-4
; Sequence 4, Application US/09841739
; Patent No. US20020094784A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841.739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID. NO. 4
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3612)
US-09-841-739-4
Alignment Scores:
Pred. No.: 0 Length: 3615
Score: 827.00 Matches: 927
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 80.76% Indels: 2
DB: 10 Gaps: 0
US-09-697-089-2 (1-1024) x US-09-841-739-4 (1-3615)
Qy 89 LeuPheHisGlnThrSerGluGlyAspLeuAspLeuAlaGlnAspLeuLysAspLeu 108
Db 736 CTTTTCATCAGACATCAGAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGACTTG 795
Qy 109 TyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleAspIlePhe 128
Db 796 TACCATACCCCATCTTTTCTGAACCTTTTATCCCTTGGTGAAGATATTCACATTATTTT 855
Qy 129 AsnLeuLysSerThrPheThrGluProValLeuThrPargLysAspGlnHisHisArg 148
Db 856 AACTTGAAGACACCTTCACAGAACCCTGCTGTGGAGGAGGACCAACACCATCACC 915
Qy 149 ValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlu 168
Db 916 GTGGAGCAGCTGACCCCTGAATGGCTCTTCAGAGCTCTTCAGAGCCCTTCATCATTTGAA 975
Qy 169 GlyClnSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTyrGlySer 188
Db 976 GGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGCGAATTCCTGCTGCGGCTCC 1035

Db 3195 ACTCGTCAAGCTTGGGTTGAAAACTCGGAGACTCAGACATACAGAGATTAGAAATTTTAGG 3254
Qy 928 yAlaPheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnAr 948
Db 3255 TGCATTTTGGAAAGAACCTCTGAAAACTCCAGCACTTGAATTTGGCGGAATCG 3314
Qy 948 gValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuVa 968
Db 3315 TGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGTATTTGAGAATCTTAAGCAATTAGT 3374
Qy 968 lPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValargLysLeuSe 988
Db 3375 GTTTTTTGACTTTAGTACTAAGAAATTTCTACCTGATCCAGCAATTAGTCAGAAAACCTAG 3434
Qy 988 rGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAs 1008
Db 3435 CCAAGTGTATCCAAGTTAACTTTCTGCAAGAGCTAGGCTTGTGGGTGGCAATTTGA 3494
Qy 1008 pAspAspLeuSerValIleThr 1016
Db 3495 TGATGATGATCTCAGTGTATTACA 3519

RESULT 5

US-09-841-739-12/c

; Sequence 12, Application US/09841739

; Patent No. US20020034784A1

; GENERAL INFORMATION:

; APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

; FILE REFERENCE: 07334-329001

; CURRENT APPLICATION NUMBER: US/09/841,739

; CURRENT FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: US 09/697,089

; PRIOR FILING DATE: 2000-10-26

; PRIOR APPLICATION NUMBER: US 60/161,822

; PRIOR FILING DATE: 1999-10-27

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 3615

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-841-739-12

Alignment Scores:

Pred. No.:	0	Length:	3615
Score:	827.00	Matches:	927
Percent Similarity:	99.78%	Conservative:	0
Best Local Similarity:	99.78%	Mismatches:	1
Query Match:	80.76%	Indels:	2
DB:	10	Gaps:	0

US-09-697-089-2 (1-1024) x US-09-841-739-12 (1-3615)

Qy 89 LeuPheHisGlnThrSerGluGlyAspLeuAspLeuAlaGlnAspLeuLysAspLeu 108
Db 2880 CTTTTCATCAGACATCAGAAAGGAGACTTGGCAGATTGGCTCAGGATTTAAAGGACTTG 2821
Qy 109 TyrHisThrProSerPheLeuAsnPheThrProLeuGlyGluAspIlePhe 128
Db 2820 TACCATACCCCACTTTTCTGAACCTTTATCCCTTGGTGAAGATATGACATATTTT 2761
Qy 129 AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHisHisArg 148
Db 2760 AACTTGAAGAGACCTTCACAGAACCTGCTCTGGAGGAAGGACCAACACCATCCGC 2701
Qy 149 ValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleLeuGlu 168
Db 2700 GTGAGCAGCTGACCTGAAATGGCTCTCGAGGCTCTTCAGAGCCCTTCATCATTTGA 2641
Qy 169 GlyGluSerGlyLysLysSerThrLeuGlnArgIleAlaMetLeuTrpGlySer 188
Db 2640 GGGAAATCTGGCAAGGCAAGTCCACTCTCTGCAGCGAAATGCCATGCTCTGGGGCTCC 2581


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QY 549 IleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLys 568
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Db 1500 ATAAACATCAATTCCTTTGTAGAGTGTGGCAATCCATTTATATCAAGAGTAGATCCAAA 1441
QY 569 SerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSer 588
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Db 1440 TCAGCCCTGAGCCAGCAAAATTTGAAGCTTCTCTTCAAGGTAAAGCTTATATATCAACTCA 1381
QY 589 GlyAsnIleProAspTyrLeuPheAspPhePheGluHisLeuProAsnCysAlaSerAla 608
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Db 1380 GGAACATCCCCGATTACTATTGTGACTTCTTTGACATTTGCCCAATTTGTGCAAGTGCC 1321
QY 609 LeuAspPheIleLysLeuAspPheTyrGlyGlyAlaMetAlaSerTyrGluLysAlaAla 628
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Db 1320 CTGGACTTCATTAACATGGACITTTATGGGGAGCTATGCTTCATGGGAAAGGCTGCA 1261
QY 629 GluAspThrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSerArgAla 648
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Db 1260 GAAGACACAGGTGGAATCCACATGGAGAGGCCCAAGAACCTTACATTTCCAGCAGGGCT 1201
QY 649 ValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuArgAsp 668
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Db 1200 GATCTCTTGTCTTCAACTGGAGAGCAAGAAATTCAGGACTCTGGAGGTCACACTCCGGGAT 1141
QY 669 PheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePheSerSerAlaTh 688
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Db 1140 TTCAGCAAGTGAATAAGCAAGATATCAG-ATATCTGGGGAATAATTCAGCTCTGCCAC 1082
QY 688 rSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaLaglySerLeuSerLeuValle 708
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Db 1081 AAGCCCTCAGCGCTGCAAAATAAGAGATGTGCTGTGTGGTGGAGGCTCAGTTTGGTCTCT 1022
QY 708 uSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAs 728
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Db 1021 CAGCAGCTGTAGAACAATTTATCTCTCATGTGGGAAGCAGTCCCTCACCATAGAAGA 962
QY 728 pGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAs 748
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Db 961 TCAGAGGCACATCACATCTGTAAACAACTGAAACCTTGAGTATTCATGACCTACAGAA 902
QY 748 nGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLe 768
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Db 901 TCACCGCTGCGCGGGTGTGACTCACAGCTTGGGTAACTTGAAGAACTTACAAAGCT 842
QY 768 uIleMetAspAsnIleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLy 788
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Db 841 CATATGGATACATAAAGATGAATCAAGAGATGCTATAAACTAGCTGAAGGCTGAA 782
QY 788 sAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGlyMe 808
|||||
Db 781 AAACCTGAAGAAGATGTGTTATTTTCAATTTGACCCACTTGTCTGACATTTGGAGAGGGAAT 722
QY 808 tAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuVa 828
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Db 721 GGATTACATAGTCAAGCTCTGTCTCAAGTGAACCTCTGACCTTGAAGAAATTCAAATTAGT 662
QY 828 lSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuVa 848
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Db 661 CTCCTGCTGCTGTCTGCAAAATGCAGTGAAATCTCTAGCTCAGATCTTCACAAATTTGGT 602
QY 848 lLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLe 868
Db 601 CAAACTGAGCATCTCTTGATTTATCAGAAAAATACCTGGGAAAAAGATGGAATCAACTCT 542
QY 868 uHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTr 888
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Db 541 TCATGAACCTGATCGACAGATGAACGTGTAGAACAGCTCAGCGCACTGATGCTGCCCTG 482
QY 888 pGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGl 908
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Db 481 GGCTGTGACGTGCAAGGAGCGCTGAGCAGCCTGTGTGAACAATTTGGAGGAGGTCCACCA 422
QY 908 nLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGl 928
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Db 421 ACTCGTCAAGCTGGGTGGAAACCTGGAGACTCACAGATACAGATTTAGG 362
QY 928 yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnAr 948
|||||
Db 361 TGCATTTTGGAAAGAACCTCTGAAAACTTTCCAGCAGTTGAATTTGGCGGAAATCG 302
QY 948 gValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuVa 968
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Db 301 TGGACAGCTGATGGATGGCTTGCCTTCATGGGTGTTATTGAGAACTTTAAGCAATTAGT 242
QY 968 lPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSe 988
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Db 241 GTTTTGTAGCTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTAG 182
QY 988 rGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAs 1008
Db 181 CCAAGTGTATCCAACTTAACCTTTCTGCAAGAAAGTAGCTTTGTTGGGTGGCAATTTGA 122
QY 1008 pAspAspAspLeuSerValIleThr 1016
Db 121 TGATGATGATCTCAGTGTATTACA 97
RESULT 6
US-09-864-921-96
; Sequence 96, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1e1 Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/379,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(3348)
US-09-864-921-96
Alignment Scores:
Pred. No.: 0 Length: 3396
Score: 721.00 Matches: 1021
Percent Similarity: 99.42% Conservativeness: 0
Best local Similarity: 99.42% Mismatches: 3
Query Match: 70.41% Indels: 6
DB: 9 Gaps: 0
US-09-697-089-2 (1-1024) x US-09-864-921-96 (1-3396)
QY 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
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Db 277 ATGAATTTCAATAAGGACAATAGCCAGCCCTTATTTCAAAGAATGGGAATGACTGTATA 336
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Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
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Db 337 AAGCAATACAGATGACCTATTGTATGAATGTTCTGAATCGCAAGAAAGTAACATC 396
Qy 41 IleCysCysGluLysValGluClnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60
|||||
Db 397 ATTTCGCTCGAAGAGGTGGAGCAGGATGCTGTAAGGGATCAATTCACATGATTGTGAA 456
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
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Db 457 AAGGTTGAGAGTCTGTAACTCTTTCTTAATCCCTTAAGGAGTGAACATCTCCTCTA 516
Qy 81 PheGlnAspLeuAsnGlyClnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
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Db 517 TTTCAGGACTTGAATGGACAAAGTCTTTTCATCAGACATCAGAAGGAGACTTGGACGAT 576
Qy 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120
|||||
Db 577 TTGGCTCAGGATTTAAGGACTTGTACCATACCCCATCTTTCTGAACCTTTTATCCCTT 636
Qy 121 GlyGluAspIleAspIlePheAsnLeuLysSerThrPheThrGluProVal -LeuTr 140
|||||
Db 637 GGTGAAGATATGACATATTTTAACTTGAAGACCCTTCACAGAACCTAT -CCTGTG 695
Qy 140 pArgLysAspGlnHisHisArgValGluClnLeuThrLeuAsnGlyLeuLeuGlnAl 160
|||||
Db 696 GAGGAAGGACCAACACCATCACCGCGTGGAGCGTGAACCTGAATGCGCTCTGCAGGC 755
Qy 160 aLeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuG1 180
|||||
Db 756 TCTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCA 815
Qy 180 nArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVa 200
|||||
Db 816 GCGCATTCGCATGCTCTGGGCTCCGGAAGTGCAGAGCTCTGACCAAGTTCAAAATTCGT 875
Qy 200 lPhePheLeuArgLeuSerArgAlaGlnGlyClyLeuPheGluThrLeuCysAspGlnLe 220
|||||
Db 876 CTTCTCTCCGCTCTCAGCAGGCGCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACT 935
Qy 220 uLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuAr 240
|||||
Db 936 CTGTATATCTGCAATCAGGAAGCAGACATTCATGGCCATTCATGCTGGAAGCTCGG 995
Qy 240 gGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProG1 260
|||||
Db 996 GCAGAGGCTCTTTTCCCTTCGTATGCTACAATGAATTCAGCCCAAGTCCGACG 1055
Qy 260 uIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrTh 280
|||||
Db 1056 AATCGAAGCCCTGATAAAGGAAACCCAGCTTCAAGAACATGCTCATCGTCACCACTAC 1115
Qy 280 rThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMe 300
|||||
Db 1116 CACTGAGTGCTGAGGCACATACGCGCAGTTGGTGGCCCTGACTGCTGAGGTGGGGATAT 1175
Qy 300 tThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluG1 320
|||||
Db 1176 GACAGAAGACACGCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGTGTAAG 1235
Qy 320 yLeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPh 340
|||||
Db 1236 CTGTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGAAATCTCATGAAGACCCCTCTCT 1295
Qy 340 eValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnTh 360
|||||
Db 1296 TGTGGTCACTACTGTGTGAATCCAGATGGGTGAAGTGAAGTTCACCTCTCACACACAAC 1355
Qy 360 rThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysG1 380
|||||
Db 1356 AACGCTGTTCCATACCTTCTATGATCTCTGATACAGAAAAACAAACAAACATAAAGG 1415
Qy 380 yValAlaAlaSerAspPheIleArgSerLeuAspHisCys -GlyAspLeuAlaLeuGluG 400
|||||

Db 1416 TGTGGCTCAAGTGACTTCATTCGAGCGCTGGACCACCG -TCGAGACCTAGTCTCTGGAGG 1474
Qy 400 lyValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspV 420
|||||
Db 1475 GTGTGTTCTCCCAAGAAGTTTGAATTCGAAGTCGAGGATGTGTCCAGCGTGAATGAGGATG 1534
Qy 420 alLeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrL 440
|||||
Db 1535 TCCTGCTGACAACTGGGCTCCTCTGTAATATACAGCTCAAAAGGTTCAAGCCAAAGTATA 1594
Qy 440 ysPhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuT 460
|||||
Db 1595 AATCTCTTCAAGTCAATTCAGGAGTACACAGCAGGACGAAGACTCAGCAGTTATTATGA 1654
Qy 460 hrSerHisGluProGluClnValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerI 480
|||||
Db 1655 CGTCTCATGAGCCAGAGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAATGGTTTCCA 1714
Qy 480 leSerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValG 500
|||||
Db 1715 TTTCCGACATTACATCCACTTATAGCAGCCTGCTCCGCTACACCTGTGGTCACTGTGG 1774
Qy 500 luAlaThrArgAlaValMetLysHisLeuAlaIleValTyrGlnHisGlyCysLeuLeuG 520
|||||
Db 1775 AAGCCACCAGGCGTGTATGAAGCACCTCGCAGCAGTGTATCAACACGCGTCCCTTCG 1834
Qy 520 lyLeuSerIleAlaLysArgProLeuTrpArgGlnGlnSerLeuGlnSerValLysAsnT 540
|||||
Db 1835 GACTTTCATCGCAAGAGGCTCTCTGGAGACAGGAATCTTGCAAAAGTGTGAAAAACA 1894
Qy 540 hrThrGluGlnGluLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleH 560
|||||
Db 1895 CCCTGAGCAGAAATCTGAAGCCATAAATCAATTCCTTTGTAGAGTGTGGCATCC 1954
Qy 560 isLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheG 580
|||||
Db 1955 ATTTATATCAAGAGAGTACATCCAAATCAGCCCTCAGCCCAAGAAATTTGAAGCTTCTTTC 2014
Qy 580 lGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheG 600
|||||
Db 2015 AAGTAAAGGCTTATATATCAACTCAGGAACATCCCCGATTACTTATTGACTTCTTTG 2074
Qy 600 luHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyA 620
|||||
Db 2075 AACATTTGCCCAATTTGTCAAGTGCCTGGACTTCATTTAAACTGGACTTTTATGGGGAG 2134
Qy 620 laMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaP 640
|||||
Db 2135 CTATGGCTTTCATGGGAAAGGCTGCAGAAAGCACAGGTGGAAATCCACATGGAAGAGGCC 2194
Qy 640 roGluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheA 660
|||||
Db 2195 CAGAAACCTACATTTCCAGCAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTC 2254
Qy 660 rgThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr -Tyr 679
|||||
Db 2255 GGACTCTGGAGGTCACACTCCGGGATTTCAAGAGTTGAATTAAGCAAGATATCAG -ATAT 2313
Qy 680 LeuGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysLagly 699
|||||
Db 2314 CTGGGGAATTTATTCAGCTCTGCCAAGCCTCAGGCTGCAAAATAAAGAGATGTCTCGT 2373
Qy 700 ValAlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetVal 719
|||||
Db 2374 GTGGTGAAGCCCTCAGTTTGGTCTCAGCAGCTGTGAAGAACATTTATCTCTCATGGTG 2433
Qy 720 GluAlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLys 739
|||||
Db 2434 GAAGCAGTCCCTCACCATAGAAGTGAAGGACACATCATCTGTAAACAAACCTGAAA 2493
Qy 740 ThrLeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeu 759
|||||


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Db 1141 TGGCTTGCTTCATCGGTGTATTTCAGAAATCTTAAGCAATAGTGTCTTTTGGACTTTAGT 1200
Qy 974 ThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnValLeuSerLys 993
Db 1201 ACTAAGAATTCACCTGATCCAGCATAGTCAGAAACTTAGCCAAAGTGTATCCAAAG 1260
Qy 994 LeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAspAspLeuSer 1013
Db 1261 TTAACCTTTCTGCAGAGCTAGCTGTGGTGCGCAATTTGATGATGATGATCTCAGT 1320
Qy 1014 ValIleThrGlyAlaPheLysLeuValThrAla 1024
Db 1321 GTTATTACAGGTGCTTTTAAACTAGTAACCTGCT 1353

RESULT 8
US-09-864-921-179
; Sequence 179, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(891)
US-09-864-921-179

Alignment Scores:
Pred. No.: 3,43e-236 Length: 891
Score: 232.00 Matches: 296
Percent Similarity: 99.33% Conservative: 0
Best Local Similarity: 99.33% Mismatches: 1
Query Match: 22.66% Indels: 2
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-921-179 (1-891)

Qy 161 LeuGlnSerProCysIleIleGluGlyCysSerGlyLysGlyLysSerThrLeuLeuGln 180
Db 1 CTTTCAGAGCCCTCATCATTTGAAGGGAATCTGCGAAGGCAAGTCCACTCTGCTGCAG 60
Qy 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db 61 CGCATTCGACGCTCGGGCTCGGAAGAGTGCAGAGGCTGACCAAGTTCAAATTCGTC 120
Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 220
Db 121 TTCCTCTCCGCTCTCAGCAGGCGCCAGGCTGTTTGAACCTCTGTGATCACTC 180
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240
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Db 181 CTGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTCAAGCTCGG 240
Qy 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
Db 241 CAGAGGGTCTCTTTTCCCTTCTTGATGGCTACAATGAATTCAGCCCAAGAACTGCCAGAA 300
Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280
Db 301 ATCGAAGCCCTGTAAAGAAACCCCGCTTCAAGAACATGGTCACTGCTCACCACCTACC 360
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
Db 361 ACTGAGTGCCTGAGGCACATACGCGCAGTTTGGTCCCTGACTGCTGAGGTGGGGATATG 420
Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
Db 421 ACAGAAGACAGCGCCCGAGGCTCTCATCCGAGAGTGTGATCAAGGAGCTTTCCTGAAAGC 480
Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
Db 481 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGATCTCATGAAGACCCCTCTCTTT 540
Qy 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
Db 541 GTGGTCATCACTTGTGCAATCCAGATGGTGAAAGTGAGTTCCACTCTCACACACAAACA 600
Qy 361 ThrLeuPheHisThrPheTyrAspLeuIleGlnLysAsnLysHisLysHisLysGly 380
Db 601 ACGCTGTTCATCACTCTTATGATCTGTGATACAGAAAAACAACACAAACATAAAAGGT 660
Qy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCys-GlyAspLeuAlaLeuGluGly 400
Db 661 GTGGCTGCAAGTGATTCATTCGGAGCGCTGGACCACCG-TGGAGACCTAGCTCTGGAGGG 719
Qy 400 yValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVa 420
Db 720 TGTGTTCTCCCAAGTTGATTTCGAACCTGCAGGATGTGTCAGCGCTGAATGAGGATGT 779
Qy 420 LLeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLy 440
Db 780 CCGCTGCACAACTGGGCTCTCTCTGTAATAATACAGCTCAAGGTTCAAGCCAAAGTATA 839
Qy 440 sPhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSer 457
Db 840 ATCTCTTTCACAAAGTCATTCAGGAGTACACAGCAGGAGGAGAGACTCAGCACT 891

RESULT 9
US-09-864-921-181
; Sequence 181, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
```

PRESENT 11


```
; TITLE OF INVENTION: NO. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(552)
US-09-864-921-100

Alignment Scores:
Pred. No.: 7.64e-85 Length: 578
Score: 89.00 Matches: 89
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.69% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-921-100 (1-578)

Qy 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
|||||
Db 277 ATGAATTCATTAAGAGACATAAGCCAGCCCTTATCAAGAATGGGAATGACTGTATA 336
|||||

Qy 21 LysGlnIleThrAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIle 40
|||||
Db 337 AAGCAATACACAGATGACCTATTGTATGGAATGTTCTGAATCGCGAAGTAACATC 396
|||||

Qy 41 IleCysCysGluIysValGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
|||||
Db 397 ATTTGCTCGGAAGGTGGAGCAGGATGCTGTAGAGGGATCATTCACATGATTTTGAA 456
|||||

Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu 80
|||||
Db 457 AAGGGTTAGAGTCTGTGAACCTCTTTCTTAATCCCTTAAGGAGTGGAACTATCTCTA 516
|||||

Qy 81 PheGlnAspLeuAsnGlyGlnSerLeu 89
|||||
Db 517 TTTCAGGACTTCAATGGACAAAGTCTT 543
|||||

RESULT 14
US-09-864-921-177
; Sequence 177, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: NO. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
```

```
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(261)
US-09-864-921-177

Alignment Scores:
Pred. No.: 4.44e-83 Length: 261
Score: 87.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.50% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-921-177 (1-261)

Qy 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
|||||
Db 1 ATGAATTCATTAAGAGACATAAGCCAGCCCTTATCAAGAATGGGAATGACTGTATA 60
|||||

Qy 21 LysGlnIleThrAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIle 40
|||||
Db 61 AAGCAATACACAGATGACCTATTGTATGGAATGTTCTGAATCGCGAAGTAACATC 120
|||||

Qy 41 IleCysCysGluIysValGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
|||||
Db 121 ATTTGCTCGGAAGGTGGAGCAGGATGCTGTAGAGGGATCATTCACATGATTTTGAA 180
|||||

Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu 80
|||||
Db 181 AAGGGTTAGAGTCTGTGAACCTCTTTCTTAATCCCTTAAGGAGTGGAACTATCTCTA 240
|||||

Qy 81 PheGlnAspLeuAsnGlyGln 87
|||||
Db 241 TTTCAGGACTTGAATGGACAA 261
|||||

RESULT 15
US-09-864-761-4236
; Sequence 4236, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4236
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011232.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 16
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
US-09-864-761-4236

Alignment Scores:
Pred. NO.: 1.9e-75 Length: 421
Score: 80.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.81% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-761-4236 (1-421)

Qy	928	GlyAlaPheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsn	947
Db	181	GGTCATATTTTGAAAGAACCCCTCTGAAAACACTCCAGCAGTTGAATTTGGCGGGAAT	240
Qy	948	ArgValSerSerAspGlyTyrLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeu	967
Db	241	CGTGTGACGACGTATGATGGCTTCCTTCATGGGTGATTTGAGAATCTTAACCAATTA	300
Qy	968	ValPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeu	987
Db	301	GTGTTTTTTGACTTTAGTACTAAAGAATTTCTACCTCATCCAGCATTTAGTCAGAAAACCTT	360
Qy	988	SerGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTyrGlnPhe	1007
Db	361	AGCCAAGTGTATCCAAAGTTAACTTTCTTCTGCAAGAACGTAGGCTTGTGGTGGCAATTT	420

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Job time : 151 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2003, 04:27:08 ; Search time 5176 Seconds
(without alignments)
4974.093 Million cell updates/sec

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Perfect score: 1024
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 24791104 seqs, 12571243825 residues

Word size: 1

Total number of hits satisfying chosen parameters: 49569006

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1024	100.0	3072	32	US-09-841-739-3
4	1024	100.0	3133	1	PCT-US00-29643-1
5	1024	100.0	3133	27	US-09-697-089-1
6	1024	100.0	3133	32	US-09-841-739-1
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					Sequence 3, Appli
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7 923 90.1 3075 41 US-10-156-733-1
8 923 90.1 3219 41 US-10-156-733-14
9 922 90.0 3213 41 PCT-US01-07143-23
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ALIGNMENTS

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; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: DNA
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; TYPE: DNA
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US-09-697-089-3

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Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220
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Db 721 CAGAGGGTCTTTCCTTCTGTATGGCTCAATGAATCAAGCCGCCCAAGTGGCCAGAA 780
Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280
Db 781 ATCGAAGCCCTGATAAAGGAACACACCGCTTCAAGAACATGGTCATCGTCACCACACTACC 840
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
Db 841 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTCCCTGACTGTGAGGTGGGGATATG 900
Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
Db 901 ACAGAAGACAGCCCGCCGCTCTCATCCGAGAGTGTGATCAGGAGCTTGTCTGAGAGGC 960
Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
Db 961 TTGTTTGCCTCAAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTT 1020
Qy 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
Db 1021 GTGGTCATCATTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACACAACA 1080
Qy 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly 380
Db 1081 ACGCTGTTCCATACCTCTATGATCTGTGTATACAGAAAAACAACAACATAAAGGT 1140
Qy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
Db 1141 GTGGCTGCAAGTGACTTTCATTCGGAGCCTGGACCCTGTGAGACCTAGCTCTGAGGGT 1200
Qy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Db 1201 GTGTTCTCCACAGTTTTGATTTGAACTGCGAGGATGTGCCAGCGTGAATGAGGATGTC 1260
Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
Db 1261 CTGCTGACAACTGGCTCTCTGTAATATACAGCTCAAGAGTTCAAGCCAAAGTATANA 1320
Qy 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuThr 460
Db 1321 TTCCTTCAAGTCAATCCAGGAGTACACAGCAGGACGAGACATCAGCAGTTTATTGAGC 1380
Qy 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db 1381 TCTCATGAGCCAGAGGAGTGCACCAAGGGGAATGGTACTTTCAGAAAAATGGTTTCCATT 1440
Qy 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
Db 1441 TCGGCATTTACATCCCTTTATAGCAGCCTGCTCCGGTACACTGTGGGTCACTGTGGAA 1500
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520
Db 1501 GCCACCAGGGCTGTATGAGCACCCTCCGACAGTGTATCAACAGGGTGCCTCTCGGA 1560
Qy 521 LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr 540
|||||

Db 1561 CTTTCCATCGCCAAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1620
Qy 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db 1621 ACTGAGCAAGAANAATCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680
Qy 561 LeuTyrGlnGlnSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
Db 1681 TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAATTTGAAGCTTCTTTTCAA 1740
Qy 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu 600
Db 1741 GGTAAAAGCTTATATATCACTCAGGGAACATCCCGGATTACTTTATTTGACTTCTTTTCAA 1800
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla 620
Db 1801 CATTTGGCCAAATTTGCAAGTGTCTGGACATTCATTAACCTGGACATTTTATGGGGAGCT 1860
Qy 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640
Db 1861 ATGGCTTCATGGGAAAAGGCTGCAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1920
Qy 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660
Db 1921 GAAACCTACATCCAGCAGGGCTGTATTTTGTCTTCAACTGGAAGCAGGAATTCAGG 1980
Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
Db 1981 ACTCTGGAGGTCACACTCCGGGATTTCAGCAAGTTGAATAGCAAGATATCACATATCTG 2040
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
Db 2041 GGGAAAAATATTCAGCTCTGCCACAAAGCTCAGGCTGCAAAATAAAGAGATGTGCTGGTGTG 2100
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
Db 2101 GCTGGAAGCCCTCAGTTTGGTCTCAGCACCTGTGAAGACATTTATTTCTCATGGTGAA 2160
Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
Db 2161 GCCAGTCCCCTCACCATAGAAGATGAGAGGCACATCATCTGTAAACAACCTGNAACACC 2220
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Db 2221 TTGAGTATTCATGACCTACAGAAATCAACGGCTGCGGGTGTCTCTGACTCAGACGTGGGT 2280
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780
Db 2281 AACTGAAGAACCCTACAAAGCTCATATGGATAACATAAAGATGAATGAAGAAGATGCT 2340
Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHis 800
Db 2341 ATAAACTAGCTGAGGCTGAAAAACCTGAAGAAGATGTGTATTATTTCAATTTGACCAC 2400
Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
Db 2401 TTGCTGCATATTGGAGAGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCGTGT 2460
Qy 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
Db 2461 GACCTTGAAGAAATTCAAATTAAGTCTCTGCTGTGTGTGTGCAAAATGCAAGTGAATCCTA 2520
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Db 2521 GCTCAGAAATCTTCAAAATTTGGTCAAACTGAGCATCTTTGATTTATTCAGAAAAATTCCTG 2580
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGluGln 880
Db 2581 GAAAAAGATGGAATGAAGCTTTCATCACTGATCGACAGATGACAGTCTAGACAG 2640
Qy 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
Db 2641 CTCACCGACTGATGCTGCCCTGGGGGTGTGACGTGAAGCAGCCTGAGCAGCCTGTGTG 2700
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QY 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920
|||||
Db 2701 AAACATTGGAGAGTCCCAACACTCGTCAAGCTTGGGTGGAAGAACTGGAGACTCACA 2760

QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
|||||
Db 2761 GATACAGAGATTAGAATTTTAGGTGCATTTTGGGAAAGAAACCTCTGAAAAAATTTCCAG 2820

QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960
|||||
Db 2821 CAGTTGAATTTGGCGGAATCGTGAGCAGTGATGGATGGCTTGCCCTTCATGGGTGTA 2880

QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
|||||
Db 2881 TTTGAGAACTTAAGCAATTAGTGTGTTTGTGACTTGTAGTACTAAAGAAATTTCTACCTGAT 2940

QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
|||||
Db 2941 CCAGCAATTAGTCAGAAACTTAGCCAAGTGTATCCAAGTTAACTTTTCTGCAAGAAGCT 3000

QY 1001 ArgLeuValClyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
|||||
Db 3001 AGCCTTGTGGGTGGCAATTTGATGATGATGATCTCAGTGTATTACAGGTGCTTTTAA 3060

QY 1021 LeuValThrAla 1024
|||||
Db 3061 CTAGTAACGTCT 3072

RESULT 4
PCT-US00-29643-1
; Sequence 1, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
PCT-US00-29643-1

Alignment Scores:
Pred. No.: 0 Length: 3133
Score: 1024.00 Matches: 1024
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x PCT-US00-29643-1 (1-3133)

QY 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
|||||
Db 36 ATGAATTTTCATAAAGGACATAAGCCGAGCCCTTATTCAAGAATGGGAATGACTGTATTA 95

QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
|||||
Db 96 AAGCAATCACAGATCACCTATTGTGTAATGTAATGTTCTGAATCGCGAAGAAGTAACATC 155

QY 41 IleCysCysLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
|||||
Db 156 ATTTGCTCGGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 215
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QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu 80
|||||
Db 216 AAGGGTTCAGAGTCCGTGAACCTCTTCTTAATCCCTTAAGGAGTGAACACTATCTCTTA 275

QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
|||||
Db 276 TTTTCAGGACTTGAATGCACAAAGCTCTTTTTCATCAGACATCAGAAGGAGACTTGGAGCAT 335

QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTrpProLeu 120
|||||
Db 336 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACATTTTATCCCTTT 395

QY 121 GlyGluAspIleAspIleLeuPheAsnLeuLysSerThrPheThrGluProValLeuTrp 140
|||||
Db 396 GGTGAAGATATTGACATATTATTTTAACTTGAAGAACACCTTCACAGAACCTGTCTGTGG 455

QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
|||||
Db 456 AGAAGGACCAACACCATCACCGCTGGAGCAGCTGACCTGAATGGCTCTCTCGCAGGCT 515

QY 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 180
|||||
Db 516 CTTTCAGAGCCCTCGCATCTATTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 575

QY 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
|||||
Db 576 CGCATTTGCCATGCTCTGGGCTCCGGNAAGTGAAGGCTGTGACCAAGTTCAATTCGCTC 635

QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220
|||||
Db 636 TTCTTCTCGCTCTCAGCAGGGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTC 695

QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240
|||||
Db 696 CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGTGAAGCTGCGG 755

QY 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
|||||
Db 756 CAGAGGGTCTCTTTCTCTTGTATGGCTACAATGAATTCAGCCCAAGAGCTGCCAGAA 815

QY 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280
|||||
Db 816 ATCGAAGCCCTGTATAAGGAAAAACCCCGCTTCAAGAACATGCTCATCGTCACACTACC 875

QY 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
|||||
Db 876 ACTGAGTGCTGAGGCACATACCGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGATATG 935

QY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
|||||
Db 936 ACAGAAGACAGCGCCCGAGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGTGAAGGC 995

QY 321 LeuLeuGlnGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
|||||
Db 996 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGAAATCTCATGAAGACCCCTCTCTTT 1055

QY 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
|||||
Db 1056 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAGTGAGTGTCCACTCTCACACACAACA 1115

QY 361 ThrLeuPheHisThrPheTrpAspLeuLeuIleGlnLysAsnLysHisLysLysGly 380
|||||
Db 1116 ACAGTGTTCATACCTTCTATGATCTGTGATACAGAAAAACAAACACAAATAAGGT 1175

QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
|||||
Db 1176 GTGGCTCAAGTGACTTCATTCGAGGCCTGGACACTGTGGAGACCTAGCTCTGGAGGT 1235

QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
|||||
Db 1236 GTGTTCTCCACAAGTTTGTATTTCGAACTGCAGATGTGTCAGCGGTGAATGAGGATGTC 1295
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Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
Db 1296 CTGCTGACAACTGGGCTCCTCTGTAATATATACAGCTCAAGGTTCAAGCCAAAGTATAAA 1355
Qy 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuThr 460
Db 1356 TTCCTTCAAGTCAATCCAGGAGTACACAGGAGTACAGGAGTATATGAGC 1415
Qy 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db 1416 TCTCATGAGCCAGAGGAGTCAACAGGGGAATGGTTACTTGCAGAAAATGGTTCCATT 1475
Qy 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
Db 1476 TCGGACATATACATCCACTATAGCAGCCTGCTCCGGTACACCTGTGGGTATCTGTGAA 1535
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuGly 520
Db 1536 GCCACCAGGGCTGTATGAAGCAGCTCGCAGCAGTGTATCAACACGGCTGCTTCTCGGA 1595
Qy 521 LeuSerIleAlaLysArgProLeuTriArgGlnGlnSerLeuGlnSerValLysAsnThr 540
Db 1596 CTTTCCATCGCAAGAGCCCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAACACC 1655
Qy 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db 1656 ACTGAGCAAGAATCTGAAAGCCATAAACATCAATCTCTTGTAGAGTGTGGCATCCAT 1715
Qy 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGlnPheGluAlaPhePheGln 580
Db 1716 TTATATCAAGAGTACATCCAAATCAGCCCTGAGCCAGGAATTTGAAGCTTTCTTTCAA 1775
Qy 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600
Db 1776 GGTAAAGCTTATATATCACTCAGGGAACATCCCGGATTAATTTGACTTCTTTGAA 1835
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620
Db 1836 CATTTGCCCAATTTGTCAAGTCTCTGGACTTCATTAACATGGACTTTATGGGGAGCT 1895
Qy 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640
Db 1896 ATGCTTTCATCGGAAAAGGCTGCAAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1955
Qy 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660
Db 1956 GAAACCTACATCCAGCAGGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGG 2015
Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
Db 2016 ACTCTGGAGGTCACACTCCGGGATTTGAGCAAGTTGAATAAGCAAGATATCACATATCTG 2075
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
Db 2076 GGGAAAATATTCAGCTCTGCCACAGGCTCAGGCTGCAAAATAAAGAGATGTGCTGGTGTG 2135
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
Db 2136 CTTGGAGCCCTCAGTTGGTCTCAGCACCTGTAGAACATTTATCTCTCATGGTGAA 2195
Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
Db 2196 GCCAGTCCCTCCACATAGAAGATGAGAGGCACATCATCTGTAACAAACCTGAAAACC 2255
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Db 2256 TTGAGTATTATGATACCTACAGAAATCAACGGCTGCGGGTGTCTGACTGACAGCTTGGGT 2315
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780
Db 2316 AACTTGAGAACTTACAAAGCTCATATGGATACATAAAGATGAATGAAGAAGAGTCT 2375
Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
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Db 2376 ATAAACTAGCTGAGGCGCTGAAAAACCTGAAGAAGATGTGTATTATTTCAATTGACCCAC 2435
Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
Db 2436 TTGCTGACATTTGAGAGGGAATGATATACATAGTCAAGTCTCTCTCAAGTGAACCCCTGT 2495
Qy 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
Db 2496 GACCTTGAAGAAATCAATTAGTCTCCTGCTGCTGTCTGCAAAATGCAGTGAATCCTA 2555
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Db 2556 GCTCAGAATCTTCAAAATTTGGTCAAACTGAGCATTTCTGATTATATCAGAAAAATACCTG 2615
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
Db 2616 GAAAAAGATGGAATGAAGCTCTTCATGACTGATCGACAGATGAAGCTGCTAGAACAG 2675
Qy 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
Db 2676 CTCACGCACTGATGCTGCCCTGGGCTGTGACGTGCAAGCAGCCTCAGCAGCCTGTG 2735
Qy 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920
Db 2736 AAACATTTGGAGAGGTCACCAACTCGTCAAGCTTGGGTTGAAAAAACCCTCTGAAAACTCCAG 2795
Qy 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 2796 GATACAGAGATTAGAAATTTTAGGTGCATTTTGGAAAGAACCCCTCTGAAAACTCCAG 2855
Qy 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyVal 960
Db 2856 CAGTTGAATTTGGCGGGAATCGGTGAGCAGTGTATGATGCTTGCCTTCATGGGTGTA 2915
Qy 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
Db 2916 TTTGAGAATCTTAAGCAATTAGTGTCTTTTACCTTACTAAGAAATTTCTACCTCAT 2975
Qy 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnAla 1000
Db 2976 CCAGCATTTAGTCAGAAAAACTTAGCCAGTGTATCCAAGTTAACTTTTCTGCAAGAGCT 3035
Qy 1001 ArgLeuValGlyTyrGlnPheAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3036 AGGCTTGTGGGTGCAATTTGATGATGATCATCTCAGTGTATTACAGGTGCTTTTAAA 3095
Qy 1021 LeuValThrAla 1024
Db 3096 CTAGTAACCTGCT 3107
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RESULT 5

US-09-697-089-1

; Sequence 1, Application US/09697089

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED

; FILE REFERENCE: 07334-136001

; CURRENT FILING DATE: 2000-10-26

; PRIOR FILING DATE: 1999-10-27

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 3133

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (36)...(3107)

US-09-697-089-1

Alignment Scores:

Pred. No.: 0 Length: 3133
Score: 1024.00 Matches: 1024
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 27 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-697-089-1 (1-3133)

Qy 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 36 ATGAATTCATAAAGAGCAATAGCGAGCCCTTATTCAAAGAAATGGGAATGACTGTATA 95
Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIle 40
Db 96 AAGCAAAATCACAGATGACCTATTGTATGGAATGTCTGAATCGGGAAGTAACATC 155
Qy 41 IleCysCysGluLysValGluGlnAspAlaAaArgGlyIleIleHisMetIleLeuLys 60
Db 156 ATTTCGCGGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 215
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu 80
Db 216 AAGGFTTCAGAGTCTGTAAACCTCTTCTTAATCCCTTAAGAGTGGAACTATCCTCTA 275
Qy 81 PheGlnAspLeuAsnGlyClnSerLeuPheHisGlnThrSerGluGlyAspLeuAsp 100
Db 276 TTTCAGGACTTGAATGGCAAAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGACGAT 335
Qy 101 LeuAlaGlnAspLeuLysAspLeuTrpHisThrProSerPheLeuAsnPheTrpProLeu 120
Db 336 TTGGCTCAGGATTAAGAGACTTGACCATACCCATCTTTCTGAACCTTTATCCCTT 395
Qy 121 GlyGluAspIleAspIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140
Db 396 GGTGAAGATATTGACATATTATTTAACTTGAAGACACCTTCACAGAACCTGTCTGTGG 455
Qy 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
Db 456 AGGAAGGACCAACACCATCACCGCTGGAGCAGCTGACCTGAATGGCTCTCGAGGCT 515
Qy 161 LeuGlnSerProCysIleIleGluGlySerGlyLysGlyLysSerThrLeuLeuGln 180
Db 516 CTTCAGAGCCCTGCATCATTTGAAGGGAATCTGGCAAGGCAAGTCCACTCTGTGCA 575
Qy 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db 576 CGCATTTGCCATGCTCTGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAAAATTCGTC 635
Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 220
Db 636 TTCTTCTCCGCTCAGCAGGCCCGAGGTGGACTTTTGAACCCCTCTGTGATCAACATC 695
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240
Db 696 CTGGATATACCTGGCAATCAGGAAGCAGACATTCATGGCCATGCTGTGAAGTGGCG 755
Qy 241 GlnArgValLeuPheLeuLeuAspGlyTrpAsnGluPheLysProGlnAsnCysProGlu 260
Db 756 CAGAGGTTCTTTCTCTTCTGATGCTACATGAATGAATCAAGCCCGCAGAACTGCCAGAA 815
Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280
Db 816 ATCGAAGCCCTGATAAAGAAAAACCCGCTTCAAGAACATGGTATCATCTCACCCTACC 875
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
Db 876 ACTGAGTCCCTGAGGCACATACGGCAGTTTGTGGCCCTGACTGCTGAGGTGGGGATATG 935
Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320

Db 936 ACAGAAGACAGCCCGCCAGGCTCTCATCCGAGAGTCTGATCAAGGAGCTTGTCTGAAGC 995
Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
Db 996 TTGTTGCTCCAAATTCAGAAATCCAGGTCCTGAGGAATCTCATGAAGACCCCTCTCTTT 1055
Qy 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
Db 1056 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCACCTCTCACACAAACA 1115
Qy 361 ThrLeuPheHisThrPheTrpAspLeuLeuIleGlnLysAsnLysHisLysLysGly 380
Db 1116 ACCTGTTCCATPACCTTCTATGATCTGTTGATACAGAAAAACACACATAAAGGT 1175
Qy 381 ValAlaIleSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
Db 1176 GTGGCTGCAAGTGACTTCATTTCGAGCCCTGGACCTGTGGAGACTAGCTCTGGAAGGT 1235
Qy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Db 1236 GTGTTCTCCCAAGTTTGATTTGNACTGCAGGATGTCTCCAGCGTGAATGAGGATGTC 1295
Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyThrAlaGlnArgPheLysProLysTyLys 440
Db 1296 CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAAAGTTCAAGCCAAAGTATAAA 1355
Qy 441 PhePheHisLysSerPheGlnGluTrpThrAlaGlyArgArgLeuSerSerLeuLeuThr 460
Db 1356 TTCTTTCACAAGTCATTCAGGAGTACACAGCAGGAGGAGACTCAGCAGTTTATTGAGC 1415
Qy 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyThrLeuGlnLysMetValSerIle 480
Db 1416 TCTCATGCCAGAGAGGCTGACCAAGGGAATGGTTACTTCGAGAAAATGGTTCCATT 1475
Qy 481 SerAspIleThrSerThrTyThrSerSerLeuLeuArgTyThrCysGlySerSerValGlu 500
Db 1476 TCGGACATTACATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGTCACTGTGGAA 1535
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaValTyThrGlnHisGlyCysLeuLeuGly 520
Db 1536 GCCACAGGGCTGTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCTCTCGGA 1595
Qy 521 LeuSerIleAlaLysArgProLeuTrpArgGlnGlnSerLeuGlnSerValLysAsnThr 540
Db 1596 CTTTCCATCGCAAGAGGCTCTCTCGAGACAGAACTCTTGCAAGTGTGAAAAACACC 1655
Qy 541 ThrGluGlnGluLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db 1656 ACTGAGCAAGAAATTCGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1715
Qy 561 LeuTyThrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPheGln 580
Db 1716 TTATATCAAGAGATACATCCAAATCAGCCCTGAGCCAGAAATTTGAAGCTTTCTTTCAA 1775
Qy 581 GlyLysSerLeuTyThrIleAsnSerGlyAsnIleProAspTyThrLeuPheAspPheGlu 600
Db 1776 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATTTACTTATTGACTTCTTTGAA 1835
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyThrGlyAla 620
Db 1836 CATTTGCCCAATGTGCAAGTGTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCT 1895
Qy 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyIleHisMetGluGluAlaPro 640
Db 1896 ATGGCTTCATGGAAAAAGGCTGCAGAAAGACACAGGTGGAATCCACATGGAAGAGCCCA 1955
Qy 641 GluThrTyThrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg 660
Db 1956 GAAACCTACATCCCGAGCAGGCTGTATCTTTCTTCAACTGGAAGCAGGAATTCAGG 2015
Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyLeu 680

Db	2016	ACTCTGGAGGTACACATCCGGGATTTCACCAAGTTGATATAGCAAGATATACATATCTG	2075
Qy	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal	700
Db	2076	GGGAAATATTACGCTCTGCCAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGTG	2135
Qy	701	AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu	720
Db	2136	GCTGGAAGCCTCAGTTTGGTCTCTCAGCAGCCTGTAAGAACATTTATTTCTCATGGTGAA	2195
Qy	721	AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr	740
Db	2196	GCAGTCCCCTCACCATAGAAATGAGAGGCACATCACATCTGTAAACAAACCTGANAACC	2255
Qy	741	LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly	760
Db	2256	TTGAGTATTACACCTACAGAAATCAAGGCTGCCGGGTGGTCTGACGACAGCTTGGGT	2315
Qy	761	AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla	780
Db	2316	AACTTGAAGAACCTTACAAAGCTCATATATGGATACATAAAGATGAATGAAGAAGATGCT	2375
Qy	781	IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis	800
Db	2376	ATAAACTAGCTGAAGCCTGAAAACCTGGAAGAAGATGTGTTATTTTCATTTGACCAC	2435
Qy	801	LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys	820
Db	2436	TTGTCTGCATTTGGAGAGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGT	2495
Qy	821	AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu	840
Db	2496	GACCTTGAGAAATTCATTTAGTCTCCTGCTGCTTGTCTGCAATGCAGTGAAATCCTA	2555
Qy	841	AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu	860
Db	2556	GCTCAGAATCTTCACAAATTTGGTCAAACTGCAGCATCTTGATTTATCAGAAAAATTACCTG	2615
Qy	861	GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGln	880
Db	2616	GAANAAGATGGAAATGAAGCTCTTCATGAACATGATCGACAGATGAACGCTGTAGAACAG	2675
Qy	881	LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu	900
Db	2676	CTCACGCACTGATGCTGCCCTGGGCTGTGACGTGCAAGCGCAGCCTGAGCAGCCTGTTG	2735
Qy	901	LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr	920
Db	2736	AAACATTTGGAGAGGTCCTCCCAACTCGTCAAGCTTGGGTTGAAAACTCGAGACTCACA	2795
Qy	921	AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln	940
Db	2796	GATACAGAGATTAGAAATTTAGTGCATTTTTTGGAAAGAACCCTCTGAAAAACTTCCAG	2855
Qy	941	GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal	960
Db	2856	CAGTTGAATTTGGCGGGAATCGTGTGACGAGTGATGGATGGCTTGCTTCATGGGTGTA	2915
Qy	961	PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp	980
Db	2916	TTTGGAAATCTTTAAGCAATTTAGTGTTTTTTGTACTTTAGTACTAAGAAGAAATTTTACCTGAT	2975
Qy	981	ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla	1000
Db	2976	CCAGCATTTAGTCAGAAAACCTTAGCCAGGTGTTATCCAAAGTTTAACCTTTCTCGAAGAAGCT	3035
Qy	1001	ArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys	1020
Db	3036	AGGCTGTTGGGTGGCAATTTGATGATGATCATCTCAGTGTATTACAGGTGCTTTTAA	3095
Qy	1021	LeuValThrAla 1024	
Db	3096	CTAGTAACCTGCT 3107	

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RESULT 6
US-09-841-739-1
; Sequence 1, Application US/09841739
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-841-739-1

Alignment Scores:
Pred. No.: 0 Length: 3133
Score: 1024.00 Matches: 1024
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 32 Gaps: 0

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Db 576 CGCAATGGCCATCTCTGGGGCTCCGAAAGTGCAAGGCTCTGACCAAGTTCAAATTCGTC 635
Qy PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220
Db TTYCTTCCTCCGCTCAGCAGGCCCCAGGGTGAGCTTTTGAACCCCTCTGTGATCAACTC 695
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240
Db CTGGATATACCTGGCCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTCAAGCTGGG 755
Qy 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
Db CAGAGGGTCTTTTCCCTCTCTGATGGCTACAAATGAATTCGAAGCCCCAGAACTGCCAGAA 815
Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280
Db ATCGNAGCCCTGATAAAGGAACCCACCGCTTCAAGAACATGGTCTCATCCACTACC 875
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
Db ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATATG 935
Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
Db ACAGAAGACAGCCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGGAGCTTGTCTGAAGGC 995
Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
Db TTGTTGCTCCAAATTCAGAAATCCAGTGCTTGGAGAAATCATGAAACCCCTCTCTCTTT 1055
Qy 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
Db GTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACAAACA 1115
Qy 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly 380
Db ACGCTGTTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAACACAAATAAAGGT 1175
Qy 381 ValAlaLaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
Db GTGGCTGCAAGTACTTCATTCGGAGCCTGGACCCTGTGGAGACTGACTGCTGGAGGGT 1235
Qy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Db GTGTTCTCCCAAGTTTGAATTCGAACCTGCAGGATGTGCCAGCGTGAATGAGGATGTC 1295
Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
Db CTGCTGACAACTGGGCTCCTCTGTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAA 1355
Qy 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr 460
Db TTCCTTCAAGTCAATCCAGAGTACACAGAGCAAGCACTGAGCAAGTATATGAGC 1415
Qy 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db TCTCATGAGCCAGAGGAGGTGACCAAGGGAAATGGTTACTTGCAGAAAATGGTTCCATT 1475
Qy 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
Db TCGGACATTTACATCCACTTATAGCAGCCTGCTCGGGTACACCTGTGGGTCTCTGTGAA 1535
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuGly 520
Db GCCACCAGGGCTGTATGAAGCACTCGCAGCAGTGTATCAACACGGCTGCTCTCCGA 1595
Qy 521 LeuSerIleAlaLysArgProLeuTriArgGlnGluSerLeuGlnSerValLysAsnThr 540
Db CTTTCCATCGCCAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAGACC 1655
Qy 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db ACTGAGCAAGAAATTTCTCAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1715

Qy 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
Db TTATATCAAGAGAGTACATCCAAATCAGCCCTGACCCCAAGAAATTTGAAGCTTCTTTCAA 1775
Qy 581 GlyLysSerLeuTyrIleAsnSerglyAsnIleProAspTyrLeuPheAspPhePheGlu 600
Db GGTAAAAGCTTATATATCAACTCAGGAACATCCCCGATTACTTATTTGACTTCTTTGAA 1835
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620
Db CATTTGCCCAATTTGCAAGTGTCTGACTTCATTAACCTGGACTTTTATGGGGAGCT 1895
Qy 621 MetAlaSerTriPGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640
Db ATGGCTTCATGGGAAAGGCTCGAGACACACAGGTGGAATCCACATGGAAGAGCCCA 1955
Qy 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTriPlyGlnGluPheArg 660
Db GAAACCTACATTTCCAGCAGGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGG 2015
Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680
Db ACTCTGGAGGTCACTCCGGGATTTCAAGAGTTGAATAAGCAAGATATACATATCTG 2075
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
Db GGGAAATATTCAGCTCTGCCACAGCCCTCAGGCTGCAAAATAAGAGATGTCTGCTGTG 2135
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720
Db GCTGGAAGCCTCAGTTTGGTCTCAGCACCTGTGAAGAACATTTATTTCTCTCATGTGAA 2195
Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
Db GCCAGTCCCTCCACATAGAAGATGAGAGGCACATCACATCTGTAAACAAACCTGAAACC 2255
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
Db TTGAGTATTCATGACTACAGNATCACGGCTGCCGGGTGGTCTGACTGCACAGCTTGGT 2315
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAla 780
Db AACTTGAAGAACCTTACAAAGCTCATATGGATAACATAAAGATCAATGAAGAAAGTGT 2375
Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
Db ATAAACTAGCTGAAGGCTGAAAAACCTGAAGAAAGATGTGTTTATTTTCATTTGACCAC 2435
Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820
Db TTGCTGTACATTTGGAGAGGAATGGATTCATAGTCAAGTCTCTCTCAAGTGAACCTGT 2495
Qy 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
Db GACCTTGAAGAAATTCATTTAGTCTCCTGCTGCTGTCTGCAAAATGCAGTGAATAATCCTA 2555
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Db GCTCAGAAATCTTCACAAATTTGGTCAAACTGAGCAATCTTGTATTTATCGAAAAATTTACCTG 2615
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
Db GAAAAAGATGGAATGAAGCTCTTCATGAATGATCGACAGATGAACGTGTGAAGACAG 2675
Qy 881 LeuThrAlaLeuMetLeuProTriPGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
Db CTCACCGACTGTATGCTGCCCTGGGGCTGTGACGTGCAAGGACGCTCAGCAGCCTGTG 2735
Qy 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTriPArgLeuThr 920
Db AAACATTTGGAGGAGGTCCCAACACTCGTCAAGCTTGGTTGGTTGAAAAACTGGAGACTACA 2795

Qy	461	SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle	480
Db	1381	TCCTCATGAGCCAGAGAGAGTGCACCAAGGGGAATGGTTACTTTCACAGAAAATGGTTTCATTT	1440
Qy	481	SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu	500
Db	1441	TCGGACATATACATCCACTTATAGCAGCCCTGCCGGTACACCTGGGGGTCACTGTGTGGAA	1500
Qy	501	AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly	520
Db	1501	GCCACCAGGGCTGTTATGAAGCACCTCGCAGCAGGTATCAACACGGCTGCCTTCGGA	1560
Qy	521	LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr	540
Db	1561	CTTTCCATCGCCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACC	1620
Qy	541	ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis	560
Db	1621	ACTGAGCAGCAAAATCTGAAAGCCATAACATCAATTCCTTTGTAGAGTGTGGCATCCAT	1680
Qy	561	LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln	580
Db	1681	TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAA	1740
Qy	581	GlyLysSerLeuTyrIleAsnSergLysAsnIleProAspTyrLeuPheAspPhePheGlu	600
Db	1741	GGTAAAGCTTATATATCAACTCAGGGACATCCCCCGATTACTTATTGTGACTTCTTTTGA	1800
Qy	601	HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla	620
Db	1801	CATTGGCCCAATTGTCCAGTGCCTTGGACTTCATTAACTGGACTTTTATGGGGGAGCT	1860
Qy	621	MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro	640
Db	1861	ATGGCTTCATGGGAAAAAGGCTGCAGAAAGACACAGGTGCAATCCACATGGAGAGAGCCCA	1920
Qy	641	GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg	660
Db	1921	GAACCTTACATTCCTCCAGCAGGCTGTATCTTTGTCTTCAACTCGAAGCAGGAATTCAGG	1980
Qy	661	ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr-TyrLe	680
Db	1981	ACTCTGGAGTCACTCCGGGATTTTCAGCAAGTTGATAGCAAGATATACAG-ATATCT	2039
Qy	680	uGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVa	700
Db	2040	GGGAAAAATTCAGCTCTGCCACAGCCTCAGGCTGCAAAATAAGAGATGTGCTGTGT	2099
Qy	700	AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValG	720
Db	2100	GGCTGGAAGCCTCAGTTTGGTCTCAGCACCTGTGAAGAACATTTATTCTCTCATGGTGA	2159
Qy	720	uAlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysTh	740
Db	2160	AGCAGTCCCTCACCATAGAGAGTGAGGGCACATCATCTGTACAAACCTGAAAC	2219
Qy	740	rLeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuG	760
Db	2220	CTTGAGTATTTCATGACTACAGAAATCAACGGCTGCCGGTGGTCTGACTGACAGCTTGGG	2279
Qy	760	YAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAlaAspAl	780
Db	2280	TAACTTGAAGAACCTTACAAAGCTCATATGGATTAACATAAAGATGAATGAAGAAGATGC	2339
Qy	780	AlaLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHi	800
Db	2340	TATAAACTAGCTGAAGGCTTGAAAAACCTGAAAGAAGATGTTTATTTCATTGTGACCCA	2399
Qy	800	sLeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProC	820
Db	2400	CTTGCTGCATTTGAGAGGGAAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCTG	2459

Qy	820	sApLeuGluGlueInLeuValSerCysLeuSerAlaAsnAlaValLysIleLe	840
Db	2460	TGACCTTTGAAGAAATTCAAATTAGTCTCCCTGCCTGTCTGCCAAATGCAGTGAAAATCCCT	2519
Qy	840	uAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLe	860
Db	2520	AGCTCAGAATCTTCACANNTTGGTCAAACTGAGCATTTCTTGNTTATCAGAAAATTAACCT	2579
Qy	860	uGluLysAspGlyAsnGluAlaLeuHisGluLeuleAspargMetAsnValLeuGluGI	880
Db	2580	GGAATAAAGATGGAATGAAGCTCTTCATCAACTGATCACAGGATGAACGTGCTAGAACA	2639
Qy	880	nLeuThrAlaLeuMetLeuproTrpGlyCysaspValGlnGlySerLeuSerSerLeuLe	900
Db	2640	GCTCACCGCACTGATGCTGCCCTGGGGCTGTGCACGTGAAGSGCAGCCTGAGCAGCCGTGT	2699
Qy	900	uLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuTh	920
Db	2700	GAACATTTGGAGAGAGGTCCCACTCGTCAAGCTTGGGTGAAAAAACTGAGACTCAC	2759
Qy	920	rAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysasnProLeuLysasnPheGI	940
Db	2760	AGATACAGACATTAGAATTTTAGTGCAATTTTTTGGAAAGAACCCCTCTGAAAAAACTTCCA	2819
Qy	940	nGlnLeuAsnLeuAlaGlyAsnArgValSerSeraspGlyTrpLeuAlaPheMetGlyVa	960
Db	2820	GCAGTTCAAATTTGCGGGAAATCGTGTGAGCAGTATGATGCGCTTGCCTTCATGGGTGT	2879
Qy	960	lPheGluAsnLeuLysGlnLeuValPhePheaspPheSerThrLysGluPheLeuProAs	980
Db	2880	ATTTGAGAANTCTTAAGCAATTAGTGTTTTTTCACCTTAGTACTAAAGAAATTTTACCCTGA	2939
Qy	980	pProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAl	1000
Db	2940	TCCAGCATTAGTCAGAAAACTTAGCCCAAGTGATTCCAAAGTTAACTTTTCTGCAGAGAGC	2999
Qy	1000	aArgLeuValglyTrpGlnPheaspAspaspLeuSerValIleThrGlyAlaPheLy	1020
Db	3000	TAGCCTTTGGTGGGCAATTTTCATGATGATGATCTCAGTGTATTACAGGTGCTTTTAA	3059
Qy	1020	sLeuValThrAla 1024	
Db	3060	ACTAGTAACCTGCT 3072	
RESULT 8 US-10-156-733-14			
; Sequence 14, Application US/10156733			
; GENERAL INFORMATION:			
; APPLICANT: Alnemri, Emad S.			
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING			
; TITLE OF INVENTION: FACTOR			
; FILE REFERENCE: 480140.477			
; CURRENT APPLICATION NUMBER: US/10/156,733			
; CURRENT FILING DATE: 2002-05-24			
; NUMBER OF SEQ ID NOS: 14			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 14			
; LENGTH: 3219			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-156-733-14			
Alignment Scores:			
Pred. No.:	0	Length:	3219
Score:	923.00	Matches:	1023
Percent Similarity:	99.80%	Conservative:	0
Best Local Similarity:	99.80%	Mismatches:	1
Query Match:	90.14%	Indels:	2
DB:	41	Gaps:	0
US-09-697-089-2 (1-1024) x US-10-156-733-14 (1-3219)			
Qy	1	MetAsnPheIleLysAspAsnSerArqAlaLeuIleGlnArgMetGlyMetThrVaille	20

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Db 145 ATGAATTTCAATAAGGACAATAGCGGCCCTTATTCAAAGAAATGGGAATGACTGTATATA 204
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
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Db 205 AAGCAAAATACAGATGACCTATTATTTGTATGGAAATCTTCTGAATCCGGAAGAAGTAACATC 264
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
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Db 265 ATTTGCTGGAGAGGTGGAGCAGATGCTGCTAGAGGGATCATTCACATGATTTTGA 324
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
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Db 325 AAGGTTTCAGAGTCTCTGAACCTTTTCTTAAATCCCTTAAGGAGTGAACATATCCCTTA 384
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
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QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120
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Db 445 TTGGCTCAGGATTTAAGGACTTGTACCATACCCCATCTTTTCGAAACTTTTATCCCCCTT 504
QY 121 GlyGluAspIleAspIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140
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Db 505 GGTGAAGATATTGACATTAATTTTAACCTTCAAAAGCACCTTCACAGAACCTGTCTGTGG 564
QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
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Db 565 AGAAGGACCAACACCATCACCCGCTGGAGCAGCTGACCCCTGAATGGCCCTCTGCAGGCT 624
QY 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 180
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Db 625 CTTTCAGAGCCCTGCATCATTTGAAGGGATCTGGCAAGGCAAGTCCACCTGTCTGCAG 684
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QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyLysPheGluThrLeuCysAspGlnLeu 220
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QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240
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QY 241 GlnArgValLeuPheLeuAspGlyTyrAsnGluPheLysAsnMetValIleValThrThr 280
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QY 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
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QY 561 LeuTyrGlnGlnSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580
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QY 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu 600
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QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla 620
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Db 2005 ATGGCTTCATGGAAAAAGCTGCAGAAGACACAGGTGGAAATCCACATGGAAGAGGCCCA 2064
QY 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660
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Db 2065 GAAACCTACATTTCCAGCAGGCTGTATCTTGTCTTCAACTGGAAGCAGGAATTCAGS 2124
QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr-TyrLe 680
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QY 1020 sLeuValThrAla 1024
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RESULT 9

PCT-US01-07143-23

; Sequence 23, Application PC/TUS0107143

; GENERAL INFORMATION:

; APPLICANT: SMITHKLINE BEECHAM CORPORATION

; APPLICANT: SMITHKLINE BEECHAM p.l.c.

; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GP50016

; CURRENT APPLICATION NUMBER: PCT/US01/07143

; CURRENT FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: 60/187,107

; PRIOR FILING DATE: 2000-03-06

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; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-07143-23

Alignment Scores:
Pred. No.: 0 Length: 3213
Score: 922.00 Matches: 1022
Percent Similarity: 99.80% Conservative: 0
Best Local Similarity: 99.80% Mismatches: 1
Query Match: 90.04% Indels: 2
Db: 1 Gaps: 0
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US-09-697-089-2 (1-1024) x PCT-US01-07143-23 (1-3213)

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QY 62 GlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeuPhe 81
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QY 162 GlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArg 181
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Db 622 CAGAGCCCTTGCATTCATTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCGAG 581
QY 182 IleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhe 201
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Db 682 ATTGCCATGCTCTGGGGCTCCGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGTCCTTC 741
QY 202 PheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeuLeu 221
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Qy 282 GluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThr 301
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Qy 422 LeuThrThrGlyLeuLeuCysLysThrThrAlaGlnArgPheLysProLysThrLysPhe 441
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Qy 482 AspIleThrSerThrThrSerSerLeuLeuArgThrThrCysGlySerSerValGluAla 501
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Qy 522 SerIleAlaLysArgProLeuThrArgGlnGlnLysSerLeuGlnSerValLysAsnThrThr 541
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Qy 562 TyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGlnCly 581
Db 1822 TATCAAGAGAGTACATCCAATCAGCCCTGAGCCCAAGAAATTTGNAGCTTCTTCAAGGT 1881
Qy 582 LysSerLeuThrIleAsnSerGlyAsnIleProAspThrLeuPheAspPheGluHis 601
Db 1882 AAAAGCTTATATATCAACTCAGGGAACATCCCGATTACTTATTTGACTTCTTTGAACAT 1941
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Qy 642 ThrThrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThr 661
Db 2062 ACCTACATTCGCCAGCAGGCTGTATCTTTGCTTCTCACTGGAAGCAGGAATTCAGGACT 2121
Qy 662 LeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlu 681
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Qy 681 yLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAl 701
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Qy 801 uSerAspIleGlyGluGlyMetAspThrIleValLysSerLeuSerSerGluProCysAs 821
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RESULT 10
US-10-221-097-23
; Sequence 23, Application US/10221097
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GPS0016
; CURRENT APPLICATION NUMBER: US/10/221,097
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-221-097-23

Alignment Scores:
Pred. No.: 0 Length: 3213
Score: 922.00 Matches: 1022
Percent Similarity: 99.80% Conservative: 0
Best Local Similarity: 99.80% Mismatches: 1
Query Match: 90.04% Indels: 2
DB: 42 Gaps: 0

US-09-697-089-2 (1-1024) x US-10-221-097-23 (1-3213)
QY 2 AsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIleLys 21
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Db 142 AATTTTCATAAAGGACATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTATATAAG 201

QY 22 GlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIleIle 41
|||||
Db 202 CAAATCAGATGACCTATTGTATGGAAATGTTCTGAATCGCGAAGATAAACATCAATT 261

QY 42 CysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLysLys 61
|||||
Db 262 TGCTCGGAGAGGTGGACGAGGATGCTGCTAGAGGATCATTCATGATGATTTTGAANAAG 321

QY 62 GlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeuPhe 81
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Db 322 GGTTCAGAGTCTGTAACTCTTTCTTAAATCCCTTAAAGGAGTGAACATATCCTCTATT 381

QY 82 GlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspLeu 101
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Db 382 CAGGACTTGAATGGCAAAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGACGATTTG 441
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QY 102 AlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeuGly 121
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Db 442 GCTCAGGATTTAAAGGACTTTGACCATACCCCATCTTTTCTGAACATTTTATCCCTTGGT 501

QY 122 GluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrpArg 141
|||||
Db 502 GAAGATATTGACATATTATTTTAACTTGAAGACACCTTACAGAACCTGCTCTGTGGAGG 561

QY 142 LysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuGlnAlaLeu 161
|||||
Db 562 AAGGACCAACACCATACCGCTGGAGCAGCTGACCTGAATGGCTCTCGAGGCTCTT 621

QY 162 GlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArg 181
|||||
Db 622 CAGAGCCCTGTCATCTGAAGGGGNACTGGCAAGGCAAGTCCACTCTGCTGCAGCGCA 681

QY 182 IleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhe 201
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Db 682 ATTGCCATGCTCTGGGGCTCCGAAAGTCAAGGCTTCAAGGCTTCAAAATTCGTCTTC 741

QY 202 PheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeuLeu 221
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Db 742 TTCCCTCCGCTCAGCAGGGCCCGAGGTGGACTTTTGAACCCCTCTGTGATCAACTCTG 801

QY 222 AspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGln 241
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Db 802 GATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCCATGCTGCTGAAGCTCGGCG 861

QY 242 ArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGluIle 261
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Db 862 AGGGTCTCTTCTTCTGATGGCTACAATGAATTCGAAGCCCAAGCTGCCAGAAATC 921

QY 262 GluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 281
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Db 922 GAAGCCCTGATAAAGGAAACCCAGCTTCAAGAACATGGTCAATGCTGCCACTACCACT 981

QY 282 GluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThr 301
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Db 982 GAGTGCTCAGGCACATACGGCAGTTGGTGGCTGACTGCTGAGTGGGGGATATGACA 1041

QY 302 GluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGlyLeu 321
|||||
Db 1042 GAAGCAGCGCCAGGCTCTCATCCGAGAAGTCTGATCAAGGAGCTTCTCTGAAGGCTTG 1101

QY 322 LeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheVal 341
|||||
Db 1102 TTGCTCCAAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1161

QY 342 ValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrThrThr 361
|||||
Db 1162 GTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACACAAACAG 1221

QY 362 LeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysLysGlyVal 381
|||||
Db 1222 CTGTTCCATACCTTCTATGATCTGTGATACAGAAAAACACACAAACATAAAGGTG 1281

QY 382 AlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlyVal 401
|||||
Db 1282 GCTGCAAGTGACTTCAATCGGAGCCCTGGACCACTGTGGAGAGACCTAGCTCTGAGG 1341

QY 402 PheSerHisLysPheAspPheGluLeuGlnAspValSerValAsnGluAspValLeu 421
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Db 1342 TTCTCCCAACAAGTTGATTTCCAGCTGCAGGATGTGTCAGCGTGAATGAGGATGCTCTG 1401

QY 422 LeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhe 441
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Db 1402 CTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAGGTTCAAGCAAGATATAATTC 1461

QY 442 PheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuThrSer 461
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Db 1462 TTTTCAAGATCATTCAGGAGGTACAGCAGGACGAAGACTCAGCAGTTTATTGAGTCT 1521
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QY	89	LeuPheHisGlnThrSerGluGlyAspLeuAspLeuAlaGlnAspLeuLysAspLeu	108
DB	736	CTTTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACTTG	795
QY	109	TyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleAspIlePhe	128
DB	796	TACCATACCCCATCTTTTCGAACTTTTATCCCTTGGTGAAGATATTGACATTATTTTT	855
QY	129	AsnLeuLysSerThrPheThrGluProValLeuTyrArgLysAspGlnHisHisArg	148
DB	856	AACCTTGAAGACACCTTCACAGAACCTGCTCTGGAGGAAGGACCAACACCATCACCGC	915
QY	149	ValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlu	168
DB	916	GTGAGCAGCTGACCTCGAATAGCCCTCCGACAGGCTTCACAGGCCCTGCATCATTTGAA	975
QY	169	GlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTyrGlySer	188
DB	976	GGGGAATCTGGCAAGCAGTCCACTCTGCTGCAGCGAATTGCCATGCTCTGGGGCTCC	1035
QY	189	GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla	208
DB	1036	GGAAAGTGCAGAGGCTGTGACCAAGTTCAAATTCGTCTCTCTCCGTCCAGCAGGGCC	1095
QY	209	GlnGlyLysLeuPheGlnThrLeuCysAspGlnLeuLeuAspIleProGlyThrIleArg	228
DB	1096	CAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCTCGGATATACCTGGCACCAATCAGG	1155
QY	229	LysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAsp	248
DB	1156	AAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGCAGAGGGTCTTTTCTCTCTTGAT	1215
QY	249	GlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGluAsn	268
DB	1216	GGCTACAAATCAAGTTCAGCCCAAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAAC	1275
QY	269	HisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArg	288
DB	1276	CACCGCTTCAAGAACATGGTCATGTCACCACTACCACTGAGTGGCTCAGGCACATACGG	1335
QY	289	GlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu	308
DB	1336	CAGTTTGGTCCCTGACTGCTGAGGTGGGGATATGACAGAAAGACAGCGCCAGGCTCTC	1395
QY	309	IleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeuGlnIleGlnLysSer	328
DB	1396	ATCCGGAAGTGTGATCAAGGAGCTGTGCTGAAGGCTGTTGCTCCAAATTCAGAAATCC	1455
QY	329	ArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCysAlaIleGln	348
DB	1456	AGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTGTGGTCATCCTGTGCAATCCAG	1515
QY	349	MetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrPheTyrAsp	368
DB	1516	ATGGGTCAAAAGTGAGTTCACCTCTCACACACAAACACGCTGTTCATACCTCTCATGAT	1575
QY	369	LeuLeuIleGlnLysAsnLysHisLysGlyValAlaAlaSerAspPheIleArg	388
DB	1576	CTGTTGTATACAGAAAAACAACAACAATAAAGGTGTGGCTGCAAGTGACTTCATTCGG	1635
QY	389	SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAspPhe	408
DB	1636	AGCCTGGACCACTGTGAGACCTTAGCTCTGGAGGGTGTCTCTCCACAGTTTGATTTC	1695
QY	409	GluLeuGlnAspValSerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCys	428
DB	1696	GAACTGCAGGATGTGCCAGCTGAATGAGGATGTCCTGCTGCACACTGGGCTCCTCTGT	1755
QY	429	LysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGlu	448
DB	1756	AAATATACAGCTCAAGGTTCAAGCCAAAGTATAAATTTCTTTTCAAGTCAATCCAGGAG	1815

Qy	449	TyrThrAlaGlyArgLeuSerSerLeuLeuThrSerHisGluProGluValThr	468
Db	1816	TACACACAGCAGCAGACACTCAGCAGCTTATTGACGTCTCATGAGCCAGAGAGGTGACC	1875
Qy	469	LysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerThrTyrSer	488
Db	1876	ANGGGGAATGGTTACTTGCAGAAATATGGTTTCCATTTTCGACATTTACATCCACTTATAGC	1935
Qy	489	SerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLysHis	508
Db	1936	AGCGTCGTCGGGTACACCTGTGTGGTCCATCTGTGGAAGCCACCAGGCGCTTTATGAAGCAC	1995
Qy	509	LeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAlaLysArgProLeu	528
Db	1996	CTCCACAGCAGTATCAACACGCGTCGCCCTTCGCGACTTTCCATGCCCAAGAGCGGCTCTC	2055
Qy	529	TrpArgGlnGluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAla	548
Db	2056	TGGAGACAGGAACTTTTGCAGAACTGTGAAAAACACCACTGAGCAAGAAATTTCTGAAAGCC	2115
Qy	549	IleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLys	568
Db	2116	ATAAACATCAATTCCTTTGTAGAGTGTGCCTCCATTTATATCAAGAGAGTACATCCAAA	2175
Qy	569	SerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSer	588
Db	2176	TCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACTCA	2235
Qy	589	GlyAsnIleProAspTyrLeuPheAspPhePheGluHisLeuProAsnCysAlaSerAla	608
Db	2236	GGGAACATCCCGAATTACTTATTGTGACTTCTTTTGAACTTTGCCCAATTTGTGCAAGTGCC	2295
Qy	609	LeuAspPheIleLysLeuAspPheTyrGlyGlyAlaMetAlaSerTrpGluLysAlaAla	628
Db	2296	CTGGACTTCATTAACTGGACTTTTATGCGGAGCTATGGCTTCATGGAAAAGGCTGCA	2355
Qy	629	GluAspThrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSerArgAla	648
Db	2356	GAAGACACAGGTGGAATCCACATGGAAGAGGCCGCCAAGAACCTACATTTCCAGCAGGCGCT	2415
Qy	649	ValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuArgAsp	668
Db	2416	GTATCTTTGTCTTCAACTGGAGCAGGAATTCAGAGCTCTCGAGGTCACACTCCGGAT	2475
Qy	669	PheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePheSerSerAlaThr	688
Db	2476	TTCAACAAGTTGAATAGCAAGATATACAG-ATATCTGGGAAAAATATTTCAGCTCTGCCAC	2534
Qy	688	rSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuValLe	708
Db	2535	AAGCCTCAGGCTGCATAAAGAGATGTGCTGTGTGGTGTGGAAGCCTCAGTTTGGTCTCT	2594
Qy	708	uSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAs	728
Db	2595	CAGCACCTGTGAAGAATTTATTCTCTCATGTGTGAAGCCAGCTGCCCTCACCATAGAAGA	2654
Qy	728	pGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAs	748
Db	2655	TGAGGCGCATCATCATCTGTACAAACCTGAAAACCTTGTAAGCTTATCATGACCTACAGAA	2714
Qy	748	nGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLe	768
Db	2715	TCAAGCGCTCCGGTGGTCTGACTGCACAGCTTGGTAACTTGAAGAACCATTACAAAGCT	2774
Qy	768	uIleMetAspAsnIleLysMetAsnGluAspAlaIleLysLeuAlaGluGlyLeuLys	788
Db	2775	CATTAATGGATAACATAAAGATGAATCAAGAAGATGCTATAAAACTAGCTGAAGGCGCTGAA	2834
Qy	788	sAsnLeuLysLysMetCysLeuPheHisIleThrHisLeuSerAspIleGlyGluGlyMe	808
Db	2835	AAACCTCAAGAAGATGTTTATTTCATTTTGACCCACTTGCTGCATTTGGAGAGGAAT	2894
Qy	808	tAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuVal	828


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Db 2895 GGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGTGACCTTGAGAAATTCATATTAGT 2954
Qy 828 lSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuVa 848
Db 2955 CTCCTGCTGCTGTCTGCAAAATGCAGTAGTCAAAATCTTACAAATTTGGT 3014
Qy 848 lLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLe 868
Db 3015 CAACTGAGCATCTTGATTATCAGAAATACCTGGAAAAAGATGGAATGAAGCTCT 3074
Qy 868 uHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTr 888
Db 3075 TCATGAATGATCGACAGGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCTG 3134
Qy 888 pClyCysaspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGl 908
Db 3135 GGGCTGTGACGTGCAAGCAGCCCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTCCCA 3194
Qy 908 nLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGl 928
Db 3195 ACTCGTCAAGCTTGGTTGAAAACTGGAGACTCACAGATACAGAGATTAGAAATTTAGG 3254
Qy 928 yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnAr 948
Db 3255 TGCATTTTTTGGAAAGAACCCCTCTGAAAAACTTCAGCAGATTGAATTTGGCGGGAATCG 3314
Qy 948 gValSerSeraspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuVa 968
Db 3315 TGTGAGCAGTAGTATGGCTTGCCTCATGGGTATTTGAGAACTTTAAGCAATTAGT 3374
Qy 968 lPhePheAspPheSerThrLysGluPheLeuProaspProAlaLeuValArgLysLeuSe 988
Db 3375 GTTTTTTGACTTTAGTACTAAGAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTAG 3434
Qy 988 rGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAs 1008
Db 3435 CCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAAGCTAGGCTTGTGGTGGCAATTTGA 3494
Qy 1008 pAspAspAspLeuSerValIleThr 1016
Db 3495 TGATGATGATCTCAGTGTTATTACA 3519
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RESULT 12

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US-09-841-739-6
; Sequence 6, Application US/09841739
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841.739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-6

Alignment Scores:
Pred. No.: 0 Length: 3612
Score: 827.00 Matches: 927
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 80.76% Indels: 2
DB: 32 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-841-739-6 (1-3612)
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Qy 89 LeuPheHisGlnThrSerGluGlyAspLeuAspLeuAlaGlnAspLeuLysAspLeu 108
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Db 736 CTTTTTCATCAGACATCAGAAAGGAGACTTGGACGATTGGCTCAGGATTTAAAGGACTTG 795
Qy 109 TyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleAspIlePhe 128
|||||
Db 796 TACCATAACCCCATCTTTTCTGAACCTTTATCCCTTGTGGAAGATATTGACATTATTTT 855
Qy 129 AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHisHisArg 148
|||||
Db 856 AACTTGAAGAAGCACCTTCACAGAACCTGCTGTGTGGAGGAAGGACCAACACCATCACCGC 915
Qy 149 ValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlu 168
|||||
Db 916 GTGAGCAGAGCTGACCTGAATGGCTCTGCAGGCTCTTCAGAGCCCTTCGACATCAATTAA 975
Qy 169 GlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySer 188
|||||
Db 976 GGGGAATCTGCAAAAGGCAAGTCCACTCTGTGCAGCGAATTGCCATGCTCTGGGGCTCC 1035
Qy 189 GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla 208
|||||
Db 1036 GGAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTCTTCTTCTCCCTCTCAGCAGGGCC 1095
Qy 209 GlnGlyGlyLeuPheGluThrLeuCysAspGlnLeuLeuLeuAspIleProGlyThrIleArg 228
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Db 1096 CAGGTGGACATTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACAATCAGG 1155
Qy 229 LysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAsp 248
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Db 1156 AAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGCAGAGGGTCTTTTCTCTTGTAT 1215
Qy 249 GlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGluAsn 268
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Db 1216 GGCTACAAATGAATTCAGCCCCAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAAC 1275
Qy 269 HisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArg 288
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Db 1276 CACCGCTTCAAGAACATCGTCTCATCGTACCACCTACCACCTGAGTGCCTGAGGCACATACGG 1335
Qy 289 GlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu 308
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Db 1336 CAGTTTGGTGGCCCTGACTGCTGAGTGGGGATATGACAGAAAGACAGAGCCCGCAGGCTCTC 1395
Qy 309 lIeArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeuGluIleGlnLysSer 328
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Db 1396 ATCCGAGAAGTGCTGATCAAGGAGCTTCTGAAGCTTGTGTGCTCCAAATTCAGAAATCC 1455
Qy 329 ArgCysLeuArgAsnLeuMetLysThrProLeuPheValValIleThrCysAlaIleGln 348
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Db 1456 AGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTGTGGTCACTACCTGTGCAATCCAG 1515
Qy 349 MetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrPheTyrAsp 368
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Db 1516 ATGGTGAAGTGAGTTCCACTCTCACACAAAACAGCTGTTCATACCTTCTATGAT 1575
Qy 369 LeuLeuIleGlnLysAsnLysHisLysHisGlyValAlaAlaSerAspPheIleArg 388
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Db 1576 CTGTGTATACAGAAAAACAAACAAATAAAGGTGGGTGCAAGTGAGCTTCATTCCG 1635
Qy 389 SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAspPhe 408
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Db 1636 AGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTGTTCTCCCAAGTTGATTTC 1695
Qy 409 GluLeuGlnAspValSerSerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCys 428
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Db 1696 GAAGTGCAGGATGTGTCCAGCGTGAATGAGGATGCTGCTGCTGACAACTGGGCTCCTCTGT 1755
Qy 429 LysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGlu 448
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Db 1756 AAATATACAGCTCAAGGTTCAAGCCAAAGTATAAAATCTTTTTCACAAAGTCATTCCAGGAG 1815
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QY	449	TyrThrAlaGlyArgLeuSerSerLeuLeuThrSerHisGluProGluValThr	468
DB	1816	TACACAGCAGGACGAAGACTCAGCAGTTATTATGACGCTCATGAGCCAGAGAGGTGACC	1875
QY	469	LysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerThrTyrSer	488
DB	1876	AAGGGGAATGGTTACTTGCAGAAATGGTTTCATTTCCGACATTACATCCACTTATAGC	1935
QY	489	SerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLysHis	508
DB	1936	AGCCTGCTCCGGTACACCTGTGGTCATCTGTGGGAAGCCACCAGGGCTGTATTGAACAC	1995
QY	509	LeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAlaLysArgProLeu	528
DB	1996	CTCGCAGCAGTGTATCAACACGGCTGCCTTCGGACTTTCATCTCGCAGCCTCTC	2055
QY	529	TrpArgGlnGluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAla	548
DB	2056	TGAGACAGGAATCTTTGCAAAAGTGTGAACAACACCCTGAGCAAGAAATTCGAAAGCC	2115
QY	549	IleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLys	568
DB	2116	ATAAACATCAATTCCTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCAAA	2175
QY	569	SerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSer	588
DB	2176	TCAGCCCTGAGCCAAAGAAATTTGAAGCTTCTTTCAAGGTAAAGCTTATATATCAACTCA	2235
QY	589	GlyAsnIleProAspTyrIleuPheAspPhePheGluHisLeuProAsnCysAlaSerAla	608
DB	2236	GGAAACATCCCCGATTACTATTTCACCTCTTTTGAACTATTTGCCCAATTTGTGCAAGTGCC	2295
QY	609	LeuAspPheIleLysLeuAspPheTyrGlyGlyAlaMetAlaSerTrpGluLysAlaAla	628
DB	2296	CTGGACTTCATTAAACTGGACCTTTTATGGGGAGGCTATGGCTTCATGGGAAAAGGCTGCA	2355
QY	629	GluAspThrGlyGlyIleHisMetGluAlaProGluThrTyrIleProSerArgAla	648
DB	2356	GAAGACACAGGTGGAATCCACATGCAAGAGGCCCCAGAAACCTACATTCCCAGCAGGGCT	2415
QY	649	ValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuArgAsp	668
DB	2416	GTATCTTGTCTTCAACTTGGGAAGCAGGAATTCAGAGACTCTGGAGGTCACACTCCGGGAT	2475
QY	669	PheSerLysLeuAsnLysGlnAspIleThrTyrLeuGlyLysIlePheSerSerAlaThr	688
DB	2476	TTCAGCAGGTTGNATPAGCAGATATCAG-ATATCTGGGGAAAATATTACGCTCTGCCAC	2534
QY	688	rSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuValLe	708
DB	2535	AAGCCTCAGCTGCAAAATAAGAGATGTGCTGGTGTGCTGGAAGCCTCAGTTTGGTCTCT	2594
QY	708	uSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAs	728
DB	2595	CAGCACCCTGTAAGAACATTTATTTCTCATGGTGGAAAGCCAGTCCCTCCACATPAGAAGA	2654
QY	728	pGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAs	748
DB	2655	TGAGAGGCACATCATCTGTAAACAAACCTGAAAACCTTGAGTATTTCATGACCTTACGAA	2714
QY	748	nGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLe	768
DB	2715	TCAACGGCTGCCGGTGGTCTGACTGACAGCTTGGGTAACTTGAAGAACCTTACAAAGCT	2774
QY	768	uIleMetAspAsnIleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLys	788
DB	2775	CATTAATGGTAATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGGCCCTGAA	2834
QY	788	sAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMe	808
DB	2835	AAACCTCAAGACAGATGTGTTTATTTTCATTGACCACCTTGTCTGACATTGGAGGGAAAT	2894
QY	808	tAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuVal	828

[illegible]

US-09-697-089-2 (1-1024) x PCT-US00-29643-4 (1-3615)	
Qy	89 LeuPheHisGlnThrSerGluGlyAspLeuAspAspLeuAlaGlnAspLeuLysAspLeu 108
Db	736 CTTTTTCATCAGACATCAGACGAGACTTGGACGATTGGCTCAGGATTTAAAGGACTTG 795
Qy	109 TyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleAspIlePhe 128
Db	796 TACCATACCCCATCTTTCTGAACCTTTTATCCCTTGGTGAAGATATTGACATATTATTTT 855
Qy	129 AsnLeuLysSerThrPheThrGluProValLeuTyrArgLysAspGlnHisHisArg 148
Db	856 AACTTTGAAAAGCACCTTTCAGAACCTGTCTGTGGAGAAGGACCAACACCATCACCGC 915
Qy	149 ValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlu 168
Db	916 GTGGAGCAGCTGACCTTGAATGCCCTCTGCAGGCTCTTCAGAGCCCTGCATCATTTGAA 975
Qy	169 GlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySer 188
Db	976 GGGGAATCTGGCAAGCAAGTCCACTCTGCTGTCAGCGAATTGCCATCTCTGGGGCTCC 1035
Qy	189 GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla 208
Db	1036 GGAAGTGTGAAGGCTCTGACCAAGTTCAAAATTCGTCTTCTCTCCGTCTCAGCAGGCCC 1095
Qy	209 GlnGlyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThrIleArg 228
Db	1096 CAGGGTGCAGCTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACAACTCAGG 1155
Qy	229 LysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAsp 248
Db	1156 AAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGCAGAGGGTTCTTTCTCTCTTGAT 1215
Qy	249 GlyTyrAsnGlnPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGluAsn 268
Db	1216 GGCTACAAATGAATTCGAAGCCCCAGAAGCTGCCAGAAATCGAAGCCCTGATAAAGGAAAC 1275
Qy	269 HisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArg 288
Db	1276 CACCGCTTCAAGAACATGGTCACTCGTACCCTACCTAGTGGCTGAGGCATCAGG 1335
Qy	289 GlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu 308
Db	1336 CAGTTTGGTCCCTGACTGCTGAGGTGGGGGATATGACAGAAGACAGCGCCAGGCTCTC 1395
Qy	309 IleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeuLeuGlnIleGlnLysSer 328
Db	1396 ATCCGGAAGTGTGATFCAAGAGCTTGCTGAAGGCTTGTTCGTCCTCAAAATTCAGAAATCC 1455
Qy	329 ArgCysLeuArgAsnLeuMetLysThrProLeuPheValValIleThrCysAlaIleGln 348
Db	1456 AGTGCTTGAAGGAATCTCATGAGACCCCTCTCTTTGTGGTCATCATCTGTGCAATCCAG 1515
Qy	349 MetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrPheTyrAsp 368
Db	1516 ATGGGTGAAAGTGAGTTCCACTCTCACACAAACACGCTGTTCATACCTTCTATGAT 1575
Qy	369 LeuLeuIleGlnLysAsnLysHisLysLysGlyValAlaAlaSerAspPheIleArg 388
Db	1576 CTGTTGTATACAGAAAAACAAACAAACATAAAGGTGTGGCTGCAAGTGACTTCATTCCG 1635
Qy	389 SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAspPhe 408
Db	1636 AGCCTGGACCACCTGTGGACACTTAGCTCTGGAGGGTGTCTCCACCAAGTTTGATTTTC 1695
Qy	409 GluLeuGlnAspValSerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCys 428
Db	1696 GAACTGCAGGATGTGCCAGGTGAATGAGGATGTCTCTGCTGACAACTGGGCTCTCTGT 1755
Qy	429 LysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGlu 448

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QY 808 tAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuVa 828
Db 2895 GgATtACATAGTCAGTCTCTCTCAAGTGAACCCCTGTGACCTTGAAGAATTCATAGT 2954
QY 828 lSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuVa 848
Db 2955 CTCCTGCTGCTGTCTGCAATGCAGTGAATAATCCTAGCTCAGAAATCTTCACAATTTGCT 3014
QY 848 lLysLeuSerIleLeuAspLeuSerGluAsnTyrIleLeuGluLysAspGlyAsnGluAlaLe 868
Db 3015 CAAACTGACATCTTGTATTTATCAAAAAATTTACCTGGAAAAAGATGGAAATGAAGCTCT 3074
QY 868 uHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProfr 888
Db 3075 TCATGAACGTGACGACAGATGACGTGTGAACAGCTCACCGCACTGATGCTGCCCTG 3134
QY 888 pGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProgl 908
Db 3135 GGGCTGTGACGTGCAAGGCAGCGCTGACGAGCGCTGTTGAAACATTTGGAGGAGGTCCAC 3194
QY 908 nLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGl 928
Db 3195 ACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACAGATACAGATTTAGAAATTTAGG 3254
QY 928 yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnAr 948
Db 3255 TGCATTTTGGAAAGAACCCCTCTGAAAACTTCACAGATTTGAATTTGGCGGGAAATCG 3314
QY 948 gValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuVa 968
Db 3315 TGTGACGACGTGATGATGGCTTGCCTTCATGGTGTATTGAGAAATCTTTAAGCAATTTAGT 3374
QY 968 lPhePheAspPheSerThrLysGluPheLeuProaspProAlaLeuValArgLysLeuSe 988
Db 3375 GTTTTGTGACTTTAGTACTAAAGATTTCTACCTGATCCAGCATTAGTCAGAAAACTTAG 3434
QY 988 rGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAs 1008
Db 3435 CCAAGGTATTCCAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGGTGGAATTTGA 3494
QY 1008 pAspAspLeuSerValIleThr 1016
Db 3495 TGATGATGATCTCAGTGTATTACA 3519
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RESULT 14

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; Sequence 6, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-29643-6
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Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 80.76% Indels: 2
Db: 1 Gaps: 0
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US-09-697-089-2 (1-1024) x PCT-US00-29643-6 (1-3615)

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Db 2880 CTTTTTCATCAGACATCAGAGGAGACTTGGACGATTTGGCTCAGATTTAAAGGACTTG 2821
QY 109 TyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleAspIlePhe 128
Db 2820 TACCATACCCCATCTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATTATTTT 2761
QY 129 AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHisHisArg 148
Db 2760 AACTTTGAAAGCACCTTCACAGAACCTGTCTGTGGAGAGAGCAACACCATCACCGC 2701
QY 149 ValGluGlnLeuThrLeuAsnGlyLeuGlnAlaLeuGlnSerProCysIleIleGlu 168
Db 2700 GTGGAGAGCTGACCTGAAATGGCCTCTGACAGGCTCTTCAGAGGCCCTTCGATCATTTGNA 2641
QY 169 GlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySer 188
Db 2640 GGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGCGAATTTGCCATGCTCTGGGGCTCC 2581
QY 189 GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla 208
Db 2580 GGAAGTGCAGAGGCTCTGACCAAGTTCAAATTCGCTTCTTCCCTCCGCTCAGCAGGGCC 2521
QY 209 GlnGlyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThrIleArg 228
Db 2520 CAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATATCCTGGCAACATCAGG 2461
QY 229 LysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAsp 248
Db 2460 AAGCAGACATTCATGCCATGCTGCTGAGCTGCGCAGAGGGTCTTTTCTCTTCTTGAT 2401
QY 249 GlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuLysGluAsn 268
Db 2400 GGCTCAATGAATTCAGGCCCCAGAACTGCCAGAAATCGAAAGCCCTGATAAGGAAAC 2341
QY 269 HisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArg 288
Db 2340 CACCGCTTCAAGAACATGGTCACTGTCACCCTACCATGAGTGGCTGAGGCGACATACGG 2281
QY 289 GlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu 308
Db 2280 CAGTTTGGTGCCCTGACTGCTGAGGTGGGGATATGACAGAAGACAGCGCCAGGCTCTC 2221
QY 309 IleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeuGlnIleGlnLysSer 328
Db 2220 ATCCGAGAAGTCTGATCAAGGAGCTTGTGAAGGCTTGTGCTCAAAATTCAGAAATCC 2161
QY 329 ArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCysAlaIleGln 348
Db 2160 AGTGCTTGAGGAATCTCATGAAGCCCTCTCTTTGTGGTCACTACCTGTGCAATCCAG 2101
QY 349 MetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrPheTyrAsp 368
Db 2100 ATGGGTGAAAGTGAGTTCACCTCTCACACACAAACAAACGCTGTTCATACCTTCTATGAT 2041
QY 369 LeuLeuIleGlnLysAsnLysHisLysHisGlyValAlaAlaSerAspPheIleArg 388
Db 2040 CTGTTGATACAGAAAAACAAACACAAACATAAAGGTGGCTGCAAGTGACTTCATTCCG 1981
QY 389 SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAspPhe 408
Db 1980 AGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTGTTCTCCACAAAGTTTGTATTC 1921
QY 409 GluLeuGlnAspValSerSerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCys 428
Db 1920 GAACTGCAGGATGTGTCCACGCGTGAATGAGGATGCTCTGCTGACAACTGGGCTCCTCTGT 1861
QY 429 LysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGlu 448
Db 1860 AAATATACAGCTCAAGAGGTTCAGGCCAAAGTATAAATCTTTTTCACAAGTCATTCCAGGAG 1801
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DB	736	CTTTTTCATCAGACATCAGAAGCAGACTTGGACGATTTGGCTCAGGATTTAAAGGACTTG	795
QY	109	TyrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleIlePhe	128
DB	796	TACCATACCCCATCTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATATTATTTT	855
QY	129	AsnLeuLysSerThrPheThrGluProValLeuTyrArgLysAspGlnHisHisAsArg	148
DB	856	AACCTGAAAGACACCTTCAGAACCTCTCTGTGGAGGAGACCAACACCATCACCGC	915
QY	149	ValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlu	168
DB	916	GTGGAGCAGCTGACCTGAATGCCCTCTCCAGGCTCTTCAGAGCCCTGCATCATTGAA	975
QY	169	GlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTyrGlySer	188
DB	976	GGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGCGAATGCCATGCTCTGGGGCTCC	1035
QY	189	GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla	208
DB	1036	GAAAGTGCAAGCTCTGCACCAAGTTCAATTCGTCTCTCCGTCTCAGCAGGGCC	1095
QY	209	GlnGlyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThrIleArg	228
DB	1096	CAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCGATATACCTGGCACAATCAGG	1155
QY	229	LysGlnThrPheMetAlaMetLeuLysLeuArgGlnArgValLeuPheLeuLeuAsp	248
DB	1156	AACGACACATTCATGGCCATGCTGCTGAAGCTCGCGCAGAGGGTCTTTCTCTCTTGAT	1215
QY	249	GlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuLysGluAsn	268
DB	1216	GGCTACAATGAATTAAGCCCAAGAACTGCCAGAAATCGAAGCCCTGATAAGGAAAC	1275
QY	269	HisArgPheLysAsnMetValIleValThrThrThrGluCysLeuArgHisIleArg	288
DB	1276	CACCGTCTCAAGAACATGTGTCATCGTCACCACTTACCACCTGAGTGCCTGAGGCACATACGG	1335
QY	289	GlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeu	308
DB	1336	CAGTTTGGTCCCTGACTGCTGAGTGGGGGATATCAGAGACAGCCCGCCAGGCTCTC	1395
QY	309	IleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeuGlnIleGlnLysSer	328
DB	1396	ATCCGAGAGTGTGATCAAGGAGCTTGCTGAAGGCTTGCTGCCAAATTCAGAAATCC	1455
QY	329	ArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCysAlaIleGln	348
DB	1456	AGTGTCTTGAGGAATCTCATGAAGACCCCTCTCTTTGGTGTCATCACTTGTGCAATCCAG	1515
QY	349	MetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrPheTyrAsp	368
DB	1516	ATGGGTGAAGTAGTGTCCACTCTCACACAAACACCGCTGTTCCTACCTTCTATGAT	1575
QY	369	LeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaSerAspPheIleArg	388
DB	1576	CTGTTGATACAGAAAAACAACAACATAAAGGTGTGGCTGCAAGTCACTTCATTCGG	1635
QY	389	SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLysPheAspPhe	408
DB	1636	AGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTCTCTCCACCAAGTTTGATTTC	1695
QY	409	GluLeuGlnAspValSerSerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCys	428
DB	1696	GAACTCAGGATGTGCCAGCGTGAATGAGGATGTCTCTGCACAACTGGGCTCCTCTGT	1755
QY	429	LysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGlu	448
DB	1756	AAATATACAGCTCAAGGTTCAAGCCAAAGTATAAATCTTTTCACAGTCAATCCAGGAG	1815
QY	449	TyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGluProGluGluValThr	468
DB	1816	TACACAGCAGGACCAAGACTCAGCAGTTATTGACGCTCTCATGAGCCAGAGGAGTGACC	1875
QY	469	LysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerThrTyrSer	488
DB	1876	AAGGGAAATGGTTACTTTCAGAAAAATGGTTTCCATTTCCGACCATTCATCCACTTAGC	1935
QY	489	SerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLysHis	508
DB	1936	AGCCTCTCCGGTACACCTGTGGTCTCATCTGTGAAAGCCACCAAGGCTGTATTAGAAGCAC	1995
QY	509	LeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAlaLysArgProLeu	528
DB	1996	CTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGACTTTCCATCCGCAAGAGCGCTCTC	2055
QY	529	TyrArgGlnGluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAla	548
DB	2056	TGGAGACAGAAATCTTTGCAAGTGTGAAAAACACCACTGAGCAGCAAGAAATTCGAAAGCC	2115
QY	549	IleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSerLys	568
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QY	569	SerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSer	588
DB	2176	TCAGCCCTCAGCCCAAGAAATTTGAAGCTTTCTTTCAAGGTAAGAAAGCTTATATATCAACTCA	2235
QY	589	GlyAsnIleProAspTyrLeuPheAspPhePheGluHisLeuProAsnCysAlaSerAla	608
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QY	609	LeuAspPheIleLysLeuAspPheTyrGlyGlyAlaMetAlaSerTrpGluLysAlaAla	628
DB	2296	CTGGACTTCATTAACATGGACTTTTATGGGAGCTATGGCTTCATGGGAAAGGCTGCA	2355
QY	629	GluAspThrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSerArgAla	648
DB	2356	GAAGACACAGGTGAATCCACATGGAAGAGGCCCCAGAACCTTACATTCACAGCGGCT	2415
QY	649	ValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuArgAsp	668
DB	2416	GTATCTTCTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGCTCACACTCCGGAT	2475
QY	669	PheSerLysLeuAsnLysGlnAspIleThr-TyrLeuGlyLysIlePheSerSerAlaTh	688
DB	2476	TTCAGCAAGTTGAATAAGCAAGATATCAG-ATATCTGGGGAAAAATATTGAGCTCTGCCAC	2534
QY	688	rSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeuSerLeuValle	708
DB	2535	AGCCTCAGGCTGCAAAATAAGAGATGTGCTGTGTGGTGGAGGCTCAGTTTGTGCTCT	2594
QY	708	uSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAs	728
DB	2595	CAGCACCCTGTAGAACAATTTATCTCTCATGGTGGAGCCAGCTCCCTCCACCATAGAGA	2654
QY	728	pGluArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAs	748
DB	2655	TGAGGACACATCACATCTGTAAACAAACCTGAAACCTTGAGTATTTCATGACCTACAGAA	2714
QY	748	nGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLe	768
DB	2715	TCAACGGCTGCCGGTGGTCTGACTGACAGCTTGGTGAATCTTGAAGAAGCTTACAAAGCT	2774
QY	768	uIleMetAspAsnIleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLys	788
DB	2775	CATAATGGATACATAAAGATGAATGAAGAAGATGTATATAAACTAGCTGAAGGCTGAA	2834
QY	788	sAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGlyLeu	808

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Db 2895 GGATTACATAGTCAAGTCTCTGTCAAGTGAACCTGTGACCTTGAAGAAATTCATTAGT 2954
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Db 3015 CAAACTGAGCATCTTGATTATCAGAAAATTACCTGGAAGATGCAATGAAGCTCT 3074
Qy 868 uHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTr 888
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Qy 888 pGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluValProGl 908
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Db 3315 TGTGAGCAGTGATGGATGGCTTGCTTCATGGTGTATTTCAGATCTTTAGCAATTAGT 3374
Qy 968 lPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSe 988
Db 3375 GTTTTTTGACTTTAGTACTAAAGAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTAG 3434
Qy 988 rGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAs 1008
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Db 3495 TGATGATGATCTCAGTGTATTACA 3519
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Job time : 5269 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
4013.976 Million cell updates/sec

Title: US-09-697-089-2

Perfect score: 1024

Sequence: 1 MNFKDNRSLRIQRMGTVI.....WQFDDDDLSVITGAFKLVT 1024

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2500250 seqs, 609544256 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4999244

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame-p2n.model -DEV=xlh
-Q/cgn2_1/USPTO_spool/US09697089/runat_29012003_091155_13527/app_query.fasta_1.1223
-DB=pending_Patents_NA_New -OFMT=fastap -SUFFIX=olip2n.rnpn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09697089 @CGN_1.1.114 @runat_29012003_091155_13527
-NCPU=6 -ICPU=3 -NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -YGAPOP=6 -DELEX=7
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

- 1: Pending_Patents_NA_New.*
- 2: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	923	90.1	3075	1	PCT-US02-21946A-1
2	923	90.1	3219	1	PCT-US02-21946A-14
3	721	70.4	3345	6	US-10-276-781-111
4	80	7.8	421	6	US-10-203-138A-4307
5	73	7.1	220	6	US-10-203-138A-9429
6	9	0.9	1956	5	US-09-620-312D-68
7	9	0.9	2685	5	US-09-134-000C-2326
8	9	0.9	2685	5	US-09-134-000C-2326
9	8	0.8	25	7	US-60-427-836-236146
10	8	0.8	212	5	US-09-531-113-8971
11	8	0.8	331	6	US-10-240-425-558

12	8	0.8	357	6	US-10-152-319A-1150
13	8	0.8	357	6	US-10-301-856-641
c 14	8	0.8	369	6	US-10-301-856-417
c 15	8	0.8	392	6	US-10-203-138A-3084
c 16	8	0.8	428	6	US-10-152-319A-103
c 17	8	0.8	428	6	US-10-301-856-73
c 18	8	0.8	471	6	US-10-276-781-683
c 19	8	0.8	484	5	US-09-513-999C-12518
c 20	8	0.8	493	6	US-10-203-138A-701
c 21	8	0.8	840	1	PCT-US02-20847-10
c 22	8	0.8	870	1	PCT-US01-43607-152
c 23	8	0.8	1018	5	US-09-724-676-25872
c 24	8	0.8	1018	5	US-09-724-676A-25872
c 25	8	0.8	1217	5	US-09-724-676-25862
c 26	8	0.8	1217	5	US-09-724-676A-25862
c 27	8	0.8	1263	5	US-09-724-676-25871
c 28	8	0.8	1263	5	US-09-724-676A-25871
c 29	8	0.8	1382	6	US-10-305-720-1427
c 30	8	0.8	1401	1	PCT-US02-02274A-2
c 31	8	0.8	1401	6	US-10-161-916A-4
c 32	8	0.8	1414	6	US-10-218-140-4531
c 33	8	0.8	1462	5	US-09-724-676-25861
c 34	8	0.8	1462	5	US-09-724-676A-25861
c 35	8	0.8	1625	5	US-09-724-676-30069
c 36	8	0.8	1625	5	US-09-724-676A-30069
c 37	8	0.8	1741	5	US-09-724-676-30058
c 38	8	0.8	1741	5	US-09-724-676A-30058
c 39	8	0.8	1745	5	US-09-724-676-25870
c 40	8	0.8	1745	5	US-09-724-676A-25870
c 41	8	0.8	1857	5	US-09-134-000C-3133
c 42	8	0.8	1857	5	US-09-134-000C-3133
c 43	8	0.8	1944	5	US-09-724-676-25860
c 44	8	0.8	1944	5	US-09-724-676A-25860
c 45	8	0.8	2074	6	US-10-218-140-3441

ALIGNMENTS

RESULT 1
PCT-US02-21946A-1
; Sequence 1, Application PC/TUS0221946A
; GENERAL INFORMATION:
; APPLICANT: Thomas Jefferson University
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; TITLE OF INVENTION: FACTOR
; FILE REFERENCE: 480140.477PC
; CURRENT APPLICATION NUMBER: PCT/US02/21946A
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3075
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3075)
PCT-US02-21946A-1

Alignment Scores:			
Pred. No.:	0	Length:	3075
Score:	923.00	Matches:	1023
Percent Similarity:	99.80%	Conservative:	0
Best Local Similarity:	99.80%	Mismatches:	1
Query Match:	90.14%	Indels:	2
DB:	1	Gaps:	0

US-09-697-089-2 (1-1024) x PCT-US02-21946A-1 (1-3075)

Qy	1	MetAspHeilelysAspAsnSerArgAlaLeuileGlnArgMetGlyMetThrValile	20
Db	1	ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTATTATCAAGAATGGGAATGACTGTATA	60

Db	2220	CTTGAGTATTCAGACCTACAGAATCAACGGCTCGCGGGTGGTCTGACTGACAGCTTGGG	2279
Qy	760	yAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAl	780
Db	2280	TAACTTGAAGAACCTTACAAAGCTCATATGATGAACATAAAGATGAATGAAGAAGATGC	2339
Qy	780	alleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHi	800
Db	2340	TATAAAACATAGCTGAAGGCCTGAAAACCTGAAGAAGATGTGTATTATTCATTATTTACCCA	2399
Qy	800	sLeuSerAspIleGlyGluGlyMetAspThrIleValLysSerLeuSerSerGluProCy	820
Db	2400	CTTGCTGTGACATTGGAGAGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTG	2459
Qy	820	sAspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLe	840
Db	2460	TGACCTTGAAGAAATTCATTAGTCTCCTGCTGCTGTCTGCAAAATGCAGTGAATACTCT	2519
Qy	840	uAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrl	860
Db	2520	AGCTCAGAATCTTCAAAATTTGGTCAAACTGAGCATTTCTGATTTATCAGAAAAATACCT	2579
Qy	860	uGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGl	880
Db	2580	GGAAAAAGATGGAAATGAAGCTTTCATCAACTGATCACAAGGATGAACGTGCTAGAACCA	2639
Qy	880	nLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLe	900
Db	2640	GCTACCGCAGTACTGCTCCCTGGGGCTGTGACGTGCAAGCGACGCTGACGACCGTGT	2699
Qy	900	uLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuth	920
Db	2700	GAACAATTTGGAGGAGGTCCCAACTCGTCAAGCTTGGGTGAAAAAAGTGGAGACTCAC	2759
Qy	920	rAspThrGluIleAArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGl	940
Db	2760	AGATACAGAGATTAGAAATTTTAGTGGCATTTTGGAAAGAACCCCTCTGAAAAATTTCCA	2819
Qy	940	nGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVa	960
Db	2820	GCAGTTGAATTTGGCGGGAAATCGTGTGACGAGTATGGATGGCTTGCCTTCATGGGTGT	2879
Qy	960	lPheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAs	980
Db	2880	ATTGTGAAATCTTAAGCAATTAAGCTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGA	2939
Qy	980	pProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAl	1000
Db	2940	TCAGAGATTAGTCAGAAAAACTTAGCCAGTGTATCCAAAGTTAACTTTCTGCAAGAACG	2999
Qy	1000	aArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys	1020
Db	3000	TAGSCTTGTTGGTGGCAATTTGATGATGATCATCTCAGTCTTATACAGGTGCTTTTAA	3059
Qy	1020	sLeuValThrAla 1024	
Db	3060	ACTAGTAACCTGCT 3072	

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RESULT 2
PCT-US02-21946A-14
; Sequence 14, Application PC/TUS0221946A
; GENERAL INFORMATION:
; APPLICANT: Thomas Jefferson University
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; TITLE OF INVENTION: FACTOR
; FILE REFERENCE: 480140.477PC
; CURRENT APPLICATION NUMBER: PCT/US02/21946A
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14

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; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-21946A-14

Alignment Scores:
Pred. No.: 0 Length: 3219
Score: 923.00 Matches: 1023
Percent Similarity: 99.80% Conservatived: 0
Best Local Similarity: 99.80% Mismatches: 1
Query Match: 90.14% Indels: 2
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x PCT-US02-21946A-14 (1-3219)

Qy 1 MetAsnPhelIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 145 ATGAATTCATAAGGACAAATAGCGAGCCCTTATTCAAGAATGGGAATGACTGTATTA 204
Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40
Db 205 AAGCAATACAGATGACCTATTTGTATGGAACTCTCTGAATCGCGAAGAAGTAAACATC 264
Qy 41 IleCysCysGluLysValGluGlnAspAlaalaargGlyIlelleHleMetIleLeuLys 60
Db 265 ATTTGCTCGGAGAAGTGGAGCAGGATGCTCTAGAGGATCATTCACATGATTTTGAA 324
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
Db 325 AAGGGTTCAGAGTCTCTGTAACTCTTTCTTAAATCCCTTAAGGAGTGGAACTATCTCTA 384
Qy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
Db 385 TTTCAGGACTTGAATGGCAAAAGTCTTTTTCATCAGACATCAGAAGAGAGACTTGGACCAT 444
Qy 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120
Db 445 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGGAACCTTTATCCCTT 504
Qy 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140
Db 505 GGTGAAGATATTGACATTTATTTTAACTTGAAGAGCACCCTTCACAGAACCCTGCTGTGG 564
Qy 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
Db 565 AGGAAGGACCAACACCATCACCGGTGGAGCAGCTGACCTGATGSCCTCTCTGCAGGCT 624
Qy 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 180
Db 625 CTTCAGAGCCCTGTCATCATTTGAAGGGGAATCTGGCAAAAGGCAAGTCCACTCTGTCAG 684
Qy 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db 685 CGAATTGGCATGCTCTGGGGCTCGCGAAGTGCAGGCTCTGACCAAGTTCAAAATTCGTC 744
Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 220
Db 745 TTCITTCCTCCGTCTCAGCAGGGGCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTC 804
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240
Db 805 CTGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTCGCG 864
Qy 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
Db 865 CAGAGGGTCTCTTTCCCTCTTGTATGGGTACATAATGAAATTCAGGCCCCAGAACTGCCCA 924
Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280
Db 925 ATCGAAGGCCCTGTATAAGGAAACACCCGCTTCAAGAACCATGGTCTCATCCACCTACC 984
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300

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Db 985 ACTGAGTGCTGAGGCACATACAGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGATATG 1044
QY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
|||||
Db 1045 ACAGAGACAGCGCCAGGCTCTCATCCGAGAAAGTGTGATCAAGGAGCTTGCTGNAGGC 1104
QY 321 LeuLeuGlnInLleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
Db 1105 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCTCTCTTT 1164
QY 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
Db 1165 GTGGTCATCATTGTCATTCAGATCCAGATGGGTGAAAGTGAGTTCACCTCTCACACAAACA 1224
QY 361 ThrLeuPheHisThrPheTyrAspLeuIleGlnLysAsnLysHisLysGly 380
Db 1225 AGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAACACAAATAAAGT 1284
QY 381 ValAlaAspSerPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400
Db 1285 GTGGCTGCAAGTACTTCATTCCGAGCCTGGACCCTGTGGAGACCTAGCTCTGGAGGCT 1344
QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420
Db 1345 GTGTTCTCCCAACAGTTTGATTTCCGAACTGCGAGGATGTCCAGCGTGAATGAGGATGTC 1404
QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440
Db 1405 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTCAAGCCAAAGTATAAA 1464
QY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr 460
Db 1465 TTCTTTTCAACAGTCAATTCAGAGAGTACAGCAGGACGAAGACTCAGCAGTTTATTGAGC 1524
QY 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db 1525 TCTCATGACCCAGAGAGGTGACCAAGGGGAATGGTTACTTCGAAAAATGGTTTCCATP 1584
QY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500
Db 1585 TCGGACATTACATCCATTATAGCAGCCTGCTCCGGTACACCTGTGGGTCTCTGTGGAA 1644
QY 501 AlaThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuGly 520
Db 1645 GGCACCCAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCTCTCGGA 1704
QY 521 LeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThr 540
Db 1705 CTTTCATCGCCACAGAGGCTCTCTGGACACAGGAATCTTTGCAAAAGTGTGAAAAACACC 1764
QY 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db 1765 ACTGAGCAAGAAATCTGAAAGCCATAACATCAATCTCTTTGTAGAGTGTGGCATCCAT 1824
QY 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPheGln 580
Db 1825 TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCAAGAAATTTGAAGCTTCTTTTCAA 1884
QY 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu 600
Db 1885 GGTAAAGCTTATATCAACTCAGGGAACATCCCGGATTTACTTTTGACTTCTTTTGA 1944
QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620
Db 1945 CATTTGCCCAATTTGCAAGTCCCTGGACTTCATTAACCTGGACTTTTATGGGGAGCT 2004
QY 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640
Db 2005 ATGGCTTCATGGAAAAAGCTCCAGAACACACAGGTGGAATCCCATGGAAGAGGCCCA 2064
QY 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660
Db 2065 GAAACCTACATTTCCAGCAGGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGG 2124

QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr-TyrLe 680
|||||
Db 2125 ACTCTGGAGGTCACTCCGGGATTTCAACAAGTTGAATAAGCAAGATATACAG-ATATCT 2183
QY 680 uGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVa 700
Db 2184 GGGGAAAAATATTAGCTCTGCCACAAGCTCAGGCTGCAAAATAAAGAGATGCTGCTGT 2243
QY 700 lAlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGl 720
Db 2244 GGCTGGAAGCCCTCAGTTGGTCTCAGCACCTGTGAACATTTATTTCTCATGGTGA 2303
QY 720 uAlaSerProLeuThrIleLeuAspGluArgHisIleThrSerValThrAsnLeuLysTh 740
Db 2304 AGCCAGTCCCTCACCATAGAAGATGAGAGGCACATCATCTGTAAACAAACCTGAAAC 2363
QY 740 rLeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGl 760
Db 2364 CTTGAGTATTATGACCTACAGAACTCAAGGCTGCGGGTGGTCTGACTGACAGCTTGG 2423
QY 760 yAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAl 780
Db 2424 TAACTTGAAGAACCCTTACAAAGCTCATATGATTAACATAAAGATGAATGAAGAAGATCC 2483
QY 780 aIleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHi 800
Db 2484 TATAAACTAGCTGAAGGCCCTGAAAAACCTGAAGAAGATGCTGTTATTTCATTGACCCA 2543
QY 800 sLeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCy 820
Db 2544 CTTGTCTGACATTGGAGAGGGAATGGATTACATAGTCTCAAGTCTCTCAAGTGAACCTG 2603
QY 820 sAspLeuGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLe 840
Db 2604 TGACCTTGAAGAAATTCAAATTAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2663
QY 840 uAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLe 860
Db 2664 AGCTCAGAATCTTCAAAATTTGGTCAAACTGAGCATTTCTTGATTTATCAGAAAAATACCT 2723
QY 860 uGluLysAspGlyAsnGluAlaLeuHisGluLeuLeuAspArgMetAsnValLeuGluGl 880
Db 2724 GAAAAAAGATGAAAAATGAAGCTCTTCATGAACCTGATCGACAGATGAAGCTGCTAGAACA 2783
QY 880 nLeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLe 900
Db 2784 GCTCACCAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2843
QY 900 uLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuTh 920
Db 2844 GAAACATTTGGAGGAGGTCCCAACTCGTCAAGCTTGGTTGAAAAAACTGGAGACTCAC 2903
QY 920 rAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGl 940
Db 2904 AGATACAGAGATTAGAAATTTAGGTGCAATTTTGGAAAGAACCCCTCTGAAAAAACTTCCA 2963
QY 940 nGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVa 960
Db 2964 GCAGTTGAATTTGGCGGGAATTCGTGTGAGCAGTGTGATGGATGGCTTGCCTTCATGGGTG 3023
QY 960 lPheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAs 980
Db 3024 ATTTGAGAAATCTTAAGCAATTAGTGTTTTTTGTACCTTTAGTACTAAAGAAATTTCTACCTGA 3083
QY 980 pProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAl 1000
Db 3084 TCCAGCATTTAGTCAGAAACCTTAGCAAGTGTATCCCAAGTTAACTTTTCTCAAGAACG 3143
QY 1000 aArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3144 TAGGCTTGTGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3203

Qy 1020 sLeuValThrAla 1024
|||||
Db 3204 ACTAGTAAGTCT 3216

RESULT 3

US-10-276-781-111
; Sequence 111, Application US/10276781
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-018 (785 contig)
; CURRENT APPLICATION NUMBER: US/10/276,781
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 2018
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-781-111

Alignment Scores:
Pred. No.: 0 Length: 3545
Score: 721.00 Matches: 1021
Percent Similarity: 99.42% Conservative: 0
Best Local Similarity: 99.42% Mismatches: 3
Query Match: 70.41% Indels: 6
Gaps: 0
DB:

US-09-697-089-2 (1-1024) x US-10-276-781-111 (1-3545)

Qy 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 232 ATGAATTTTCATAAAGGACATAGCGGAGCCCTTATTCAAAGAAATGGGAATGACTGTTATA 291
Qy 21 LysGlnIleThrAspLeuPheValTrpAsnValLeuAsnArgGluValAsnIle 40
Db 292 AAGCAATTCACAGATGACCTATTGTTATGGAATGTTCTGAAATCGCAAGAGAAATGAACATC 351
Qy 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 352 ATTTGCTCGAAGAGGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGAA 411
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu 80
Db 412 AAGGTTTCAGAGTCTGTAACTCTTTTAAATCCCTTAAGGAGTGAACATATCTCTTA 471
Qy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
Db 472 TTTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAAAGAGACTTGGACCAT 531
Qy 101 LeuAlaGlnAspLeuLysAspLeuTrpHisThrProSerPheLeuAsnPheTrpProLeu 120
Db 532 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTCAACTTTTATCCCTT 591
Qy 121 GlyGluAspIleAspIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140
Db 592 GGTGAAGATATTTGACATATTTTAACTTGAAGACACCTTTCACAGAACCTGTCTGTGG 651
Qy 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160
Db 652 AGGAAGGCCAACACCATCAGCGGTGGAGCAGCTGACCCCTGAATGGCTCTCTCGAGGCT 711
Qy 161 LeuGlnSerProCysIleIleGluSerGlyLysGlyLysSerThrLeuLeuGln 180
Db 712 CTTACAGCCCCCTGCATCATTTGAAGGGAATCTGGCAAGCAAGTCCACCTGCTGTCGAG 771
Qy 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db 772 CGCATTTGCCATGCTCTGGGGTCCGGAAGTGCAGAGGCTCTGACCAAGTTCAAATTCGTC 831

Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 220
Db 832 TTCTTCTCCGCTCAGCAGGGCCCCAGGGTGACATTTTGAACCCCTCTGTGATCAACTC 891
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240
Db 892 CTGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGG 951
Qy 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
Db 952 CAGAGGGTCTTTCTTCTTGTATGGCTACAAATGAATCAAGCCCCAGAACTGCCAGAA 1011
Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 280
Db 1012 ATCGAAGCCCTGATAAAGAAACCCGCCCTTCAAGAACATGGTCTATGCTCACCACCTACC 1071
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
Db 1072 ACTGAGTGCCTGAGGCACATACGGCAGTTTGTGTCCTGACTGCTGAGTGGGGATATG 1131
Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320
Db 1132 ACAGAAGACAGCGCCCGGCTCTCATCCGAGAAGTGTCTGATCAAGGAGCTTCTCTGAAGGC 1191
Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340
Db 1192 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1251
Qy 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360
Db 1252 GTGGTTCATCACTTGTGCAATCCAGATGGTGAAGTGAAGTTCCTCTCACACACAAACA 1311
Qy 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly 380
Db 1312 AGCGTGTTCATACCTTCTATGATCTGTGATACAGAAACAAACACAAACATAAAGGT 1371
Qy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAsp-LeuAlaLeuGluGln 400
Db 1372 GTGGCTGCAAGTGACTTCATTCGGAGCCTGGACCACTGTGGATA-CCTAGCTCTGGAGG 1430
Qy 400 yValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVa 420
Db 1431 TGTGTCTCTCCACAAAGTTTGATTTCGAATCGCAGGATGTGTCCAGCGTGAATGAGGATGT 1490
Qy 420 IleLeuThrThrGlyLeuLeuCysLysTrpThrAlaGlnArgPheLysProLysTrpLys 440
Db 1491 CCTGCTGACAACTGGGCTCCTCTGTAAATATATACGCTCAAAGGTTCAAGCCAAAGTATAA 1550
Qy 440 sPhePheHisLysSerPheGlnGluTrpThrAlaGlyArgArgLeuSerSerLeuLeuTh 460
Db 1551 ATCTTTTCACAAGTTCATTCAGGAGTACACAGCAGGACGAGACTCAGCAGTTTATTGAC 1610
Qy 460 rSerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480
Db 1611 GTCTCATGAGCAGAGGAGGTGACCAAGGGGAATGGTTACTTTCAGAAAAATGGTTTCCAT 1670
Qy 480 eSerAspIleThrSerThrTrpSerSerLeuLeuArgTrpThrCysGlySerSerValGln 500
Db 1671 TTCGACATTCATCCACTTATAGCAGCTGCTCGGTTACACCTGTGGGTGATCTGTGGA 1730
Qy 500 uAlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGln 520
Db 1731 AGCCACAGGCTGTATGAGACCTCGCAGCAGTGTATCAACAGCGCTGCTCTCTCGG 1790
Qy 520 yLeuSerIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnTh 540
Db 1791 ACTTTCCATCGCAAGAGGCTCTCTGGAGACAGGAATCTTTTGAAGTGTGAAAAACAC 1850
Qy 540 rThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560
Db 1851 CACTGAGCAAGAAATTCGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCA 1910

Qy	560	sLeuTyrgInGlnSerThrSerLysSerAlaLeuSerGlnGlnPheGluAlaPhePheG1	580
Db	1911	TTTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAAGAAATTTGAAGCTTCTTTCA	1970
	580	nGlyLysSerLeuTyriLeAsnSerGlyAsnIleProAspTyriLeuPheAspPheG1	600
	1971	AGGTAAAGCTTATATATCAACTCAGGGAACATCCCGGATTACTTATTGTGACTTCTTTGA	2030
Qy	600	uHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAsp - PheTyriGlyGlyA	620
Db	2031	ACATTGCCCAATGTGCAAGTCTCTGGACNCTCATTAACNCTGG - CTTTTATGGGGAG	2089
Qy	620	laMetalSerTrpGluLysAlaAlaGluAspThrGlyIleHisMetGluGluAlap	640
Db	2090	CTATGGCTTCATGGGAAAGGCTGCAGAGACACAGGTGGAATCCACATGGAAGAGGCC	2149
Qy	640	roGluThrTyriIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheA	660
Db	2150	CAGAAACCTCATTTCCACAGAGGCTGTATCTTCTTCTTCAACTGGAAGCAGGAATTC	2209
Qy	660	rgThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThr - Tyr	679
Db	2210	GGACTCTGGAGGTCACACTCCGGGATTCAGCAAGTTGNAATPAAGCAGATATCAG - ATAT	2268
Qy	680	LeuGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGly	699
Db	2269	CTGGGAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCRAATAAAGAGATGTCTGGT	2328
Qy	700	ValAlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyriSerLeuMetVal	719
Db	2329	GTGGCTGGAAAGCCTCAGTTTGGTCTCAGCAGCCTGTAAGAACAATTTATCTCTCATGTG	2388
Qy	720	GluAlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLys	739
Db	2389	GAAGCAGTCCCTTCACCATAGAAGATGAGAGGCACATCACATCTGTAAACAACTGAAA	2448
Qy	740	ThrLeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeu	759
Db	2449	ACCTTGAGTATTCATGNCTTACAGATCAACGGCTGCCGGTGGTCTCACTGCACAGCTTG	2508
Qy	760	GlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysP	779
Db	2509	GGTAACCTGAAGAACCTTCAAAAGCTCATAAATGGATACATAAAGATCAATGAAGAAG	2568
Qy	780	AlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThr	799
Db	2569	GCTATAAACTAGCTGAAGGCCCTGAAAAACCTGAGAAGATGTGTTTATTTTCATTTGACC	2628
Qy	800	HisLeuSerAspIleGlyGluGlyMetAspTyriIleValLysSerLeuSerSerGluPro	819
Db	2629	CACTTGTCTCACATTCGAGAGGAATGGATTACATAGTCAAGTCTCTCAAGTGAACCC	2688
Qy	820	CysAspLeuGluIleGlnLeuValSerCysLysLeuSerAlaAsnAlaValLysIle	839
Db	2689	TGTGACCTTGAAGAAATTCAAATAGTCTCCTGCTGCTGTCTGCAAAATGCAGTGAATAATC	2748
Qy	840	LeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyri	859
Db	2749	CTAGCTCAGAAATCTTCACAAATTTGGTCAAACTGAGCATCTTGATTTATCAGAAAAATTC	2808
Qy	860	LeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlu	879
Db	2809	CTGGAAAAAGATGGAATGAAGCTCTTCATGAACTGATCGACAGATGAAGCTGCTAGAA	2868
Qy	880	GlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeu	899
Db	2869	CAGCTCACCCACTGATGTGCTGGGCTGTGAGCTGCAAGGAGGAGCCTGAGCAGCCTG	2928
Qy	900	LeuLysHisLeuGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeu	919
Db	2929	TTGAAACATTTGAGAGAGGTCCACAACTCTGCAAGCTTGGGTTGGTAAACCTGGAGACT	2988
Qy	920	ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe	939

[illegible]

FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 558
LENGTH: 331
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. AI309223
US-10-240-425-558

Alignment Scores:
Pred. No.: 215 Length: 331
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x US-10-240-425-558 (1-331)

QY 759 SerLeuAlaThrSerLeuArgLeuThr 766
DB 145 TCCAGCGCCACCTCACTGAGACTT 186

RESULT 12

US-10-152-319A-1150
Sequence 1150, Application US/10152319A
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1150
LENGTH: 357
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:

OTHER INFORMATION: Genbank Accession No. A1179407
US-10-152-319A-1150
Alignment Scores:
Pred. No.: 232 Length: 357
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x US-10-152-319A-1150 (1-357)

QY 685 SerSerAlaThrSerLeuArgLeu 692
DB 163 TCCAGCGCCACCTCACTGAGACTT 186

RESULT 13

US-10-301-856-641
Sequence 641, Application US/10301856
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Nephrotoxicology Modeling
FILE REFERENCE: 44921-5089-01
CURRENT APPLICATION NUMBER: US/10/301,856
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US 10/152,319
PRIOR FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1261
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 641
LENGTH: 357
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:

OTHER INFORMATION: Genbank Accession No. A1179407
US-10-301-856-641

Alignment Scores:
Pred. No.: 232 Length: 357
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x US-10-301-856-641 (1-357)

QY 685 SerSerAlaThrSerLeuArgLeu 692

Db 163 TCCAGCGCCACCTCACTGAGACTT 186
|||||

RESULT 14

US-10-301-856-417/c
; Sequence 417, Application US/10301856
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Elashoff, Michael
; FILE OF INVENTION: Molecular Nephrotoxicology Modeling
; CURRENT APPLICATION NUMBER: US/10/301,856
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1261
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 417
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AI029017
US-10-301-856-417

Alignment Scores:
Pred. No.: 239 Length: 369
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x US-10-301-856-417 (1-369)

QY 849 LysLeuSerIleLeuAspLeuSer 856
|||||
Db 84 AAGCTGAGTACTACTGACTTATCA 61

RESULT 15

US-10-203-138A-3084/c
; Sequence 3084, Application US/10203138A
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474

; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203,138A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: CB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 3084
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031864.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
US-10-203-138A-3084

Alignment Scores:
Pred. No.: 254 Length: 392
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 0.78% Indels: 0
DB: 6 Gaps: 0

US-09-697-089-2 (1-1024) x US-10-203-138A-3084 (1-392)

QY 316 GluLeuAlaGluGlyLeuLeu 323
Db 174 GAAGTTCAGAGGTCGTCTCTT 151

Search completed: January 31, 2003, 08:44:50
Job time : 336 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 22:46:10 : Search time 7683 seconds
(without alignments)
11636.577 Million cell updates/sec

Title: US-09-697-089-3
Perfect score: 3072
Sequence: 1 atgaattcataaaggacaa.....cttttaactagtaactgct 3072

Scoring table: **OLIGO_NUC**
Gapop 60.0, Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues
Word size 6 12
Total number of hits satisfying chosen parameters: 824982

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl.*

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- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
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- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
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- 24: em_ph.*
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- 27: em_sts.*
- 28: em_un.*
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- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3072	100.0	3133	9	AY032589	Homo sapi
2	2919	95.0	3219	9	AY035391	Homo sapi
3	2919	95.0	3360	9	BC031555	Homo sapi
4	2868	93.4	3355	9	AK095467	Homo sapi
5	2868	93.4	3396	6	AX318091	Sequence
6	2868	93.4	3396	9	AY027787	Homo sapi
7	2868	93.4	3581	9	AF376061	Homo sapi
8	1946	63.3	160583	2	AC010968	Homo sapi
9	1844	60.0	138909	9	CNS01DS3	Sequence
10	1267	41.2	1355	9	IR2005417	Homo sapi
11	840	27.3	891	6	AX318174	Sequence
12	815	26.5	1395	6	AX318093	Sequence
13	815	26.5	1395	9	AY027788	Homo sapi
14	618	20.1	618	6	AX318176	Sequence
15	461	15.0	768	6	AX318097	Sequence
16	461	15.0	768	9	AY027789	Homo sapi
17	292	9.5	162692	9	CNS01DS8	Sequence
18	292	9.5	185281	2	AC011232	Homo sapi
19	269	8.8	578	6	AX318095	Sequence
20	269	8.8	578	9	AY027790	Homo sapi
21	261	8.5	261	6	AX318172	Sequence
22	170	5.5	553	11	G55568	SHGC-100923
23	114	3.7	165	6	AX318178	Sequence
24	39	1.3	185469	2	AC101793	Mus muscu
25	29	0.9	29	6	AX318155	Sequence
26	25	0.8	25	6	AX318156	Sequence
27	25	0.8	25	6	AX318157	Sequence
28	25	0.8	25	6	AX318160	Sequence
29	25	0.8	175205	2	AC128434	Rattus no
30	24	0.8	24	6	AX318154	Sequence
31	24	0.8	33	6	AX318152	Sequence
32	23	0.7	23	6	AX318148	Sequence
33	23	0.7	23	6	AX318158	Sequence
34	23	0.7	169406	2	AC090582	Homo sapi
35	23	0.7	175152	2	AC074195	Homo sapi
36	23	0.7	183556	2	AC019059	Homo sapi
37	22	0.7	42513	9	AL592438	Human DNA
38	22	0.7	79431	2	AC098256	Rattus no
39	22	0.7	87834	9	AF002957	Sequence
40	22	0.7	137897	9	AL161913	Human DNA
41	22	0.7	151088	9	AC020917	Homo sapi
42	22	0.7	153733	2	AC011980	Homo sapi
43	22	0.7	155531	2	AL592213	Homo sapi
44	22	0.7	157021	2	AC129066	Didelphis
45	22	0.7	159946	2	AC079194	Homo sapi
46	21	0.7	21	6	AX318151	Sequence
47	21	0.7	30	6	AX318153	Sequence
48	21	0.7	7067	6	AX286953	Sequence
49	21	0.7	7595	4	BTCAK35	Bovine gene
50	21	0.7	9257	1	AE010385	Methanopy
51	21	0.7	35357	2	AC131526	Rattus no
52	21	0.7	37906	9	AC005199	Homo sapi
53	21	0.7	45496	2	AC017948	Drosophil
54	21	0.7	76526	2	AC027055	Homo sapi
55	21	0.7	80346	8	ATM4E13	Arabidops
56	21	0.7	84499	8	ATT1235	Arabidops
57	21	0.7	86710	8	ATF23E12	Arabidops
58	21	0.7	91573	10	AL732313	Mouse DNA
59	21	0.7	119141	2	AC096826	Rattus no
60	21	0.7	130117	9	AC004907	Homo sapi
61	21	0.7	157308	2	AC079351	Homo sapi
62	21	0.7	160931	3	AC093498	Drosophil
63	21	0.7	180176	10	AL671190	Mouse DNA
64	21	0.7	181277	2	AC120594	Rattus no
65	21	0.7	181477	9	AC024590	Homo sapi

c 66	21	0.7	184864	9	AC013553	AC013553 Homo sapi	139	20	0.7	163604	4	AC092727	AC092727 Bos tauru
c 67	21	0.7	194874	8	AC080090	AC080090 Homo sapi	c 140	20	0.7	164067	2	AC115162	AC115162 Rattus no
c 68	21	0.7	195165	8	ATCHRIV82	AL161586 Arabidops	c 141	20	0.7	164648	2	AC115014	AC115014 Mus muscu
c 69	21	0.7	197859	8	ATCHRIV83	AL161587 Arabidops	c 142	20	0.7	164688	2	AL732360	AL732360 Mus muscu
c 70	21	0.7	198935	2	AC068573	AC068573 Homo sapi	c 143	20	0.7	165333	9	AC023822	AC023822 Homo sapi
c 71	21	0.7	200398	9	AC025566	AC025566 Homo sapi	c 144	20	0.7	166953	3	AC093104	AC093104 Drosophil
c 72	21	0.7	201415	2	AC107239	AC107239 Mus muscu	c 145	20	0.7	167031	2	AC124468	AC124468 Mus muscu
c 73	21	0.7	206452	10	AL593857	AL593857 Mouse DNA	c 146	20	0.7	167469	2	AC113882	AC113882 Rattus no
c 74	21	0.7	211194	10	AL513468	AL513468 Mouse DNA	c 147	20	0.7	168038	2	AC112052	AC112052 Rattus no
c 75	21	0.7	213473	2	AC094371	AC094371 Rattus no	c 148	20	0.7	168231	9	AL589863	AL589863 Human DNA
c 76	21	0.7	214433	2	AL627184	AL627184 Mus muscu	c 149	20	0.7	170279	2	AC027053	AC027053 Homo sapi
c 77	21	0.7	221341	2	AC092992	AC092992 Homo sapi	c 150	20	0.7	171031	2	AC104020	AC104020 Homo sapi
c 78	21	0.7	227194	2	AC020727	AC020727 Homo sapi	c 151	20	0.7	171256	9	AC105193	AC105193 Homo sapi
c 79	21	0.7	242265	2	AC126460	AC126460 Mus muscu	c 152	20	0.7	172526	2	AC107467	AC107467 Rattus no
c 80	21	0.7	256933	10	AC099771	AC099771 Mus Muscu	c 153	20	0.7	174098	9	AC005737	AC005737 Homo sapi
c 81	21	0.7	303367	3	AE003538	AE003538 Drosophil	c 154	20	0.7	174612	9	CNS07EF6	AL512357 Human chr
c 82	20	0.7	475	6	AX437848	AX437848 Sequence	c 155	20	0.7	175274	9	AP004286	AP004286 Homo sapi
c 83	20	0.7	768	6	AX318097	AX318097 Sequence	c 156	20	0.7	175345	9	AC073065	AC073065 Homo sapi
c 84	20	0.7	768	9	AY027789	AY027789 Homo sapi	c 157	20	0.7	178861	2	AC068231	AC068231 Homo sapi
c 85	20	0.7	1198	14	REOS3NSB	M18390 Reovirus se	c 158	20	0.7	178864	9	AC022535	AC022535 Homo sapi
c 86	20	0.7	1688	8	SCYBR141C	236010 S.cerevisia	c 159	20	0.7	178868	9	AL357752	AL357752 Human DNA
c 87	20	0.7	2833	8	SCYBR142W	236011 S.cerevisia	c 160	20	0.7	180110	2	AC122001	AC122001 Mus muscu
c 88	20	0.7	3709	3	AF116341	AF116341 Drosophil	c 161	20	0.7	180303	9	AL672045	AL672045 Human DNA
c 89	20	0.7	10467	1	AE010860	AE010860 Methanosa	c 162	20	0.7	180836	2	AC025241	AC025241 Homo sapi
c 90	20	0.7	12595	8	SCIRAI	X78937 S.cerevisia	c 163	20	0.7	182870	2	AC016563	AC016563 Homo sapi
c 91	20	0.7	25474	2	AC110773	AC110773 Homo sapi	c 164	20	0.7	184003	2	AC011058	AC011058 Homo sapi
c 92	20	0.7	36631	9	HUMCOL7AlX	L23982 Homo sapien	c 165	20	0.7	185104	2	AC118763	AC118763 Rattus no
c 93	20	0.7	40937	3	CER01E6	758118 Caenorhabdi	c 166	20	0.7	185108	2	AC101860	AC101860 Mus muscu
c 94	20	0.7	45459	2	AC066103	AC066103 Homo sapi	c 167	20	0.7	185405	2	AP001887	AP001887 Homo sapi
c 95	20	0.7	69672	2	AC107863	AC107863 Mus muscu	c 168	20	0.7	185835	2	AC092007	AC092007 Bos tauru
c 96	20	0.7	71463	9	AC080088	AC080088 Homo sapi	c 169	20	0.7	186183	9	AC026827	AC026827 Homo sapi
c 97	20	0.7	81875	2	AC131203	AC131203 Rattus no	c 170	20	0.7	186381	2	AC109708	AC109708 Rattus no
c 98	20	0.7	83669	9	AC005210	AC005210 citib_179	c 171	20	0.7	186869	2	AC102392	AC102392 Mus muscu
c 99	20	0.7	86155	9	AL159169	AL159169 Human DNA	c 172	20	0.7	187998	2	AC125909	AC125909 Rattus no
c 100	20	0.7	86719	9	AP000885	AP000885 Homo sapi	c 173	20	0.7	189291	2	AC102326	AC102326 Mus muscu
c 101	20	0.7	88326	9	AC005923	AC005923 Homo sapi	c 174	20	0.7	191748	2	AL662902	AL662902 Mus muscu
c 102	20	0.7	88839	3	AC084447	AC084447 Caenorhab	c 175	20	0.7	192029	2	AC123986	AC123986 Mus muscu
c 103	20	0.7	89748	2	AC106195	AC106195 Rattus no	c 176	20	0.7	193999	2	AC113413	AC113413 Homo sapi
c 104	20	0.7	91733	2	AL391278	AL391278 Homo sapi	c 177	20	0.7	194973	9	AP002008	AP002008 Homo sapi
c 105	20	0.7	93409	2	AC073294	AC073294 Mus muscu	c 178	20	0.7	196031	2	AL844564	AL844564 Mus muscu
c 106	20	0.7	99225	2	AC114149	AC114149 Rattus no	c 179	20	0.7	197576	2	AC123476	AC123476 Rattus no
c 107	20	0.7	102165	2	AC083819	AC083819 Mus muscu	c 180	20	0.7	198501	2	AC118410	AC118410 Rattus no
c 108	20	0.7	106601	9	AL357352	AL357352 Human DNA	c 181	20	0.7	199903	2	AC113503	AC113503 Mus muscu
c 109	20	0.7	109810	9	AL139036	AL139036 Human DNA	c 182	20	0.7	204618	10	AF146793	AF146793 Mus muscu
c 110	20	0.7	111777	2	AP004089	AP004089 Oryza sat	c 183	20	0.7	206745	2	AC096481	AC096481 Rattus no
c 111	20	0.7	111851	9	AC090564	AC090564 Homo sapi	c 184	20	0.7	207411	2	AC084746	AC084746 Mus muscu
c 112	20	0.7	114169	9	AC010902	AC010902 Homo sapi	c 185	20	0.7	207541	2	AC121252	AC121252 Homo sapi
c 113	20	0.7	120733	9	AC022124	AC022124 Homo sapi	c 186	20	0.7	207873	2	AL807753	AL807753 Mus muscu
c 114	20	0.7	121931	9	AC008390	AC008390 Homo sapi	c 187	20	0.7	208095	2	AC118606	AC118606 Mus muscu
c 115	20	0.7	121963	2	AC095337	AC095337 Rattus no	c 188	20	0.7	208524	2	AC123260	AC123260 Mus muscu
c 116	20	0.7	124347	9	AC010072	AC010072 Homo sapi	c 189	20	0.7	213889	2	AL807242	AL807242 Mus muscu
c 117	20	0.7	129837	9	AC004829	AC004829 Homo sapi	c 190	20	0.7	216698	2	AC092006	AC092006 Bos tauru
c 118	20	0.7	130221	2	AC125495	AC125495 Oryza sat	c 191	20	0.7	217217	2	AC129085	AC129085 Mus muscu
c 119	20	0.7	130981	2	AC087702	AC087702 Trypanoso	c 192	20	0.7	218074	9	AC023283	AC023283 Homo sapi
c 120	20	0.7	132171	3	AC008370	AC008370 Drosophil	c 193	20	0.7	221689	2	AC097195	AC097195 Rattus no
c 121	20	0.7	132641	2	AC100539	AC100539 Mus muscu	c 194	20	0.7	226060	2	AC079583	AC079583 Mus muscu
c 122	20	0.7	132641	2	AC100539	AC100539 Mus muscu	c 195	20	0.7	226833	3	AE003838	AE003838 Drosophil
c 123	20	0.7	135497	2	AC102346	AC102346 Mus muscu	c 196	20	0.7	232827	2	AC125329	AC125329 Mus muscu
c 124	20	0.7	137955	9	AL359752	AL359752 Human DNA	c 197	20	0.7	235314	2	AC121848	AC121848 Mus muscu
c 125	20	0.7	141079	8	AP002868	AP002868 Oryza sat	c 198	20	0.7	327357	2	AC098504	AC098504 Rattus no
c 126	20	0.7	142203	2	AC079521	AC079521 Mus muscu	c 199	20	0.7	340000	9	AP001707	AP001707 Homo sapi
c 127	20	0.7	145576	8	AP002541	AP002541 Oryza sat	c 200	19	0.6	223	4	AF152590	AF152590 Capreolus
c 128	20	0.7	147474	2	AC117872	AC117872 Rattus no	c 201	19	0.6	275	11	G41356	G41356 21351 Zebra
c 129	20	0.7	147728	9	AC034113	AC034113 Homo sapi	c 202	19	0.6	375	14	AV655518	AV655518 Hepatitis
c 130	20	0.7	149207	9	AC010435	AC010435 Homo sapi	c 203	19	0.6	384	14	AV657142	AV657142 Hepatitis
c 131	20	0.7	150183	2	AC126985	AC126985 Rattus no	c 204	19	0.6	422	11	G21255	G21255 human STS W
c 132	20	0.7	151991	9	AP004289	AP004289 Homo sapi	c 205	19	0.6	558	1	AF437054	AF437054 Unculture
c 133	20	0.7	153031	2	AC105458	AC105458 Felis cat	c 206	19	0.6	581	11	G62797	G62797 SHGC-140335
c 134	20	0.7	155798	2	AC099431	AC099431 Rattus no	c 207	19	0.6	669	11	G58716	G58716 SHGC-105508
c 135	20	0.7	157559	2	AC020344	AC020344 Drosophil	c 208	19	0.6	755	8	STPOACUTR	X55748 S.tuberosum
c 136	20	0.7	158574	2	AC024895	AC024895 Homo sapi	c 209	19	0.6	770	9	HOMLC107	M61840 Human lacta
c 137	20	0.7	159158	9	AL359915	AL359915 Human DNA	c 210	19	0.6	888	3	DDU66524	U66524 Dictyostell
c 138	20	0.7	160392	9	AC104236	AC104236 Homo sapi	c 211	19	0.6	1260	1	S38128	S38128 lciA-lactoc

c 212	19	0.6	1494	10	RNU09228	U09228 Rattus norv	c 285	19	0.6	88735	2	AF165178	AF165178 Homo sapi
c 213	19	0.6	1578	9	AF236882	AF236882 Homo sapi	c 286	19	0.6	90041	2	AC095553	AC095553 Rattus no
c 214	19	0.6	1843	2	AC014303	AC014303 Drosophil	c 287	19	0.6	90902	8	AXF28M20	AXF28M20 Arabidops
c 215	19	0.6	2005	10	MUSKTEPII	K02108 Mouse kerat	c 288	19	0.6	91081	2	AC096165	AC096165 Rattus no
c 216	19	0.6	2064	8	AF191494	AF191494 Arabidops	c 289	19	0.6	91955	2	AL006613	AL006613 Rattus no
c 217	19	0.6	2249	10	BC003756	BC003756 Mus muscu	c 290	19	0.6	92138	9	AL590391	AL590391 Human DNA
c 218	19	0.6	2490	8	AF105142	AF105142 Brassica	c 291	19	0.6	93173	2	AC094918	AC094918 Rattus no
c 219	19	0.6	2494	9	HS0801051	AL117408 Homo sapi	c 292	19	0.6	94081	9	HSJ820B18	AL109946 Human DNA
c 220	19	0.6	2533	9	HS0805082	AL833769 Homo sapi	c 293	19	0.6	94366	2	AC112468	AC112468 Rattus no
c 221	19	0.6	2626	5	AE002145	AE002145 Rana cate	c 294	19	0.6	94453	9	AC019070	AC019070 Homo sapi
c 222	19	0.6	2790	9	AK054790	AK054790 Homo sapi	c 295	19	0.6	96577	2	AC128037	AC128037 Rattus no
c 223	19	0.6	2800	8	STPOAC58	X55749 S. tuberosum	c 296	19	0.6	96577	2	AC128037	AC128037 Rattus no
c 224	19	0.6	2825	9	AK023073	AK023073 Homo sapi	c 297	19	0.6	96577	2	AC128037	AC128037 Rattus no
c 225	19	0.6	3037	3	AF203971	AF203971 Entamoeba	c 298	19	0.6	99055	2	AC105465	AC105465 Rattus no
c 226	19	0.6	3151	8	AF089003	AF089003 Arabidops	c 299	19	0.6	99781	9	AC115082	AC115082 Homo sapi
c 227	19	0.6	3173	8	AF160500	AF160500 Arabidops	c 300	19	0.6	100099	10	AE008684_3	Continuation (4 of
c 228	19	0.6	4048	8	AF277737	AF277737 Arabidops	c 301	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 229	19	0.6	4080	8	SCADR6	XL12493 Yeast ADP6	c 302	19	0.6	101846	9	AL450324	AL450324 Human DNA
c 230	19	0.6	6274	9	HSLPH	X07994 Human mRNA	c 303	19	0.6	101912	9	AC000100	AC000100 Homo sapi
c 231	19	0.6	8801	14	AF037273	AY037273 Human imm	c 304	19	0.6	101912	9	AC000100	AC000100 Homo sapi
c 232	19	0.6	10029	1	AE006202	AE006202 Pasteurel	c 305	19	0.6	101912	9	AC000100	AC000100 Homo sapi
c 233	19	0.6	10379	1	AE007943	AE007943 Agrobacte	c 306	19	0.6	101912	9	AC000100	AC000100 Homo sapi
c 234	19	0.6	10581	1	AE008975	AE008975 Agrobacte	c 307	19	0.6	101912	9	AC000100	AC000100 Homo sapi
c 235	19	0.6	10917	6	AX384783	AX384783 Sequence	c 308	19	0.6	101912	9	AC000100	AC000100 Homo sapi
c 236	19	0.6	10939	1	AE000813	AE000813 Methanoba	c 309	19	0.6	101912	9	AC000100	AC000100 Homo sapi
c 237	19	0.6	12496	1	AE000634	AE000634 Helicobac	c 310	19	0.6	104334	5	AL606751	AL606751 Zebrafish
c 238	19	0.6	12526	1	AE001548	AE001548 Helicobac	c 311	19	0.6	104334	5	AL606751	AL606751 Zebrafish
c 239	19	0.6	13684	1	AE010466	AE010466 Fusobacte	c 312	19	0.6	104334	5	AL606751	AL606751 Zebrafish
c 240	19	0.6	14515	4	CFY15484	Y15484 Canis famli	c 313	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 241	19	0.6	22939	3	CEW04E12	Z82070 Caenorhabdi	c 314	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 242	19	0.6	23087	1	SCD40A	AL161691 Streptomy	c 315	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 243	19	0.6	27413	2	AC127051	AC127051 Rattus no	c 316	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 244	19	0.6	30589	3	CEZK666	Z49132 Caenorhabdi	c 317	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 245	19	0.6	31638	10	AF259073	AF259073 Mus muscu	c 318	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 246	19	0.6	35550	8	U33335	U33335 Saccharomyc	c 319	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 247	19	0.6	36019	9	AC008726	AC008726 Homo sapi	c 320	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 248	19	0.6	36630	9	AC006541	AC006541 Homo sapi	c 321	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 249	19	0.6	40638	10	AC005403	AC005403 Mus muscu	c 322	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 250	19	0.6	42248	2	AC105943	AC105943 Homo sapi	c 323	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 251	19	0.6	43351	9	AC004800	AC004800 Homo sapi	c 324	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 252	19	0.6	44027	3	CBRG41F07	AC084587 Caenorhab	c 325	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 253	19	0.6	44236	3	U80027	U80027 Caenorhabdi	c 326	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 254	19	0.6	47733	3	L14433	L14433 Caenorhabdi	c 327	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 255	19	0.6	49393	2	AC101083	AC101083 Mus muscu	c 328	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 256	19	0.6	52831	2	AC100274	AC100274 Mus muscu	c 329	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 257	19	0.6	54727	9	AL357336	AL357336 Human DNA	c 330	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 258	19	0.6	55801	2	AC131505	AC131505 Lytechinu	c 331	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 259	19	0.6	58330	2	AL353694_3	Continuation (4 of	c 332	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 260	19	0.6	58796	2	AC112983	AC112983 Mus muscu	c 333	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 261	19	0.6	58796	2	AC112983	AC112983 Mus muscu	c 334	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 262	19	0.6	61796	2	AC100321	AC100321 Mus muscu	c 335	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 263	19	0.6	61973	2	AC094631	AC094631 Rattus no	c 336	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 264	19	0.6	63347	2	AC110526	AC110526 Mus muscu	c 337	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 265	19	0.6	63809	2	AC100512	AC100512 Mus muscu	c 338	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 266	19	0.6	66204	2	AC084699	AC084699 Homo sapi	c 339	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 267	19	0.6	66204	2	AC084699	AC084699 Homo sapi	c 340	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 268	19	0.6	69208	2	AC020466	AC020466 Drosophil	c 341	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 269	19	0.6	71225	9	AL358196	AL358196 Human DNA	c 342	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 270	19	0.6	72085	2	AC118655	AC118655 Homo sapi	c 343	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 271	19	0.6	72891	2	AC124128	AC124128 Mus muscu	c 344	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 272	19	0.6	73546	2	AC129938	AC129938 Mus muscu	c 345	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 273	19	0.6	73579	2	AC117704	AC117704 Mus muscu	c 346	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 274	19	0.6	73656	2	AC027536	AC027536 Homo sapi	c 347	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 275	19	0.6	76193	9	AL451081	AL451081 Human DNA	c 348	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 276	19	0.6	77547	2	AC016804	AC016804 Homo sapi	c 349	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 277	19	0.6	77690	8	NC18A7	AL670542 Neurospor	c 350	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 278	19	0.6	78215	2	AC105803	AC105803 Rattus no	c 351	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 279	19	0.6	79376	2	AC105652	AC105652 Rattus no	c 352	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 280	19	0.6	79829	2	AC036211	AC036211 Homo sapi	c 353	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 281	19	0.6	83698	8	AB010072	AB010072 Arabidops	c 354	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 282	19	0.6	83341	2	AC106700	AC106700 Rattus no	c 355	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 283	19	0.6	88098	9	AL451042	AL451042 Human DNA	c 356	19	0.6	104757	2	AC095721	AC095721 Rattus no
c 284	19	0.6	88211	2	AC130247	AC130247 Rattus no	c 357	19	0.6	104757	2	AC095721	AC095721 Rattus no

358	19	0.6	131753	9	AL358790	Human DNA	431	19	0.6	158095	2	AC016224	Homo sapi
359	19	0.6	133708	2	AC120074	Rattus no	c 432	19	0.6	158591	9	AC012597	Homo sapi
360	19	0.6	133708	9	AC092270	Homo sapi	433	19	0.6	158677	2	CNS01DUR	Homo sapi
361	19	0.6	134965	9	AL354923	Human DNA	c 434	19	0.6	158817	2	AC127442	Rattus no
362	19	0.6	135245	9	AL354923	Rattus no	435	19	0.6	159312	2	AC096878	Pan trogl
363	19	0.6	135430	9	AC112131	Homo sapi	436	19	0.6	159476	9	AL441963	Human DNA
364	19	0.6	135598	9	AC099344	Homo sapi	437	19	0.6	159510	9	AC023156	Homo sapi
365	19	0.6	137150	2	AC125856	Rattus no	438	19	0.6	159859	9	AC074010	Homo sapi
366	19	0.6	137539	9	AC130193	Felis cat	c 439	19	0.6	160242	9	AP002778	Homo sapi
367	19	0.6	138783	9	HS564M11	Human DNA	c 440	19	0.6	160509	2	AC121749	Rattus no
368	19	0.6	140150	9	AC072057	Homo sapi	441	19	0.6	160736	2	AC027477	Homo sapi
369	19	0.6	140756	9	AL139038	Human DNA	442	19	0.6	160804	2	AC011828	Homo sapi
370	19	0.6	141212	2	AC113859	Rattus no	c 443	19	0.6	161003	2	AC121888	Mus muscu
371	19	0.6	142225	9	AC110053	Homo sapi	444	19	0.6	161150	2	AC126240	Felis cat
372	19	0.6	142367	2	AC109899	Rattus no	c 445	19	0.6	161648	9	AC108462	Homo sapi
373	19	0.6	142776	10	AC006404	Mus muscu	446	19	0.6	161682	2	AC024438	Homo sapi
374	19	0.6	143124	2	AC123074	Felis cat	447	19	0.6	161737	2	AC044901	Homo sapi
375	19	0.6	143281	2	AP000614	Homo sapi	448	19	0.6	161879	9	AC017005	Homo sapi
376	19	0.6	143677	2	AC102481	Mus muscu	c 449	19	0.6	162208	9	AC073321	Homo sapi
377	19	0.6	143710	2	AC036109	Homo sapi	450	19	0.6	162322	9	AC093027	Homo sapi
378	19	0.6	143723	2	AC012248	Homo sapi	c 451	19	0.6	162599	9	AL3560230	Human DNA
379	19	0.6	143823	9	AC019195	Homo sapi	c 452	19	0.6	163108	2	AC016741	Homo sapi
380	19	0.6	143842	2	AC096401	Rattus no	c 453	19	0.6	163228	2	AC127812	Rattus no
381	19	0.6	144480	2	AP004276	Human DNA	454	19	0.6	163528	2	AC130416	Homo sapi
382	19	0.6	146327	9	AL162253	Human DNA	455	19	0.6	163632	2	AC069057	Homo sapi
383	19	0.6	147061	2	AC119597	Rattus no	456	19	0.6	164223	2	AC109727	Rattus no
384	19	0.6	147140	9	AC010226	Homo sapi	c 457	19	0.6	164302	9	AC127457	Homo sapi
385	19	0.6	147489	2	AP001926	Homo sapi	458	19	0.6	164404	4	AC092874	Sus scrofa
386	19	0.6	147676	2	AC098065	Rattus no	c 459	19	0.6	164510	2	AC115711	Mus muscu
387	19	0.6	147993	2	AC094580	Rattus no	c 460	19	0.6	164668	9	AC091925	Homo sapi
388	19	0.6	148039	2	AC131388	Homo sapi	461	19	0.6	164820	2	AC109420	Rattus no
389	19	0.6	148082	9	AL139115	Human DNA	462	19	0.6	165158	2	AC103184	Rattus no
390	19	0.6	148147	9	AC044787	Homo sapi	c 463	19	0.6	165191	9	HSJ1140A9	Human DNA
391	19	0.6	148352	9	AC025309	Homo sapi	c 464	19	0.6	165337	2	AC096212	Rattus no
392	19	0.6	148469	2	AC128226	Rattus no	c 465	19	0.6	165456	9	AC090733	Homo sapi
393	19	0.6	148517	2	AC011147	Homo sapi	c 466	19	0.6	165589	9	AL356584	Human DNA
394	19	0.6	148557	2	AC116827	Mus muscu	467	19	0.6	165743	2	AL691459	Homo sapi
395	19	0.6	148703	2	AP004879	Oryza sat	c 468	19	0.6	165854	2	AC091539	Canis fam
396	19	0.6	148930	9	AC073316	Homo sapi	469	19	0.6	165945	2	AC104296	Mus muscu
397	19	0.6	149061	2	AC118888	Rattus no	c 470	19	0.6	166022	9	AL354950	Human DNA
398	19	0.6	149794	2	AC007273	Homo sapi	471	19	0.6	166143	9	AC013447	Homo sapi
399	19	0.6	150889	9	AC106881	Homo sapi	472	19	0.6	166305	9	AC012447	Homo sapi
400	19	0.6	151104	2	AC096123	Rattus no	c 473	19	0.6	166765	9	AC009721	Homo sapi
401	19	0.6	151117	2	AL357128	Homo sapi	c 474	19	0.6	167269	10	AC083894	Mus muscu
402	19	0.6	151121	2	AC012276	Homo sapi	475	19	0.6	167446	2	AC122292	Mus muscu
403	19	0.6	151321	2	AP004790	Oryza sat	c 476	19	0.6	167463	9	AC108489	Homo sapi
404	19	0.6	152408	2	AP005537	Oryza sat	c 477	19	0.6	167611	9	AL583859	Human DNA
405	19	0.6	152546	9	AL391221	Human DNA	478	19	0.6	167614	2	AC119641	Rattus no
406	19	0.6	152787	2	AC026623	Homo sapi	c 479	19	0.6	167616	2	AC106290	Rattus no
407	19	0.6	153300	2	AC011933	Homo sapi	480	19	0.6	167783	2	AC094651	Rattus no
408	19	0.6	153328	2	AC122111	Rattus no	c 481	19	0.6	167888	2	AC121651	Rattus no
409	19	0.6	153590	9	AP001284	Homo sapi	c 482	19	0.6	167998	9	AL353662	Human DNA
410	19	0.6	154001	9	AC083904	Homo sapi	483	19	0.6	168239	2	AC021367	Homo sapi
411	19	0.6	154076	2	AC023273	Homo sapi	c 484	19	0.6	168367	2	AC017830	Mus muscu
412	19	0.6	154159	2	AC104645	Homo sapi	485	19	0.6	168468	9	AC005510	Homo sapi
413	19	0.6	154289	2	AC027714	Homo sapi	c 486	19	0.6	168668	2	CNS07Y08	Oryza sat
414	19	0.6	154371	9	AP003466	Homo sapi	c 487	19	0.6	169106	2	AP005261	Oryza sat
415	19	0.6	154685	9	AP001595	Homo sapi	c 488	19	0.6	169184	9	AC022398	Homo sapi
416	19	0.6	155507	2	AL831747	Danio rer	c 489	19	0.6	169204	9	AP001486	Homo sapi
417	19	0.6	155619	9	CNS01DFT	Human chr	c 490	19	0.6	169514	2	AC122449	Mus muscu
418	19	0.6	155705	9	AC093823	Homo sapi	c 491	19	0.6	169833	2	AC107249	Rattus no
419	19	0.6	155763	2	AC099449	Rattus no	c 492	19	0.6	169880	2	AC107288	Rattus no
420	19	0.6	155818	9	AC073504	Homo sapi	c 493	19	0.6	170000	2	OSJN00133	Oryza sat
421	19	0.6	156149	2	AC027556	Homo sapi	c 494	19	0.6	170387	2	AC115225	Rattus no
422	19	0.6	156238	2	AC104862	Mus muscu	495	19	0.6	170494	2	AP001919	Homo sapi
423	19	0.6	156361	2	AC108612	Rattus no	496	19	0.6	170676	9	AC026258	Homo sapi
424	19	0.6	156381	2	AC021087	Homo sapi	c 497	19	0.6	170711	2	AC032020	Homo sapi
425	19	0.6	156452	2	AC096043	Rattus no	c 498	19	0.6	170829	2	AP001316	Homo sapi
426	19	0.6	156856	2	AC097235	Rattus no	c 499	19	0.6	170906	2	AC084314	Mus muscu
427	19	0.6	156891	2	AC108550	Rattus no	c 500	19	0.6	171349	2	AC020735	Homo sapi
428	19	0.6	156992	9	AC093581	Homo sapi	c 501	19	0.6	171369	2	AC113690	Rattus no
429	19	0.6	157511	2	AC021383	Homo sapi	502	19	0.6	171486	2	AC120330	Rattus no
430	19	0.6	157562	2	AC011574	Homo sapi	503	19	0.6	171676	9	AC107904	Homo sapi

c 650	19	0.6	199102	2	AC079315	AC079315 Homo sapi	c 723	19	0.6	229296	2	AL645969	AL645969 Mus muscu
c 651	19	0.6	199725	2	AC1100787	AC1100787 Homo sapi	724	19	0.6	232453	2	AC105985	AC105985 Mus muscu
c 652	19	0.6	199785	2	AC1119085	AC1119085 Rattus no	725	19	0.6	233363	2	AC078919	AC078919 Homo sapi
c 653	19	0.6	200257	2	AC122301	AC122301 Mus muscu	c 726	19	0.6	234649	2	AC109577	AC109577 Rattus no
c 654	19	0.6	200630	2	AC110424	AC110424 Rattus no	727	19	0.6	235841	2	AC126250	AC126250 Mus muscu
c 655	19	0.6	201027	9	AC025105	AC025105 Homo sapi	728	19	0.6	235996	2	AC107235	AC107235 Mus muscu
c 656	19	0.6	201035	2	AC016744	AC016744 Homo sapi	c 729	19	0.6	238554	2	AC124573	AC124573 Mus muscu
c 657	19	0.6	201114	2	AC131108	AC131108 Mus muscu	c 730	19	0.6	239570	2	AC111335	AC111335 Rattus no
c 658	19	0.6	201365	2	AL773563	AL773563 Mus muscu	c 731	19	0.6	240233	2	AC127342	AC127342 Mus muscu
c 659	19	0.6	201444	2	AL807810	AL807810 Mus muscu	c 732	19	0.6	240938	2	AL731665	AL731665 Mus muscu
c 660	19	0.6	201598	2	AL772335	AL772335 Mus muscu	c 733	19	0.6	247544	2	AC092741	AC092741 Mus muscu
c 661	19	0.6	201599	2	AC068790	AC068790 Homo sapi	c 734	19	0.6	248461	2	AC099619	AC099619 Mus muscu
c 662	19	0.6	201676	2	AC105367	AC105367 Sus scrof	c 735	19	0.6	255396	2	AC117201	AC117201 Mus muscu
c 663	19	0.6	201815	2	AC113497	AC113497 Mus muscu	736	19	0.6	255927	2	AC097689	AC097689 Rattus no
c 664	19	0.6	201897	2	AC098810	AC098810 Papio cyn	737	19	0.6	260252	3	AE003736	AE003736 Drosophil
c 665	19	0.6	202638	10	AL671492	AL671492 Mouse DNA	c 738	19	0.6	270361	2	AC114005	AC114005 Mus muscu
c 666	19	0.6	202640	2	AC090008	AC090008 Mus muscu	739	19	0.6	274947	2	AL731766	AL731766 Mus muscu
c 667	19	0.6	202719	9	AC006379	AC006379 Homo sapi	740	19	0.6	282895	2	AL133478	AL133478 Homo sapi
c 668	19	0.6	202849	2	AC130630	AC130630 Rattus no	741	19	0.6	295225	3	AE003461	AE003461 Drosophil
c 669	19	0.6	202945	9	AC008038	AC008038 Homo sapi	c 742	19	0.6	315986	2	AL627316	AL627316 Homo sapi
c 670	19	0.6	203286	10	AL606829	AL606829 Mouse DNA	743	19	0.6	321250	1	MPULM02	AL445564 Mycoplasma
c 671	19	0.6	204177	9	AC040926	AC040926 Homo sapi	744	19	0.6	321708	2	AC087142	AC087142 Mus muscu
c 672	19	0.6	204185	2	AL844521	AL844521 Danio rer	745	19	0.6	329752	2	AC096334	AC096334 Rattus no
c 673	19	0.6	204568	2	AC115547	AC115547 Rattus no	c 746	19	0.6	338116	2	AC087159	AC087159 Mus muscu
674	19	0.6	205331	2	AC124470	AC124470 Mus muscu	c 747	19	0.6	346940	2	AC107420	AC107420 Homo sapi
675	19	0.6	205770	2	AC102597	AC102597 Mus muscu	c 748	19	0.6	349980	6	AX344563	AX344563 Sequence
676	19	0.6	205793	2	AC103615	AC103615 Mus muscu	c 749	19	0.6	349980	6	AX344564	AX344564 Sequence
677	19	0.6	206222	2	AC108891	AC108891 Bos tauru	750	18	0.6	148	3	AX318150	AX318150 Sequence
678	19	0.6	207017	2	AC023373	AC023373 Homo sapi	751	18	0.6	148	3	S5918951	S591895 Drosophila
c 679	19	0.6	207183	9	AP001533	AP001533 Homo sapi	752	18	0.6	159	3	AY035318	AY035318 Lirionomyza
c 680	19	0.6	207457	2	AC102631	AC102631 Mus muscu	753	18	0.6	180	11	G56063	G56063 SHGC-101325
c 681	19	0.6	207514	2	AC094261	AC094261 Rattus no	c 754	18	0.6	184	9	HSNDSUJAY	222495 H.sapiens D
c 682	19	0.6	207694	9	AL354984	AL354984 Human DNA	c 755	18	0.6	201	9	HSLN2C10	U66742 Human lamin
c 683	19	0.6	208073	2	AC073226	AC073226 Homo sapi	c 756	18	0.6	226	9	HS119C2R	264430 H.sapiens C
684	19	0.6	208098	2	AL627251	AL627251 Mus muscu	c 757	18	0.6	244	9	HS7H5F	263261 H.sapiens C
685	19	0.6	208443	2	AC120207	AC120207 Canis fam	c 758	18	0.6	256	9	HSNASEAJ	222350 H.sapiens D
686	19	0.6	208571	9	AC010906	AC010906 Homo sapi	759	18	0.6	257	9	HS133BI2F	256643 H.sapiens C
c 687	19	0.6	208994	2	AC113448	AC113448 Mus muscu	c 760	18	0.6	269	9	HS21A8F	257913 H.sapiens C
c 688	19	0.6	209487	2	AC122422	AC122422 Mus muscu	c 761	18	0.6	295	9	HS133BI2R	256644 H.sapiens C
c 689	19	0.6	209743	9	AL354896	AL354896 Human DNA	c 762	18	0.6	295	9	HS26F4F	260518 H.sapiens C
c 690	19	0.6	209930	10	AC092751	AC092751 Genomic s	c 763	18	0.6	299	9	HS26F4F	260519 H.sapiens C
c 691	19	0.6	211574	2	AC125765	AC125765 Rattus no	c 764	18	0.6	319	9	HS26A7R	266380 H.sapiens C
c 692	19	0.6	213045	2	AC093640	AC093640 Homo sapi	c 765	18	0.6	321	9	HS59F6R	255711 H.sapiens C
c 693	19	0.6	214396	10	AL671968	AL671968 Mouse DNA	c 766	18	0.6	345	8	AF182368	AF182368 Coleochaee
c 694	19	0.6	214654	10	AC098716	AC098716 Mus muscu	c 767	18	0.6	375	8	AY039088	AY039088 Tayloria
c 695	19	0.6	214852	9	CNS05TCZ	AL355888 Human chr	768	18	0.6	377	8	AF020531	AF020531 Homo sapi
c 696	19	0.6	214986	2	AC122378	AC122378 Mus muscu	c 769	18	0.6	411	11	G62203	G62203 EST837 Foot
c 697	19	0.6	215172	2	AC126983	AC126983 Rattus no	770	18	0.6	480	11	AU046727	AU046727 Rattus no
c 698	19	0.6	216032	2	AC095703	AC095703 Rattus no	c 771	18	0.6	513	11	AF239035	AF239035 Oncorhynch
c 699	19	0.6	216095	2	AC107714	AC107714 Mus muscu	c 772	18	0.6	522	9	HS3434200	HS3434200 Homo sapi
700	19	0.6	216180	2	AC124347	AC124347 Mus muscu	c 773	18	0.6	554	3	AF248853	AF248853 Chironomu
701	19	0.6	216408	2	AC092466	AC092466 Homo sapi	c 774	18	0.6	554	3	AF248854	AF248854 Chironomu
702	19	0.6	218386	2	AC121589	AC121589 Mus muscu	c 775	18	0.6	578	9	HUMUG3PE	M14061 Human U3 sm
c 703	19	0.6	219151	2	AC115353	AC115353 Rattus no	c 776	18	0.6	580	4	BTWTCSD7	227077 B.taurus (C
c 704	19	0.6	220103	2	AC073781	AC073781 Mus muscu	c 777	18	0.6	585	8	SCYGL220W	Z72742 S.cerevisia
c 705	19	0.6	220384	2	AC078926	AC078926 Homo sapi	778	18	0.6	597	11	G39975	G39975 Z11944 Zebr
706	19	0.6	221157	2	AC091540	AC091540 Canis fam	c 779	18	0.6	634	9	HS34324130	HS34324130 Homo sapi
707	19	0.6	221912	10	AL672003	AL672003 Mouse DNA	c 780	18	0.6	634	9	HSU3B3	HSU3B3 Homo sapi
c 708	19	0.6	222048	2	AL844481	AL844481 Mus muscu	c 781	18	0.6	634	9	HSU3BTWO1	AF020534 Homo sapi
c 709	19	0.6	222472	2	AL732317	AL732317 Mus muscu	c 782	18	0.6	647	9	HSRPE65G08	AF039862 Homo sapi
710	19	0.6	222605	9	AC010973	AC010973 Homo sapi	783	18	0.6	656	11	PM11B2B	AL684121 Penicilli
711	19	0.6	222726	2	AL807747	AL807747 Mus muscu	c 784	18	0.6	660	9	HSRPE65G09	AF039863 Homo sapi
712	19	0.6	223664	2	AC125204	AC125204 Mus muscu	c 785	18	0.6	663	8	AY083348	AY083348 Solanum t
713	19	0.6	225119	2	AC015894	AC015894 Homo sapi	786	18	0.6	674	11	G56596	G56596 SHGC-102162
714	19	0.6	225260	2	AC108330	AC108330 Rattus no	c 787	18	0.6	688	9	HS3429826	HS3429826 Homo sapi
715	19	0.6	225924	2	AC074210	AC074210 Mus muscu	c 788	18	0.6	768	12	AF488703	AF488703 Synthetic
c 716	19	0.6	226467	2	AC121855	AC121855 Mus muscu	c 789	18	0.6	772	3	D83705	D83705 Drosophila
c 717	19	0.6	226685	2	AC121583	AC121583 Mus muscu	c 790	18	0.6	817	8	STU30814	STU30814 Solanum tub
718	19	0.6	227368	2	AC094262	AC094262 Rattus no	c 791	18	0.6	856	3	DROS3APEN	LI3690 Drosophila
c 719	19	0.6	227368	2	AC094262	AC094262 Rattus no	c 792	18	0.6	881	8	AY015079	AY015079 Gastrolob
c 720	19	0.6	227849	2	AC129322	AC129322 Mus muscu	c 793	18	0.6	883	5	GGU28241	U28241 Gallus gall
721	19	0.6	228584	2	AC122388	AC122388 Mus muscu	c 794	18	0.6	927	10	AY074035	AY074035 Mus muscu
c 722	19	0.6	229118	2	AC122272	AC122272 Mus muscu	c 795	18	0.6	928	3	AY118971	AY118971 Drosophila

796	18	0.6	960	6	AX122205	AX122205 Sequence	c 869	18	0.6	2689	1	BSU19898	UI9898 Bacillus sp
c 797	18	0.6	962	4	SHPPLAC	M31660 Ovine place	c 870	18	0.6	2740	1	P30TRA	M62986 Plasmid p30
798	18	0.6	1023	8	AF155762	AF155762 Pismum sat	c 871	18	0.6	2841	10	RATTCBC3	M63795 Rat T-cell
799	18	0.6	1047	5	AF317271	AF317271 Pelvicach	c 872	18	0.6	2854	8	SCYDL180W	Z74228 S. cerevisia
800	18	0.6	1083	6	AX064929	AX064929 Sequence	c 873	18	0.6	2904	9	AK096138	AK096138 Homo sapi
801	18	0.6	1094	9	HSU3	X14945 Human gene	c 874	18	0.6	2987	10	MMIDDGENE	X95460 M.musculus
c 802	18	0.6	1205	6	AX013773	AX013773 Sequence	c 875	18	0.6	3000	6	ARI72809	ARI72809 Sequence
c 803	18	0.6	1216	4	OAPLE2	AF079546 Ovis arie	c 876	18	0.6	3157	3	AY058362	AY058362 Drosophill
c 804	18	0.6	1254	1	AF369028	AF369028 Streptoco	c 877	18	0.6	3165	3	DMP13K59F	X99912 D.melanogas
c 805	18	0.6	1264	1	ECPSU233	X55896 E.coli plas	c 878	18	0.6	3275	6	AX078760	AX078760 Sequence
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c 807	18	0.6	1339	3	AF058340	AF058340 Drosophill	c 880	18	0.6	3614	8	RCHCHS2	DI0160 Rhizopus oi
c 808	18	0.6	1348	3	AF252639	AF252639 Drosophill	c 881	18	0.6	3671	14	AF291703	AF291703 Andes vir
c 809	18	0.6	1348	3	AF252641	AF252641 Drosophill	c 882	18	0.6	3881	8	SCU07228	U7228 Saccharomyc
c 810	18	0.6	1353	9	HS326249	AJ326249 Homo sapi	c 883	18	0.6	3968	1	MYCMBPRP	L11447 Mycoplasma
c 811	18	0.6	1389	9	AF154847	AF154847 Homo sapi	c 884	18	0.6	3969	6	AR203450	AR203450 Sequence
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c 814	18	0.6	1433	3	AFSECAATP	X79331 A.franciscs	c 887	18	0.6	3999	10	MUSMEGL	D78641 Mouse mRNA
c 815	18	0.6	1473	8	AY084564	AY084564 Arabidops	c 888	18	0.6	4116	8	AB055105	AB055105 Oryza sat
c 816	18	0.6	1506	8	AY052232	AY052232 Arabidops	c 889	18	0.6	4197	3	AF163835	AF163835 Dictyoste
c 817	18	0.6	1515	6	AR170122	AR170122 Sequence	c 890	18	0.6	4220	8	ENU86620	U86620 Emericella
c 818	18	0.6	1515	6	AR170123	AR170123 Sequence	c 891	18	0.6	4255	9	AK024455	AK024455 Homo sapi
c 819	18	0.6	1561	9	HUMNELI	M20199 Human neutr	c 892	18	0.6	4451	1	WSAJ3049	AJ003049 Wolinella
c 820	18	0.6	1579	9	AK000918	AF157497 Mus muscu	c 893	18	0.6	4796	5	XLXOLL	Y09661 X.laevis mR
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c 823	18	0.6	1634	10	MMU09930	U09930 Mus musculu	c 896	18	0.6	5028	8	SCU49845	U49845 Saccharomyc
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c 831	18	0.6	1792	9	BC007391	BC007391 Homo sapi	c 904	18	0.6	5867	9	HSL241B9A	Z69362 Human DNA s
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c 839	18	0.6	1930	9	AK057359	AK057359 Homo sapi	c 912	18	0.6	8810	9	AY040206	AY040206 Homo sapi
c 840	18	0.6	1935	9	D83730	D83730 Homo sapien	c 913	18	0.6	8868	6	AX399206	AX399206 Sequence
c 841	18	0.6	1943	5	GM6PR46K	X95501 G.gallus mR	c 914	18	0.6	8868	9	HSU16720	U16720 Human inter
c 842	18	0.6	1962	6	AK014865	AX014865 Sequence	c 915	18	0.6	8873	6	AX251820	AX251820 Sequence
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ALIGNMENTS

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DEFINITION
cvs.
ACCESSION  AY032589
VERSION    AY032589.1  GI:13899172
KEYWORDS   Homo sapiens.
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ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 3133) Geddes,B.J., Wang,L., Huang,W.-J., Lavellee,M., Manji,G.A., Brown,M., Jurman,M., Morganstern,J., Merriam,S., Glucksmann,A., DiStefano,P.S. and Bertin,J.
TITLE	Human CARD12 is a novel CED4/Apaf-1 family member that induces apoptosis
JOURNAL	Biochem. Biophys. Res. Commun. 284 (1), 77-82 (2001)
MEDLINE	21268963
PUBMED	11374873
REFERENCE	2 (bases 1 to 3133) Bertin,J.
TITLE	Direct Submission
JOURNAL	Submitted (15-APR-2001) Neurobiology, Millennium Pharmaceuticals Inc., 640 Memorial Drive, Cambridge, MA 02139, USA
FEATURES	Location/Qualifiers
source	1..3133
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ORIGIN	
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Best Local Similarity	100.0%; Pred. No. 0;
Matches 3072; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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QY 61	AAGCAATACAGATGACCTATTGTGTAATGCTTCTGAATCGGAAGTAACATC 120
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QY 121	ATTTCGTCGAGAGGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTGAAA 180
Db 156	ATTTCGTCGAGAGGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTGAAA 215
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Db 216	AAGGGTTCAGAGTCCTGTAACCTCTTCTTAAATCCCTTAAGGAGTGGAACTATCCTCTA 275

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DEFINITION	Homo sapiens, caspase recruitment domain protein 12, clone		
ACCESSION	MGC:35330 IMAGE:5179909, mRNA, complete cds.		
VERSION	BC031555		
KEYWORDS	MGC.		
SOURCE	BC031555.1 GI:21594975		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	1 (bases 1 to 3360)		
REMARK	Strausberg, R.		
COMMENT	Direct Submission		
	Submitted (06-JUN-2002) National Institutes of Health, Mammalian		
	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
	NIH-MGC Project URL: http://mgc.nci.nih.gov		
	Contact: MGC help desk		
	Email: cgapbs-r@mail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Baylor College of Medicine Human Genome		
	Sequencing Center		
	Center code: BCM-HGSC		
	Web site: http://www.hqsc.bcm.tmc.edu/cdna/		
	Contact: amg@bcm.tmc.edu		
	Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,		
	Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,		
	Richards, S., Gibbs, R.A.		
	Clone distribution: MGC clone distribution information can be found		
	through the I.M.A.G.E. Consortium/LLNE at: http://image.llnl.gov		
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LOCUS AX318091 3396 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 96 from Patent WO0190156.
ACCESSION AX318091
VERSION AX318091.1 GI:17900820
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Reed J.C., Pio F.F., Godzik A., Stehlik C., Damiano J.S., Lee S.H.,
Oliveira V.A., Hayashi H. and Pawlowski K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 96 29-NOV-2001;
The Burnham Institute (US)
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RESULT 7
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LOCUS
DEFINITION
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cds.
AF376061
AF376061.1 GI:14040074
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3581)
Gingras,M.-C., Qiu,J. and Margolin,J.F.
Differential expression of the caspase recruitment domain protein
12 (CARD12) during monocytic differentiation
Unpublished
2 (bases 1 to 3581)
Gingras,M.-C., Qiu,J. and Margolin,J.F.
Direct Submission
Submitted (03-MAY-2001) Pediatric/Texas Children's Cancer Center,
Baylor College of Medicine, 6621 Fannin St. MC3-3320, Houston, TX
77030, USA
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Matches 3068; Conservative 0; Mismatches 4; Indels 0; Gaps 0;									
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*	2181	2280:	gap of	unknown	length	
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of library CIBT_978_SKB from chromosome 2 of Homo sapiens (Human).
ACCESSION  AL121653
VERSION     AL121653.2 GI:7159616
KEYWORDS    SPG4 genomic DNA interval.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 138909)
AUTHORS     Hazan,J., Fonknechten,N., Mavel,D., Paternotte,C., Samson,D.,
Artiguenave,F., Davoine,C.S., Cruaud,C., Durr,A., Wincker,P.,
Brothier,P., Cattolico,L., Barbe,V., Burgunder,J.M.,
Prud'Homme,J.F., Brice,A., Fontaine,B., Heilig,R. and
Weissenbach,J.
TITLE       Spastin, a novel AAA protein, is altered in the most frequent form
of autosomal dominant spastic paraplegia
JOURNAL     Nat. Genet. (1999) In press
REFERENCE   2 (bases 1 to 138909)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (18-APR-2002) Genoscope - Centre National de Sequencage :
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT     On Mar 6, 2000 this sequence version replaced gi:6002386.
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Best Local Similarity 99.8%; Pred. No. 0;
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ACCESSION AL389934
VERSION AL389934.1 GI:9367839
KEYWORDS Full_cDNA.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1355)
Auffray,C., Ansoenge,W., Ballabio,A., Estivill,X., Gibson,K.,
Lehrach,H., Poustka,A. and Lundberg,J.
The European IMAGE consortium for Integrated Molecular analysis of
human gene transcripts
Unpublished
2 (bases 1 to 1355)
Pluvinet,R., Estivill,X., Escarceller,M. and Sumoy,L.
Direct Submission
Submitted (15-JUL-2000) Dept. Genetica Molecular, Institut de
Recerca Oncologica (IRO), Hospital Duran i Reynals, Av. Gran Via
s/n Km 2,7 L'Hospitalet de Llobregat, 08907 Barcelona, Catalunya,
SPAIN. Tel: ++34-93-260-7775 Fax: ++34-93-260-7776 WWW site:
http://www.iro.es e-mail enquiries: lsumoy@iro.es
EURO-IMAGE Consortium Contact: Auffray C
CNRS UPR 420 - Genetique Molculaire et Biologie du Developement
IFR 1221 - Rue Guy Moquet 19, Batiment G - Bp 8
94801 Villejuif Cedex, FRANCE
Tel: ++33-1-49 58 34 98
Fax: ++33-1-49 58 35 09
e-mail: auffray@infobiogen.fr
This clone is available royalty-free through IMAGE Consortium
Distributors.
IMPORTANT: This sequence represents the full insert of this IMAGE
cDNA clone. No attempt has been made to verify whether this
corresponds to the full-length of the original mRNA from which it
was derived.
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REFERENCE 2 (bases 1 to 1395)
AUTHORS Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
Research, The Burnham Institute, 10901 North Torrey Pines Road, La
Jolla, CA 92037, USA
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LOCUS Sequence 181 from Patent WO0190156.
DEFINITION AX318176
ACCESSION AX318176
VERSION AX318176.1 GI:17900867
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 181 29-NOV-2001;
The Burnham Institute (US)
FEATURES
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Query Match 20.1%; Score 618; DB 6; Length 618;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 15
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DEFINITION Sequence 102 from Patent WO0190156.
ACCESSION AX318097
VERSION AX318097.1 GI:17900826
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 102 29-NOV-2001;
FEATURES
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ACCESSION AY027789
VERSION AY027789.1 GI:14324116
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REFERENCE
1 (bases 1 to 768)
AUTHORS Damiano,J.S., Stehlik,C., Pio,F., Godzik,A. and Reed,J.C.
TITLE Clan, a novel human ced-4-like gene
JOURNAL Genomics 75 (1-3), 77-83 (2001)
MEDLINE 21365712
PUBMED 11472070
REFERENCE
2 (bases 1 to 768)
AUTHORS Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
Research, The Burnham Institute, 10901 North Torrey Pines Road, La
Jolla, CA 92037, USA
FEATURES
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.4e-237;
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QY 61 AAGCAAAATCACAGATGACCTATTGTATGGAATGTCTGAATCGCGAAGATGAACATC 120
Db 337 AAGCAAAATCACAGATGACCTATTGTATGGAATGTCTGAATCGCGAAGATGAACATC 396
QY 121 ATTGCTGCGAGAAGTGGAGGAGGATGCTGTAGAGGATCATTCACATGATTTTGA 180
Db 397 ATTGCTGCGAGAAGTGGAGGAGGATGCTGTAGAGGATCATTCACATGATTTTGA 456
QY 181 AAGGTTTCAGAGTCCCTGTACCTCTTCTTAATCCCTTAAGGAGTGAACATCCTCTA 240
Db 457 AAGGTTTCAGAGTCCCTGTACCTCTTCTTAATCCCTTAAGGAGTGAACATCCTCTA 516
QY 241 TTTAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGACGAT 300
Db 517 TTTAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGACGAT 576
QY 301 TTGGCTCAGATTAAAGGACTGTACCATACCCCATCTTTCTGAACATTTTATCCCTT 360
Db 577 TTGGCTCAGATTAAAGGACTGTACCATACCCCATCTTTCTGAACATTTTATCCCTT 636
QY 361 GTGAGATATTCACATATTTTAACTTGAAGACACCTTCACAGAACTGTCTGTGG 420
Db 637 GTGAGATATTCACATATTTTAACTTGAAGACACCTTCACAGAACTGTCTGTGG 696
QY 421 AGGAGGACCAACACCATCACCGCGTGGAGCAGTGACCT 461
Db 697 AGGAGGACCAACACCATCACCGCGTGGAGCAGTGACCT 737

RESULT 17
CNS01D58/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
BASE COUNT
ORIGIN

CNS01D58 162692 bp DNA linear PRI 18-APR-2002
BAC sequence from the SPG4 candidate region at 2p21-2p22 BAC 563N04
of library RPCI-11 from chromosome 2 of Homo sapiens (Human).
AL121658
AL121658.4 GI:20218783
SPG4 genomic DNA interval.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Hazan,J., Fonknechten,N., Mavel,D., Paternotte,C., Samson,D.,
Artiguenave,F., Davoine,C.S., Cruaud,C., Durr,A., Wincker,P.,
Brottier,P., Catolico,L., Barbe,V., Burgunder,J.M.,
Pruet/Homme,J.F., Brice,A., Fontaine,B., Heilig,R. and
Weissenbach,J.
Spastin, a novel AAA protein, is altered in the most frequent form
of autosomal dominant spastic paraplegia
Nat. Genet. (1999) In press
2 (bases 1 to 162692)
Direct Submission
Genoscope.
Submitted (18-APR-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Apr 19, 2002 this sequence version replaced gi:20160242.
Location/Qualifiers
1..162692
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="563N04"
44981 a 32017 c 32887 g 52792 t 15 others

Query Match 9.5%; Score 292; DB 9; Length 162692;
Best Local Similarity 100.0%; Pred. No. 6e-146;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2781 AGGTGCATTTTGGAAAGAACCCCTCTGAAAACTTCCAGCAGTTGGAATTTGGCGGAAA 2840
Db 152218 AGGTGCATTTTGGAAAGAACCCCTCTGAAAACTTCCAGCAGTTGGAATTTGGCGGAAA 152159
QY 2841 TCGTGTGACAGTGGATGGCTTGCCTTCATGGGTGTATTGAGAACTTTAAGCAAT 2900
Db 152158 TCGTGTGACAGTGGATGGCTTGCCTTCATGGGTGTATTGAGAACTTTAAGCAAT 152099
QY 2901 AGTGTGTTTGTACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCAATTAGTCAGAAAAC 2960
Db 152098 AGTGTGTTTGTACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCAATTAGTCAGAAAAC 152039
QY 2961 TAGCCAAAGTGTATCCAACTTAACCTTTCTGCAAGAAGTAGCTTTGTTGGGTCGCAAT 3020
Db 152038 TAGCCAAAGTGTATCCAACTTAACCTTTCTGCAAGAAGTAGCTTTGTTGGGTCGCAAT 151979
QY 3021 TGATGATGATGATCTCAGTGTATTATACAGTGTCTTTTAACTAGTAACTGCT 3072
Db 151978 TGATGATGATGATCTCAGTGTATTATACAGTGTCTTTTAACTAGTAACTGCT 151927

RESULT 18
AC011232/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AC011232 185281 bp DNA linear HTG 10-MAR-2001
Homo sapiens chromosome 2 clone RP11-78E13, WORKING DRAFT SEQUENCE,
7 unordered pieces.
AC011232
AC011232.7 GI:13270720
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Waterston,R.H.
1 (bases 1 to 185281)
The sequence of Homo sapiens clone
Unpublished
JOURNAL
2 (bases 1 to 185281)
Waterston,R.H.
Direct Submission
Submitted (04-OCT-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Mar 10, 2001 this sequence version replaced gi:9799811.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0078E13
----- Summary Statistics -----
Sequencing vector: M13; 57%
Sequencing vector: plasmid; 40%
Chemistry: Dye-primer ET; 48% of reads
Chemistry: Dye-terminator Big Dye; 50% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 182798 bases at least Q40
Consensus quality: 183538 bases at least Q30
Consensus quality: 184045 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 184681; sum-of-contigs
Quality coverage: 7.07 in Q20 bases; agarose-fp
Quality coverage: 7.33 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
```

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1985: contig of 1985 bp in length
* 1986 2085: gap of unknown length
* 2086 8183: contig of 6098 bp in length
* 8184 8283: gap of unknown length
* 8284 22741: contig of 14458 bp in length
* 22742 22841: gap of unknown length
* 22842 41446: contig of 18605 bp in length
* 41447 69183: contig of 27636 bp in length
* 69183 69283: gap of unknown length
* 69283 112131: contig of 42849 bp in length
* 112132 112232: gap of unknown length
* 112232 185281: contig of 73050 bp in length.

FEATURES

source
1. 185281
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-78E13"

misc_feature

1. 1985
/note="assembly_name:Contig11"
2086. 8183
/note="assembly_name:Contig12"
8284. 22741
/note="assembly_name:Contig13"
22842. 41446
/note="assembly_name:Contig14"
41547. 69182
/note="assembly_name:Contig15"
69283. 112131
/note="assembly_name:Contig16"
112232. 185281
/note="assembly_name:Contig17"

BASE COUNT 52719 a 36957 c 37187 g 57816 t 602 others
ORIGIN

Query Match 9.58; Score 292; DB 2; Length 185281;
Best Local Similarity 100.0%; Pred. No. 5.9e-146;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2781 AGGTGCATTTTGTGGAAGAACCCTCTGAAAACTTCACGAGTTGAATTTGGCGGAAA 2840
|||||
Db 160183 AGGTGCATTTTGTGGAAGAACCCTCTGAAAACTTCACGAGTTGAATTTGGCGGAAA 160124
|||||

Qy 2841 TCGTGTGAGCAGTGATGGCTTGCCCTTCATGGGTATTTGAGAACTTTAAGCAATT 2900
|||||
Db 160123 TCGTGTGAGCAGTGATGGCTTGCCCTTCATGGGTATTTGAGAACTTTAAGCAATT 160064
|||||

Qy 2901 AGTGTGTTTTCACCTTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAACT 2960
|||||
Db 160063 AGTGTGTTTTCACCTTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAACT 160004
|||||

Qy 2961 TAGCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGGGTGGCAATT 3020
|||||
Db 160003 TAGCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGGGTGGCAATT 159944
|||||

Qy 3021 TGATGATGATGATCTCAGTGTATTACAGGTCGCTTTTAAACTAGTAAGTCT 3072
|||||

Db 159943 TGATGATGATGATCTCAGTGTATTACAGGTCGCTTTTAAACTAGTAAGTCT 159892
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RESULT 19

AX318095
LOCUS AX318095 578 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 100 from Patent W00190156.
ACCESSION AX318095
VERSION AX318095.1 GI:17900824
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 100 29-NOV-2001;
The Burnham Institute (US)
FEATURES
source
1. 578
/organism="Homo sapiens"
/db_xref="taxon:9606"
277. 555
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD19342.1"
/db_xref="GI:17900825"
/translation="MNFIKDSRLIORMGMTVIKQITDLDLFVNNVLRREVNIIICCE
KVEQDAARGIIHMLKKGSESLFLKSLKEWNYPLFQDLNGQSLLTA"

BASE COUNT 172 a 106 c 143 g 157 t
ORIGIN

Query Match 8.88; Score 269; DB 6; Length 578;
Best Local Similarity 100.0%; Pred. No. 2.3e-133;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATTTTCATAAAGGACATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTTATA 60
|||||

Db 277 ATGAATTTTCATAAAGGACATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTTATA 336
|||||

Qy 61 AAGCAATACAGATGACCTATTGTTATGGAATGCTCTGAATCGCGAAGAGTAACATC 120
|||||

Db 337 AAGCAATACAGATGACCTATTGTTATGGAATGCTCTGAATCGCGAAGAGTAACATC 396
|||||

Qy 121 ATTTGCTGCGAAGAGGTGGAGCAGGATGCTCTAGAGGATCATTCACATGATTTTGAAA 180
|||||

Db 397 ATTTGCTGCGAAGAGGTGGAGCAGGATGCTCTAGAGGATCATTCACATGATTTTGAAA 456
|||||

Qy 181 AAGGTTTCAGAGTCTCTGAACCTCTTCTTAAATCCCTTAAGGAGTGAACATCTCTCTA 240
|||||

Db 457 AAGGTTTCAGAGTCTCTGAACCTCTTCTTAAATCCCTTAAGGAGTGAACATCTCTCTA 516
|||||

Qy 241 TTTCAGGACTTGAATGGACAAAGCTTTT 269
|||||

Db 517 TTTCAGGACTTGAATGGACAAAGCTTTT 545
|||||

RESULT 20

AY027790
LOCUS AY027790 578 bp mRNA linear PRI 20-JUL-2001
DEFINITION Homo sapiens CLAND (CLAN1) mRNA, complete cds.
ACCESSION AY027790
VERSION AY027790.1 GI:14324118
KEYWORDS
SOURCE Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 578)

AUTHORS Damiano,J.S., Stehlik,C., Pio,F., Godzik,A. and Reed,J.C.

TITLE Clon, a novel human ced-4-like gene

JOURNAL Genomics 75 (1-3), 77-83 (2001)

MEDLINE 21365712

PUBMED 11472070

REFERENCE 2 (bases 1 to 578)

AUTHORS Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.

TITLE Direct Submission

JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death

Research, The Burnham Institute, 10901 North Torrey Pines Road, La
Jolla, CA 92037, USA

FEATURES
source

Location/Qualifiers
1..578

/organism="Homo sapiens"
/db_xref="taxon:9606"

/chromosome="2"

/map="2p22-p21"

/tissue_type="lung"

1..578

/gene="CLAN1"

277..555

/gene="CLAN1"

/note="CARD protein; alternatively spliced"

/codon_start=1

/product="CLAND"

/protein_id="AAK14779.1"

/db_xref="GI:14324119"

/translation="MNFIKDNRSRALIQRMGTVIKQITDDLFVWVNLNREEVNIICCE
KVEQDAARGIIHMLKKGSECNFLKSLKEWNYPLFQDLNGQSLTTA"

BASE COUNT 172 a 106 c 143 g 157 t

ORIGIN

Query Match 8.8%; Score 269; DB 9; Length 578;

Best Local Similarity 100.0%; Pred. No. 2.3e-133;

Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTCATTAAGGACAAATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTATA 60

Db 277 ATGAATTCATTAAGGACAAATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTATA 336

QY 61 AAGCAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAAGTAACATC 120

Db 337 AAGCAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAAGTAACATC 396

QY 121 ATTGCTGCGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 180

Db 397 ATTGCTGCGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 456

QY 181 AAGGTTTCAGAGTCTGTAACTCTTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 240

Db 457 AAGGTTTCAGAGTCTGTAACTCTTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 516

QY 241 TTTCAGGACTTGAATGGACAAATGCTTTT 269

Db 517 TTTCAGGACTTGAATGGACAAATGCTTTT 545

RESULT 21

AX318172

LOCUS AX318172 261 bp DNA linear PAT 14-DEC-2001

DEFINITION Sequence 177 from Patent WO0190156.

ACCESSION AX318172

VERSION AX318172.1 GI:17900863

KEYWORDS human.

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

REFERENCE

AUTHORS

Reed, J.C., Pio, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H.,

Oliveira, V.A., Hayashi, H. and Pawlowski, K.

Card domain containing polypeptides, encoding nucleic acids, and

methods of use

JOURNAL

Patent: WO 0190156-A 177 29-NOV-2001;

The Burnham Institute (US)

FEATURES

Location/Qualifiers

1..261

/organism="Homo sapiens"

/db_xref="taxon:9606"

1..>261

/note="unnamed protein product"

/codon_start=1

/protein_id="CAD19349.1"

/db_xref="GI:17900864"

FEATURES
source

/translation="MNFIKDNRSRALIQRMGTVIKQITDDLFVWVNLNREEVNIICCE
KVEQDAARGIIHMLKKGSECNFLKSLKEWNYPLFQDLNGQ"

BASE COUNT 86 a 44 c 59 g 72 t

ORIGIN

Query Match 8.5%; Score 261; DB 6; Length 261;

Best Local Similarity 100.0%; Pred. No. 5.1e-129;

Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTCATTAAGGACAAATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTATA 60

Db 1 ATGAATTCATTAAGGACAAATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTATA 60

QY 61 AAGCAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAAGTAACATC 120

Db 61 AAGCAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAAGTAACATC 120

QY 121 ATTGCTGCGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 180

Db 121 ATTGCTGCGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 180

QY 181 AAGGTTTCAGAGTCTGTAACTCTTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 240

Db 181 AAGGTTTCAGAGTCTGTAACTCTTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 240

QY 241 TTTCAGGACTTGAATGGACAA 261

Db 241 TTTCAGGACTTGAATGGACAA 261

RESULT 22

G55568/c

LOCUS SHGC-100923 Human Homo sapiens STS genomic, sequence tagged site.

DEFINITION G55568

ACCESSION G55568

VERSION G55568.1 GI:6120887

KEYWORDS STS.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 553)

REFERENCE

AUTHORS

Olivier, M. and Cox, D.R.

Unpublished, Olivier, M., Cox, D.R. (2000)

JOURNAL

Unpublished (2000)

COMMENT

Contact: Michael Olivier, David R. Cox

Stanford Human Genome Center

Stanford University School of Medicine

4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA

Tel: (650) 320-5800

Fax: (650) 320-5801

Email: olivier@shgc.stanford.edu

Primer A: AATAAGGGGGGCAAAATAAGCAAA

Primer B: TAACACCCCTTTGTTCTCTCTCA

STS size: 322

PCR Profile:

Initial incubation: 95 degrees C for 10 minutes

Denaturation: 94 degrees C for 30 seconds

Annealing: 60 degrees C for 30 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9700

Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

AmpliTaq Gold Polymerase: 0.07 units/ul

Total Vol: 5 ul

Buffer:

MgCl2: 2.5 mM

KCl: 50 mM

Tris-HCl: 10 mM
pH: 8.3

BAC ends sequenced at TIGR from the RPC111 BAC library. Designed and developed at the Stanford Human Genome Center.

FEATURES

source
Location/Qualifiers
1. .553
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="2"
/clone_lib="Human"
5. .326
5. .27
primer_bind
primer_bind
complement(304..326)
BASE COUNT 170 a 107 c 114 g 162 t
ORIGIN

Query Match 5.5% Score 170; DB 11; Length 553;

Best Local Similarity 100.0%; Pred. No. 9.4e-80;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2615 TCGACAGGATGAAGCTGTAGAACAGCTCACCAGCTGATGCTGCCCTGGGGCTGTGACG 2674

Db 258 TCGACAGGATGAAGCTGTAGAACAGCTCACCAGCTGATGCTGCCCTGGGGCTGTGACG 199

Qy 2675 TGCAGGCGAGCTGAGCAGCCTGTGTAACATTTGGAGGAGTCCACAACTCGTCAAGC 2734

Db 198 TGCAGGCGAGCTGAGCAGCCTGTGTAACATTTGGAGGAGTCCACAACTCGTCAAGC 139

Qy 2735 TTGGTTGAAAACTGGAGACTCACAGTACAGAGATAGAAATTTAGGT 2784

Db 138 TTGGTTGAAAACTGGAGACTCACAGTACAGAGATAGAAATTTAGGT 89

RESULT 23

AX318178
LOCUS AX318178 165 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 183 from Patent WO0190156.
ACCESSION AX318178
VERSION AX318178.1 GI:17900869

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

Reed, J.C., Pio, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H.,

Oliveira, V.A., Hayashi, H., and Pawlowski, K.

Card domain containing polypeptides, encoding nucleic acids, and

methods of use

Patent: WO 0190156-A 183 29-NOV-2001;

The Burnham Institute (US)

FEATURES

source

1. .165

/organism="Homo sapiens"

/db_xref="taxon:9606"

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/note="unnamed protein product"

/codon_start=1

/protein_id="CAD19352.1"

/db_xref="GI:17900870"

/translation="TYPISRAVSLFFNWKQEFRTLEVTLRDFSKLNKQDIRYLKIFS

SATSLRLQIKR"

BASE COUNT 51 a 37 c 38 g 39 t

ORIGIN

Query Match 3.7% Score 114; DB 6; Length 165;

Best Local Similarity 99.4%; Pred. No. 2.1e-49;

Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1984

CTGGAGGTACACCTCCGGGATTTTCAGCAAGTTGAATAGCAAGATATCAGATATCTGGG 2043

Db 61 CTGGAGGTACACCTCCGGGATTTTCAGCAAGTTGAATAGCAAGATATCAGATATCTGGG 120

Qy 2044 AAAATATTACGCTCTGCCACAGCCTCAGCTGCAAAATAAAGAGA 2088

Db 121 AAAATATTACGCTCTGCCACAGCCTCAGCTGCAAAATAAAGAGA 165

RESULT 24

AC101793/c

LOCUS

DEFINITION

185469 bp DNA linear HTG 21-AUG-2002

Mus musculus clone RP24-178L2, WORKING DRAFT SEQUENCE, 43 unordered

pieces.

AC101793

AC101793.2 GI:22381529

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

house mouse.

Mus musculus

1 (bases 1 to 185469)

Birren, B., Nusbaum, C., and Lander, E.

Unpublished

2 (bases 1 to 185469)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,

Brown, A., Camarata, J., Campopiano, A., Chang, J., Chararo, B.,

Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,

Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,

Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,

Giude, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,

Jones, C., Kamat, A., Karatas, A., Kells, C., Lakocque, K.,

Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,

MacLean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C.,

McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrum, J.,

Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,

Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,

Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,

Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,

Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,

Seaman, S., Severi, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,

Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 185469)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,

Camarata, J., Chang, J., Chazaro, B., Choepe, Y., Collymore, A.,

Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,

Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,

Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,

Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,

Liu, G., MacLean, C., MacDonald, P., Major, J., Matthews, C.,

McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V.,

Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,

O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,

Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severi, P.,

Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,

Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,

Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome

COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 21, 2002 this sequence version replaced gi:17060568.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L17408
Center clone name: 178_L_2
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 173992 bases at least Q40
Consensus quality: 177954 bases at least Q30
Consensus quality: 180012 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 181269; sum-of-contigs
Quality coverage: 7.1 in Q20 bases; agarose-fp
Quality coverage: 6.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 43 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 60: contig of 60 bp in length
* 61 160: gap of 100 bp
* 161 824: contig of 664 bp in length
* 825 924: gap of 100 bp
* 925 1843: contig of 919 bp in length
* 1844 1943: gap of 100 bp
* 1944 2615: contig of 672 bp in length
* 2616 2715: gap of 100 bp
* 2716 3318: contig of 603 bp in length
* 3319 3418: gap of 100 bp
* 3419 4524: contig of 1106 bp in length
* 4525 4624: gap of 100 bp
* 4625 5485: contig of 861 bp in length
* 5486 5585: gap of 100 bp
* 5586 6384: contig of 799 bp in length
* 6385 6484: gap of 100 bp
* 6485 7162: contig of 678 bp in length
* 7163 7262: gap of 100 bp
* 7263 7456: contig of 194 bp in length
* 7457 7556: gap of 100 bp
* 7557 8160: contig of 604 bp in length
* 8161 8260: gap of 100 bp
* 8261 8941: contig of 681 bp in length
* 8942 9041: gap of 100 bp
* 9042 9922: contig of 881 bp in length
* 9923 10022: gap of 100 bp
* 10023 11459: contig of 1437 bp in length
* 11460 11559: gap of 100 bp
* 11560 12040: contig of 481 bp in length
* 12041 12140: gap of 100 bp
* 12141 13305: contig of 1165 bp in length
* 13306 13405: gap of 100 bp
* 13406 14296: contig of 891 bp in length
* 14297 14396: gap of 100 bp
* 14397 15353: contig of 957 bp in length
* 15354 15453: gap of 100 bp
* 15454 16520: contig of 1067 bp in length
* 16521 16620: gap of 100 bp
* 16621 18291: contig of 1671 bp in length
* 18292 18391: gap of 100 bp

* 18392 19794: contig of 1403 bp in length
* 19795 19894: gap of 100 bp
* 19895 21659: contig of 1765 bp in length
* 21660 21759: gap of 100 bp
* 21760 23729: contig of 1970 bp in length
* 23730 23829: gap of 100 bp
* 23830 25103: contig of 1274 bp in length
* 25104 25203: gap of 100 bp
* 25204 27230: contig of 2027 bp in length
* 27231 27330: gap of 100 bp
* 27331 29923: contig of 2593 bp in length
* 29924 30023: gap of 100 bp
* 30024 32248: contig of 2225 bp in length
* 32249 32348: gap of 100 bp
* 32349 35145: contig of 2797 bp in length
* 35146 35245: gap of 100 bp
* 35246 38595: contig of 3350 bp in length
* 38596 38695: gap of 100 bp
* 38696 41857: contig of 3162 bp in length
* 41858 41957: gap of 100 bp
* 41958 45734: contig of 3777 bp in length
* 45735 45834: gap of 100 bp
* 45835 50585: contig of 4751 bp in length
* 50586 50685: gap of 100 bp
* 50686 58532: contig of 7847 bp in length
* 58533 58632: gap of 100 bp
* 58633 64513: contig of 5881 bp in length
* 64514 64613: gap of 100 bp
* 64614 72116: contig of 7503 bp in length
* 72117 72216: gap of 100 bp
* 72217 79497: contig of 7281 bp in length
* 79498 79597: gap of 100 bp
* 79598 89239: contig of 9642 bp in length
* 89240 89339: gap of 100 bp
* 89340 100740: contig of 11401 bp in length
* 100741 100840: gap of 100 bp
* 100841 112859: contig of 12019 bp in length
* 112860 112959: gap of 100 bp
* 112960 125403: contig of 12444 bp in length
* 125404 125503: gap of 100 bp
* 125504 140153: contig of 14650 bp in length
* 140154 140253: gap of 100 bp
* 140254 160616: contig of 20363 bp in length
* 160617 160716: gap of 100 bp
* 160717 185469: contig of 24753 bp in length.
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Db 151494 CCTGAGCCAGAAATTGAAGCTTCTTTCAGAGGTAAAG 151456

RESULT 25
AX318155/c
LOCUS AX318155 29 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 160 from Patent WO0190156.
ACCESSION AX318155
VERSION AX318155.1 GI:17900846
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Read,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 160 29-NOV-2001;
The Burnham Institute (US)
FEATURES
source Location/Qualifiers
1. .25
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/db_xref="taxon:32630"
/note="primer"
BASE COUNT 8 a 8 c 8 g 5 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1152 TGACTTCATTCGGAGCCTGGACCACCTGTG 1180
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Db 29 TGACTTCATTCGGAGCCTGGACCACCTGTG 1

RESULT 26
AX318156
LOCUS AX318156 25 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 161 from Patent WO0190156.
ACCESSION AX318156
VERSION AX318156.1 GI:17900847
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Read,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 161 29-NOV-2001;
The Burnham Institute (US)
FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 CATCATTTGCTGCGAGAAGTGGAG 141
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Db 1 CATCATTTGCTGCGAGAAGTGGAG 25

RESULT 27
AX318157/c

LOCUS AX318157 25 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 162 from Patent WO0190156.
ACCESSION AX318157
VERSION AX318157.1 GI:17900848
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Read,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 162 29-NOV-2001;
The Burnham Institute (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32630"
/note="primer"
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ORIGIN
Query Match 0.8%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2959 CTTAGCCCAAGTGTATCCCAAGTTAA 2983
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Db 25 CTTAGCCCAAGTGTATCCCAAGTTAA 1

RESULT 28
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LOCUS AX318160 25 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 165 from Patent WO0190156.
ACCESSION AX318160
VERSION AX318160.1 GI:17900851
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Read,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 165 29-NOV-2001;
The Burnham Institute (US)
FEATURES
source Location/Qualifiers
1. .25
/organism="synthetic construct"
/db_xref="taxon:32630"
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BASE COUNT 11 a 4 c 5 g 5 t
ORIGIN
Query Match 0.8%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AATTTCAAGAGGACAAATAGCCGAG 28
|||||
Db 1 AATTTCAAGAGGACAAATAGCCGAG 25

RESULT 29
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LOCUS AC128434 175205 bp DNA linear HTG 19-JUL-2002
DEFINITION Rattus norvegicus clone CH230-104C1, *** SEQUENCING IN PROGRESS
*** 60 unordered pieces.
ACCESSION AC128434
VERSION AC128434.1 GI:21909117

KEYWORDS HTGS_PHASE1.
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 175205)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbieri,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brivea,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delantewate,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthett,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Haviak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Jarlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Ljoulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwundu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Teifrod,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 175205)
Worley,K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GYXN
Center clone name: CH230-104C1
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 117421 bases at least Q40
Consensus quality: 124465 bases at least Q30
Consensus quality: 129193 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft.html).

* NOTE: This is a 'working draft' sequence. It currently
* consists of 60 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1561: contig of 1561 bp in length
* 1561: gap of unknown length
* 1562 2884: contig of 1223 bp in length
* 1562 2884: gap of unknown length
* 2885 4160: contig of 1176 bp in length
* 2885 4160: gap of unknown length
* 4161 5643: contig of 1383 bp in length
* 4161 5643: gap of unknown length
* 5644 7371: contig of 1628 bp in length
* 5644 7371: gap of unknown length
* 7372 9191: contig of 1720 bp in length
* 7372 9191: gap of unknown length
* 9192 10351: contig of 1060 bp in length
* 9192 10351: gap of unknown length
* 10352 12006: contig of 1555 bp in length
* 10352 12006: gap of unknown length
* 12007 13864: contig of 1758 bp in length
* 12007 13864: gap of unknown length
* 13865 15179: contig of 1215 bp in length
* 13865 15179: gap of unknown length
* 15180 16514: contig of 1235 bp in length
* 15180 16514: gap of unknown length
* 16515 17837: contig of 1223 bp in length
* 16515 17837: gap of unknown length
* 17838 19892: contig of 1955 bp in length
* 17838 19892: gap of unknown length
* 19893 21501: contig of 1509 bp in length
* 19893 21501: gap of unknown length
* 21502 23094: contig of 1493 bp in length
* 21502 23094: gap of unknown length
* 23095 23194: contig of 1974 bp in length
* 23095 23194: gap of unknown length
* 23195 25268: gap of unknown length
* 23195 25268: contig of 1914 bp in length
* 25269 27182: gap of unknown length
* 25269 27182: contig of 1250 bp in length
* 27183 28532: gap of unknown length
* 27183 28532: gap of unknown length
* 28533 30371: contig of 1739 bp in length
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* 30372 31973: contig of 1502 bp in length
* 30372 31973: gap of unknown length
* 31974 32073: gap of unknown length
* 31974 32073: contig of 1561 bp in length
* 32074 33635: gap of unknown length
* 32074 33635: contig of 2777 bp in length
* 33636 36512: gap of unknown length
* 33636 36512: contig of 1221 bp in length
* 36513 37832: gap of unknown length
* 36513 37832: contig of 2574 bp in length
* 37833 40506: gap of unknown length
* 37833 40506: contig of 2666 bp in length
* 40507 43272: gap of unknown length
* 40507 43272: contig of 2027 bp in length
* 43273 45399: gap of unknown length
* 43273 45399: contig of 1721 bp in length
* 45400 47220: gap of unknown length
* 45400 47220: contig of 1928 bp in length
* 47221 49248: gap of unknown length
* 47221 49248: contig of 2876 bp in length
* 49249 52224: gap of unknown length
* 49249 52224: contig of 1809 bp in length
* 52225 54133: gap of unknown length
* 52225 54133: contig of 1901 bp in length
* 54134 56134: gap of unknown length
* 54134 56134: contig of 1996 bp in length
* 56135 58330: gap of unknown length
* 56135 58330: contig of 3605 bp in length
* 58331 61935: contig of 3605 bp in length
* 58331 61935: gap of unknown length

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* 61936 62035: gap of unknown length
* 62036 63849: contig of 1814 bp in length
* 63850 63949: gap of unknown length
* 63950 66368: contig of 2419 bp in length
* 66369 66468: gap of unknown length
* 66469 70087: contig of 3619 bp in length
* 70088 70187: gap of unknown length
* 70188 73499: contig of 3312 bp in length
* 73500 73599: gap of unknown length
* 73600 73699: contig of 2380 bp in length
* 73700 76079: gap of unknown length
* 76080 76674: contig of 3595 bp in length
* 76675 79774: gap of unknown length
* 79775 82514: contig of 2740 bp in length
* 82515 82615: gap of unknown length
* 82616 85238: contig of 2824 bp in length
* 85239 85338: gap of unknown length
* 85339 87656: contig of 2318 bp in length
* 87657 87757: gap of unknown length
* 87758 89651: contig of 1895 bp in length
* 89652 89751: gap of unknown length
* 89752 93019: contig of 3268 bp in length
* 93020 93119: gap of unknown length
* 93120 97532: contig of 4413 bp in length
* 97533 97632: gap of unknown length
* 97633 100905: contig of 3273 bp in length
* 100906 101005: gap of unknown length
* 101006 102927: contig of 1922 bp in length
* 102928 103027: gap of unknown length
* 103028 106601: contig of 3574 bp in length
* 106602 106701: gap of unknown length
* 106702 110014: contig of 3313 bp in length
* 110015 110114: gap of unknown length
* 110115 115019: contig of 4905 bp in length
* 115020 115119: gap of unknown length
* 115120 119985: contig of 4866 bp in length
* 119986 120085: gap of unknown length
* 120086 124854: contig of 4769 bp in length
* 124855 124954: gap of unknown length
* 124955 129028: contig of 4074 bp in length
* 129029 129129: gap of unknown length
* 129130 134385: contig of 5257 bp in length
* 134386 134486: gap of unknown length
* 134487 139933: contig of 5448 bp in length
* 139934 140033: gap of unknown length
* 140034 146041: contig of 6008 bp in length
* 146042 146141: gap of unknown length
* 146142 152958: contig of 6817 bp in length
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Query Match      0.8%; Score 25; DB 2; Length 175205;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1109 TGATACAGAAACAAACACACAAACA 1133
Db 134182 TGATACAGAAACAAACACACAAACA 134206

RESULT 30
AX318154
LOCUS AX318154 24 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 159 from Patent WO0190156.
ACCESSION AX318154
VERSION AX318154.1 GI:17900845
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
         Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
        methods of use
JOURNAL Patent: WO 0190156-A 153 29-NOV-2001;
        The Burnham Institute (US)
FEATURES
        source
        1. .23
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methods of use
Patent: WO 0190156-A 159 29-NOV-2001;
The Burnham Institute (US)
FEATURES
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        1. .24
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Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 GGTGGAGCAGGATGCTGTAGAGG 158
Db 1 GGTGGAGCAGGATGCTGTAGAGG 24

RESULT 31
AX318152
LOCUS AX318152 33 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 157 from Patent WO0190156.
ACCESSION AX318152
VERSION AX318152.1 GI:17900843
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
         Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
        methods of use
JOURNAL Patent: WO 0190156-A 157 29-NOV-2001;
        The Burnham Institute (US)
FEATURES
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        Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGACAATAGC 24
Db 10 ATGAATTTTCATAAAGGACAATAGC 33

RESULT 32
AX318148/c
LOCUS AX318148 23 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 153 from Patent WO0190156.
ACCESSION AX318148
VERSION AX318148.1 GI:17900839
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
         Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
        methods of use
JOURNAL Patent: WO 0190156-A 153 29-NOV-2001;
        The Burnham Institute (US)
FEATURES
        source
        Location/Qualifiers
        1. .23
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"

BASE COUNT 6 a 6 c 5 g 6 t
ORIGIN

Query Match 0.7%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 CTGCTAGAGGATCATTCACATG 171
Db 23 CTGCTAGAGGATCATTCACATG 1

RESULT 33
AX318158
LOCUS AX318158 23 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 163 from Patent WO0190156.
ACCESSION AX318158
VERSION AX318158.1 GI:17900849

KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
Reed, J.C., Pio, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H.,
Oliveira, V.A., Hayashi, H. and Pawlowski, K.

TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use

JOURNAL Patent: WO 0190156-A 163 29-NOV-2001;
The Burnham Institute (US)

FEATURES
Location/Qualifiers
1..23

/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"

BASE COUNT 8 a 4 c 5 g 6 t
ORIGIN

Query Match 0.7%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 GTAACATCATTTGTCGCGAGAA 134
Db 1 GTAACATCATTTGTCGCGAGAA 23

RESULT 34
AC090582/c

LOCUS AC090582 169406 bp DNA linear HTG 24-AUG-2002
DEFINITION Homo sapiens chromosome 11 clone RP11-125F14 map 11, *** SEQUENCING
IN PROGRESS ***, 6 unordered pieces.

ACCESSION AC090582

VERSION AC090582.6 GI:22474963

KEYWORDS HTG: HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 169406)

REFERENCE Birren, B., Nusbaum, C. and Lander, E.

AUTHORS Birren, B., Nusbaum, C. and Lander, E.

TITLE Homo sapiens chromosome 11, clone RP11-125F14

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 169406)

AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Boguslavskiy, L., Boukhgalter, B., Brown, A.,
Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J.,
Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,

Jones, C., Karatas, A., LaRoque, K., Lamazares, R., Landers, T.,
Lehoczyk, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,
Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,
McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P.,
Sounez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (03-MAR-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 169406)

REFERENCE
AUTHORS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cooke, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Aug 24, 2002 this sequence version replaced gi:20334596.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L11783

Center clone name: 125_F14

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 5671: contig of 5671 bp in length
* 5672 5771: gap of 100 bp
* 5772 43769: contig of 37998 bp in length
* 43770 43869: gap of 100 bp
* 43870 51226: contig of 7357 bp in length
* 51227 51326: gap of 100 bp
* 51327 90886: contig of 39560 bp in length
* 90887 90986: gap of 100 bp
* 90987 111813: contig of 20827 bp in length
* 111814 111913: gap of 100 bp
* 111914 169406: contig of 57493 bp in length.
Location/Qualifiers
1..169406

FEATURES

SOURCE

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-125F14"
/clone_lib="RPCI-11 Human Male BAC"
BASE COUNT 40775 a 44420 c 43265 g 40363 t 503 others
ORIGIN

Query Match 0.78; Score 23; DB, 2; Length 169406;
Best Local Similarity 100.0%; Pred. NO. 2.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1887 AGACACAGGTGGATCCACATGG 1909
|||||
Db 96369 AGACACAGGTGGATCCACATGG 96347

RESULT 35
AC074195/c
LOCUS AC074195 175152 bp DNA linear HTG 20-AUG-2000
DEFINITION Homo sapiens chromosome 11 clone RP11-750A9, WORKING DRAFT
AC074195
VERSION AC074195.3 GI:9799883
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Waterston,R.H.
The sequence of Homo sapiens clone
2 (bases 1 to 175152)
Waterston,R.H.
Direct Submission
Submitted (16-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 13, 2000 this sequence version replaced gi:9743495.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0750A09
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 155181 bases at least Q40
Consensus quality: 161068 bases at least Q30
Consensus quality: 163835 bases at least Q20
Insert size: 174000; agarose-fp
Insert size: 172752; sum-of-contigs
Quality coverage: 4.16 in Q20 bases; agarose-fp
Quality coverage: 4.34 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1335: contig of 1335 bp in length
* 1336 1435: gap of unknown length
* 1436 3074: contig of 1639 bp in length

3075 3174: gap of unknown length
3175 5334: contig of 2360 bp in length
5335 5634: gap of unknown length
5635 8287: contig of 2653 bp in length
8288 8388: gap of unknown length
8389 10416: contig of 2028 bp in length
10417 10515: gap of unknown length
10516 12875: contig of 2360 bp in length
12876 12975: gap of unknown length
12976 16283: contig of 3308 bp in length
16284 16384: gap of unknown length
16385 19547: contig of 3163 bp in length
19548 19646: gap of unknown length
19647 24020: contig of 4374 bp in length
24021 24121: gap of unknown length
24122 28747: contig of 4626 bp in length
28748 33535: gap of unknown length
33536 33636: contig of 4689 bp in length
33637 38255: gap of unknown length
38256 38355: contig of 4620 bp in length
38356 43277: gap of unknown length
43278 43377: contig of 4922 bp in length
43378 47903: gap of unknown length
47904 48003: contig of 4526 bp in length
48004 52384: gap of unknown length
52385 52484: contig of 4381 bp in length
52485 58975: gap of unknown length
58976 59075: contig of 6491 bp in length
59076 59703: gap of unknown length
59704 67403: contig of 8228 bp in length
67404 74849: gap of unknown length
74850 83615: contig of 7446 bp in length
83616 83715: gap of unknown length
83716 94881: contig of 8666 bp in length
94882 94981: contig of 11166 bp in length
94982 104766: gap of unknown length
104767 104866: contig of 9785 bp in length
104867 118097: gap of unknown length
118098 118197: contig of 13231 bp in length
118198 132815: gap of unknown length
132816 132915: contig of 14618 bp in length
132916 148952: gap of unknown length
148953 149052: contig of 16037 bp in length
149053 175152: gap of unknown length
175153: contig of 26100 bp in length.

FEATURES
Location/Qualifiers
1..175152
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/clone="RP11-750A9"
misc_feature 1..1335
/ note="assembly_name:Contig13"
1436..3074
/ note="assembly_name:Contig16"
3175..5534
/ note="assembly_name:Contig17"
5635..8287
/ note="assembly_name:Contig18"
8388..10415
/ note="assembly_name:Contig19"
10516..12875
/ note="assembly_name:Contig20"
12976..16283
/ note="assembly_name:Contig21"
16384..19546
/ note="assembly_name:Contig22"
19647..24020
/ note="assembly_name:Contig23"
24121..28746
/ note="assembly_name:Contig24"
28847..33535

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* 128333 128432: gap of unknown length
* 128433 139368: contig of 10936 bp in length
* 139369 139468: gap of unknown length
* 139469 154140: contig of 14672 bp in length
* 154141 154240: gap of unknown length
* 154241 167223: contig of 13483 bp in length
* 167224 167823: gap of unknown length
* 167824 183556: contig of 15733 bp in length.
```

FEATURES

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Location/Qualifiers
1..183556
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/db_xref="taxon:9606"
/chromosome="11"
/clone="RP11-125F14"
1..1181
/note="assembly_name:Contig7"
1282..2783
/note="assembly_name:Contig8"
2884..4618
/note="assembly_name:Contig9"
4719..6318
/note="assembly_name:Contig10"
6419..8952
/note="assembly_name:Contig11"
9053..11436
/note="assembly_name:Contig12"
11537..14108
/note="assembly_name:Contig13"
14209..16184
/note="assembly_name:Contig14"
16285..20536
/note="assembly_name:Contig15"
20637..25264
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41743..47291
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68582..73841
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/note="assembly_name:Contig27"
80020..86721
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86822..92876
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92977..98096
/note="assembly_name:Contig30"
98197..106663
/note="assembly_name:Contig31"
106764..117153
/note="assembly_name:Contig32"
117254..128332
/note="assembly_name:Contig33
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vector_side:left"
128433..139368
/note="assembly_name:Contig34
clone_end:T7
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vector_side:right"
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/note="assembly_name:Contig35"
154241..167723
/note="assembly_name:Contig36"
167824..183556
/note="assembly_name:Contig37"
BASE COUNT 43865 a 46765 c 45344 g 44562 t 3020 others
ORIGIN

Query Match 0.7%; Score 23; DB 2; Length 183556;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1887 AGACACAGGTGGTAATCCACATGG 1909
|||||
Db 103946 AGACACAGGTGGTAATCCACATGG 103924
|||||

RESULT 37
AL592438/c 42513 bp DNA linear PRI 21-OCT-2001
LOCUS Human DNA sequence from clone RP11-187G6 on chromosome 9, complete
DEFINITION sequence.
ACCESSION AL592438
VERSION AL592438.7 GI:16412381
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Wall, M.
Direct Submission
Submitted (20-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Requests: clonerquest@sanger.ac.uk
On Oct 24, 2001 this sequence version replaced gi:15021052.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; SW:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RP11-187G6 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-187G6 it may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true right end of clone RP11-187G6 is at 42513 in this
sequence. The true left end of clone RP11-99J1 is at 3799 in this
sequence. The true right end of clone RP11-161E22 is at 2000 in
this sequence.
FEATURES
Location/Qualifiers
1..42513
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-187G6"
/clone_lib="RPC1-11.1"
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misc_feature
BASE COUNT 13395 a 8244 c 7878 g 12996 t
ORIGIN
Query Match 0.7%; Score 22; DB 9; Length 42513;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1060 TTCACACTCTCACACAAACAA 1081
|||||
Db 42350 TTCACACTCTCACACAAACAA 42329

RESULT 38
AC098256
LOCUS 79431 bp DNA linear HTG 31-JUL-2002
DEFINITION Rattus norvegicus clone CH230-1G22, *** SEQUENCING IN PROGRESS ***,
48 unordered pieces.
ACCESSION AC098256
VERSION AC098256.3 GI:21953970
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 79431)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbarya,J., Benton,J., Bimake,K., Blankenburg,K., Bonnin,D.,
Bouch,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burrell,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyte,M.D., Dathorne,S.R., David,R.,
Devila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlssoon,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,P., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseghe,H.,
Lozardo,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Monabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenwo,S., Ogih,M., Okuwonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savary,G.,
Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,
Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
```

Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 79431)
Worley,K.C.
Direct Submission
Submitted (23-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 79431)
Worley,K.C.
Direct Submission
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 24, 2002 this sequence version replaced gi:20976511.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: TUDU
Center clone name: CH230-1G22
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 33875 bases at least Q40
Consensus quality: 35563 bases at least Q30
Consensus quality: 36799 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 48 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1072: contig of 1072 bp in length
* 1073 1172: gap of unknown length
* 1173 2181: contig of 1009 bp in length
* 2182 2281: gap of unknown length
* 2282 3489: contig of 1208 bp in length
* 3490 3589: gap of unknown length
* 3590 4669: contig of 1080 bp in length
* 4670 4769: gap of unknown length
* 4770 5841: contig of 1072 bp in length
* 5842 7188: contig of 1247 bp in length
* 7189 7288: gap of unknown length
* 7289 8373: contig of 1085 bp in length
* 8374 8474: gap of unknown length
* 8475 9595: contig of 1122 bp in length
* 9596 10856: contig of 1161 bp in length
* 10857 10956: gap of unknown length
* 10957 12528: contig of 1572 bp in length
* 12529 14017: contig of 1389 bp in length
* 14018 14117: gap of unknown length
* 14118 15306: contig of 1189 bp in length
* 15307 15406: gap of unknown length
* 15407 16997: contig of 1591 bp in length
* 16998 17097: gap of unknown length
* 17098 18675: contig of 1578 bp in length
* 18676 20284: contig of 1489 bp in length
* 20285 20365: gap of unknown length
* 20366 21735: contig of 1371 bp in length
* 21736

* 21736 21835: gap of unknown length
* 21836 23176: contig of 1341 bp in length
* 23177 23276: gap of unknown length
* 23277 24327: contig of 1051 bp in length
* 24328 24427: gap of unknown length
* 24428 25499: contig of 1072 bp in length
* 25500 26599: gap of unknown length
* 26600 26756: contig of 1157 bp in length
* 26757 26856: gap of unknown length
* 26857 28201: contig of 1345 bp in length
* 28202 28301: gap of unknown length
* 28302 30133: contig of 1832 bp in length
* 30134 30233: gap of unknown length
* 30234 31984: contig of 1751 bp in length
* 31985 32084: gap of unknown length
* 32085 33479: contig of 1395 bp in length
* 33480 33579: gap of unknown length
* 33580 34838: contig of 1259 bp in length
* 34839 34938: gap of unknown length
* 34939 36511: contig of 1573 bp in length
* 36512 36611: gap of unknown length
* 36612 38672: contig of 2061 bp in length
* 38673 38772: gap of unknown length
* 38773 40686: contig of 1914 bp in length
* 40687 40786: gap of unknown length
* 40787 41840: contig of 1054 bp in length
* 41841 41940: gap of unknown length
* 41941 42364: contig of 1024 bp in length
* 42365 43064: gap of unknown length
* 43065 44307: contig of 1243 bp in length
* 44308 44407: gap of unknown length
* 44409 45721: contig of 1314 bp in length
* 45722 45821: gap of unknown length
* 45822 47317: contig of 1496 bp in length
* 47318 47417: gap of unknown length
* 47419 48844: contig of 1427 bp in length
* 48845 48944: gap of unknown length
* 48945 50750: contig of 1806 bp in length
* 50751 50850: gap of unknown length
* 50851 52232: contig of 1382 bp in length
* 52233 52332: gap of unknown length
* 52333 53122: contig of 1480 bp in length
* 53123 53912: gap of unknown length
* 53913 56448: contig of 2536 bp in length
* 56449 56548: gap of unknown length
* 56549 57717: contig of 1168 bp in length
* 57717 57816: gap of unknown length
* 57817 59387: contig of 1571 bp in length
* 59388 59487: gap of unknown length
* 59488 61488: contig of 2001 bp in length
* 61489 61588: gap of unknown length
* 61589 64695: contig of 3107 bp in length
* 64696 64795: gap of unknown length
* 64796 66580: contig of 1785 bp in length
* 66581 66680: gap of unknown length
* 66681 68096: contig of 1416 bp in length
* 68097 68196: gap of unknown length
* 68197 70443: contig of 2247 bp in length
* 70444 70543: gap of unknown length
* 70544 73543: contig of 3000 bp in length
* 73544 73643: gap of unknown length
* 73644 78874: contig of 2231 bp in length
* 78875 79574: gap of unknown length
* 79575 79631: contig of 3457 bp in length.

FEATURES

source

Location/Qualifiers
1..79431
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-1G22"

BASE COUNT 21375 a 15325 c 15238 g 22670 t 4823 others
ORIGIN

Query Match

0.7%; Score 22; DB 2; Length 79431;

Best Local Similarity 100.0%; Pred. No. 9.9; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1112 TACAGAAAAACAAACAAACA 1133
|||||
Db 61169 TACAGAAAAACAAACAAACA 61190
|||||

RESULT 39
AP002957 87834 bp DNA linear PRI 26-APR-2001
LOCUS Homo sapiens genomic DNA, chromosome 11q, clone:CTD-2337I7,
DEFINITION complete sequences.
ACCESSION AP002957
VERSION AP002957.2 GI:13810522
KEYWORDS HTG.
SOURCE Homo sapiens DNA, clone:CTD-2337I7.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in DataBase (2000)
REFERENCE 2 (bases 1 to 87834)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (28-NOV-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@psc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel.:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Apr 26, 2001 this sequence version replaced gi:11526584.
FEATURES
source
1..87834
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="CTD-2337I7"
BASE COUNT 23650 a 20616 c 20127 g 23441 t
ORIGIN

Query Match 0.7%; Score 22; DB 9; Length 87834;
Best Local Similarity 100.0%; Pred. No. 9.9; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1117 AAAAAACAAACAAACATAAAG 1138
|||||
Db 18515 AAAAAACAAACAAACATAAAG 18536
|||||

RESULT 40
AL161913/c 137897 bp DNA linear PRI 15-NOV-2001
LOCUS Human DNA sequence from clone RP11-64P11 on chromosome 9, complete
DEFINITION sequence.
ACCESSION AL161913
VERSION AL161913.11 GI:16972809
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 137897)
AUTHORS Mashreghi-Mohammadi,M.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Nov 16, 2001 this sequence version replaced gi:14329900.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr9>

RP11-64P11 is from the library RPCI-11.1 constructed by the group

of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone

RP11-64P11. It may be shorter because we sequenced overlapping

sections only once, except for a short overlap.

The true left end of clone RP11-36615 is at 135898 in this

sequence. The true right end of clone RP11-18766 is at 2000 in this sequence.

```

FEATURES             Location/Qualifiers
     source            1..137897
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="9"
                     /clone="RP11-64P11"
                     /clone_lib="RPCI-11.1"
BASE COUNT           44788 a 26058 c 25186 g 41865 t
ORIGIN

```

```

Query Match          0.7%; Score 22; DB 9; Length 137897;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1060 TTCCACTCTCACACAAACAA 1081
      |||||||
Db 1837 TTCCACTCTCACACAAACAA 1816

```

```

RESULT 41
AC020917 AC020917 151088 bp DNA linear PRI 08-NOV-2000
LOCUS      Homo sapiens chromosome 19 clone CTD-2013N17, complete sequence.
DEFINITION
ACCESSION AC020917
VERSION    AC020917.4 GI:11120760
KEYWORDS   HTG.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE    1 (bases 1 to 151088)
AUTHORS      DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE        Direct Submission
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 151088)
AUTHORS      DOE Joint Genome Institute.
TITLE        Direct Submission
JOURNAL      Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE    3 (bases 1 to 151088)
AUTHORS      DOE Joint Genome Institute and Stanford Human Genome Center.

```

```

TITLE
JOURNAL
COMMENT

```

```

Direct Submission
Submitted (08-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Nov 8, 2000 this sequence version replaced gi:7704958.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.3.
STS Content:
SHGC-57513 G37313.

```

```

Location/Qualifiers
     source            1..151088
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /clone="CTD-2013N17"
BASE COUNT           40571 a 38233 c 38536 g 33748 t
ORIGIN

```

```

Query Match          0.7%; Score 22; DB 9; Length 151088;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1778 ATTACTTATTGACTTCTTTGA 1799
      |||||||
Db 117449 ATTACTTATTGACTTCTTTGA 117470

```

```

RESULT 42
AC011980/c AC011980 153733 bp DNA linear HTG 12-MAR-2000
LOCUS      Homo sapiens clone RP11-16H7, WORKING DRAFT SEQUENCE, 11 unordered
DEFINITION pieces.
ACCESSION AC011980
VERSION    AC011980.3 GI:7230122
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE    1 (bases 1 to 153733)
AUTHORS      Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE        Homo sapiens, clone RP11-16H7
JOURNAL      Unpublished
AUTHORS

```

```

REFERENCE    2 (bases 1 to 153733)
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Bouckghalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
            Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Horton,L.,
            Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
            McSwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severi,P.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Wyman,D., Ye.W.J., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
            Zimmer,A. and Zody,M.

```

```

Direct Submission
Submitted (17-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 12, 2000 this sequence version replaced gi:6453966.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

```

```

----- Project Information
Center project name: L3543
Center clone name: 16_H.7
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 117952 bases at least Q40
Consensus quality: 136478 bases at least Q30
Consensus quality: 146705 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 152733; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1
* 3262: contig of 3262 bp in length
* 3263 3362: gap of 100 bp
* 3363 9412: contig of 6050 bp in length
* 9413 9512: gap of 100 bp
* 9513 14144: contig of 4632 bp in length
* 14145 14244: gap of 100 bp
* 14245 24193: contig of 9949 bp in length
* 24194 24293: gap of 100 bp
* 24294 37092: contig of 12799 bp in length
* 37093 37192: gap of 100 bp
* 37193 49508: contig of 12316 bp in length
* 49509 49608: gap of 100 bp
* 49609 60861: contig of 11253 bp in length
* 60862 60961: gap of 100 bp
* 60962 76206: contig of 15245 bp in length
* 76207 76306: gap of 100 bp
* 76307 89151: contig of 12845 bp in length
* 89152 89251: gap of 100 bp
* 89252 107693: contig of 18442 bp in length
* 107694 107793: gap of 100 bp
* 107794 153733: contig of 45940 bp in length.
FEATURES
source
1..153733
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-16H7"
/clone_lib="RPCI-11 Human Male BAC"
1..3262
/note="assembly_fragment"
3363..9412
/note="assembly_fragment"
9513..14144
/note="assembly_fragment"
14245..24193
/note="assembly_fragment"
24294..37092
/note="assembly_fragment"
37193..49508
/note="assembly_fragment"
49609..60861
/note="assembly_fragment"
60962..76206
/note="assembly_fragment"
76307..89151
/note="assembly_fragment"
89152..107693
/note="assembly_fragment"
107694..107793
/note="assembly_fragment"

```

```

misc_feature /note="assembly_fragment"
107794..153733
/note="assembly_fragment"
BASE COUNT 42218 a 34152 c 33610 g 42710 t 1043 others
ORIGIN
Query Match 0.7%; Score 22; DB 2; Length 153733;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1117 AAAACAAACACAAACATAAAG 1138
|||||
Db 120518 AAAACAAACACAAACATAAAG 120497
|||||
RESULT 43
AL592213 155531 bp DNA linear HTG 04-AUG-2001
Homo sapiens chromosome 9 clone RP11-99J1, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
ACCESSION AL592213 AC007951
VERSION 1
KEYWORDS HTG; HTGS_PHASE2; HTGS_CANCELLED.
SOURCE human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 155531)
Hammond.S.
REFERENCE Direct Submission
AUTHORS Submitted (03-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
TITLE CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk
JOURNAL requests: clonerequest@sanger.ac.uk
COMMENT On Aug 9, 2001 this sequence version replaced gi:15029558.
Draft Sequence Produced by Whitehead Institute/MIT Center for
Genome Research, 320 Charles Street,
Cambridge, MA 02141, USA
http://www-seq.wi.mit.edu
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA99J1
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 30% of reads
Chemistry: Dye-terminator Big Dye; 68% of reads
Dye-terminator Big Dye; 68% of reads
Chemistry: Dye-terminator Big Dye; 68% of reads
Consensus quality: 155436 bases at least Q40
Consensus quality: 155453 bases at least Q30
Consensus quality: 155482 bases at least Q20
Insert size: 155531; sum-of-contigs
Insert size: 144681; 16.2% error; agarose-fp
Quality coverage: 15.49x in Q20 bases; sum-of-contigs Quality
coverage: 16.65x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source
1..155531
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-99J1"
/clone_lib="RPCI-11.1"
1..155531
/note="assembly_fragment:03518"

```

clone_end:SP6
vector_side:right"
BASE COUNT 50143 a 29768 c 28721 g 46899 t
ORIGIN

Query Match 0.7%; Score 22; DB 2; Length 15531;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1060 TTCCACTCTCACACAAACAA 1081
|||||
Db 38569 TTCCACTCTCACACAAACAA 38548

RESULT 44
AC129066/c 157021 bp DNA linear HTG 16-AUG-2002
LOCUS Didelphis virginiana clone LB3-8N21, WORKING DRAFT SEQUENCE, 3
DEFINITION ordered pieces.
ACCESSION AC129066
VERSION AC129066.2 GI:22267576
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE North American opossum.
ORGANISM Didelphis virginiana

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
1 (bases 1 to 157021)
Benjamin, B., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P.,
Lee-Lin, S.-Q., Legaspi, R., Madero, Q.L., Madero, V.B.,
Marquies, E.H., Masello, C., Maskeri, B., Mastrian, S.D.,
McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R.,
Portnoy, M.E., Prasad, A., Schueler, M.G., Stantropop, S., Thomas, J.W.,
Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 157021)

TITLE
JOURNAL Direct Submission
REFERENCE Green, E.D.
AUTHORS
JOURNAL Submitted (25-JUL-2002) NIH Intramural Sequencing Center, 8717
Government Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 157021)
Green, E.D.
Direct Submission
Submitted (16-AUG-2002) NIH Intramural Sequencing Center, 8717
Government Circle, Gaithersburg, MD 20877, USA
On Aug 16, 2002 this sequence version replaced gi:21955001.
----- Genome Center

Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc_zoehghri.nih.gov
----- Project Information
Center Project name: dvd
Center Clone name: 008N21

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones), alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 155497 bases at least Q40
Consensus quality: 156249 bases at least Q30
Consensus quality: 156658 bases at least Q20
Insert size: 138000; agarose-fp
Quality coverage: 7.19x in Q20 bases; agarose-fp
Quality coverage: 6.33x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 31400: contig of 31400 bp in length
* 31401 31500: gap of unknown length
* 31501 40794: contig of 9294 bp in length
* 40795 40894: gap of unknown length
* 40895 157021: contig of 116127 bp in length.

FEATURES
source

1..157021

/organism="Didelphis virginiana"

/db_xref="taxon:9267"

/clone="LB3-8N21"

/clone_lib="LB3"

1..31400

/note="assembly_fragment"

clone_end:T7

vector_side:left

31501..40794

/note="assembly_fragment"

40895..157021

/note="assembly_fragment"

clone_end:SP6

vector_side:right"

BASE COUNT 49123 a 27264 c 26805 g 53629 t 200 others

ORIGIN

Query Match 0.7%; Score 22; DB 2; Length 157021;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2587 GATGGAATGAAGCTCTTCATG 2608
|||||
Db 113039 GATGGAATGAAGCTCTTCATG 113018

RESULT 45
AC079194/c 159946 bp DNA linear HTG 22-NOV-2000
LOCUS Homo sapiens chromosome 11 clone RP11-475C4 map 11, WORKING DRAFT
DEFINITION SEQUENCE, 37 unordered pieces.
ACCESSION AC079194
VERSION AC079194.2 GI:11276162
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159946)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 11, clone RP11-475C4
JOURNAL Unpublished
2 (bases 1 to 159946)
REFERENCE Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bida, F., Boguslavsky, L.,
Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Choepe, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

misc_feature 9659..11181
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1117 AAAACAACACAAACATAAAG 1138
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Db 150590 AAAACAACACAAACATAAAG 150569

RESULT 46
AX318151
LOCUS AX318151 21 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 156 from Patent WO0190156.
ACCESSION AX318151
VERSION AX318151.1 GI:17900842
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 156 29-NOV-2001;
The Burnham Institute (US)
FEATURES
source
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTATGGAATGTTCTGAATCGC 21
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RESULT 47
AX318153/c
LOCUS AX318153 30 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 158 from Patent WO0190156.
ACCESSION AX318153
VERSION AX318153.1 GI:17900844
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,
Oliveira,V.A., Hayashi,H. and Pawlowski,K.
TITLE Card domain containing polypeptides, encoding nucleic acids, and
methods of use
JOURNAL Patent: WO 0190156-A 158 29-NOV-2001;
The Burnham Institute (US)
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QY 232 TATCCTCTATTTCAGGACTTG 252
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Db 30 TATCCTCTATTTCAGGACTTG 10
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RESULT 48
AX286953
LOCUS AX286953 7067 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 21 from Patent WO0181598.
ACCESSION AX286953
VERSION AX286953.1 GI:17048966
KEYWORDS
SOURCE Candida albicans.
ORGANISM Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE 1
AUTHORS Nelissen,B.J., de Becker,M.D. and Luyten,W.H.
TITLE Multiple retrotransposon families in Candida albicans
JOURNAL Patent: WO 0181598-A 21 01-NOV-2001;
JANSSEN PHARMACEUTICA N.V. (BE)
FEATURES
source
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 49

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LOCUS 7595 bp DNA linear MAM 24-JUN-2000
DEFINITION Bovine gene for kappa-casein exons 3-5.
ACCESSION X14908 X14326
VERSION X14908.1 GI:180
KEYWORDS casein; kappa-casein; repetitive sequence: Alu-like repetitive sequence; restriction fragment linked polymorphism.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 7595)
AUTHORS Alexander,L.J., Stewart,A.F., Mackinlay,A.G., Kapelinskaya,T.V., Tkach,T.M. and Gordetsky,S.I.
TITLE Isolation and characterization of the bovine kappa-casein gene
JOURNAL Eur. J. Biochem. 178 (2), 395-401 (1988)
MEDLINE 89091174
PUBMED 3208764
REFERENCE 2 (bases 1 to 7595)
AUTHORS Valman,D., Mercier,D., Moazami-Goudarzi,K., Eggen,A., Ciampolini,R., Lepingale,A., Velmala,R., Kaukinen,J., Varvio,S.L., Martin,P. et al.
TITLE A set of 99 cattle microsatellites: characterization, syntenic mapping, and polymorphism
JOURNAL Mamm. Genome 5 (5), 288-297 (1994)
MEDLINE 94355772
PUBMED 7545949
REFERENCE 3 (bases 1 to 7595)
AUTHORS Mackinlay,A.G.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1989) A.G. Mackinlay, The University of New South Wales, P.O. Box 1 Kensington New South Wales Australia
FEATURES
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variation 5345
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variation 5406
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variation 5413
/note="a is t in kappa-casein B variant"
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variation 7382
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polyA_site 7416
variation 7484

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Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 6007 TTTTAACTTGAAGACACCT 6027
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RESULT 50
AE010385/c
LOCUS AE010385 9257 bp DNA linear BCT 01-AUG-2002
DEFINITION Methanopyrus kandleri AV19 section 84 of 157 of the complete genome.
ACCESSION AE010385 AE009439
VERSION AE010385.1 GI:19887459
KEYWORDS Methanopyrus kandleri AV19.
SOURCE Methanopyrus kandleri AV19.
ORGANISM Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae; Methanopyrus.
REFERENCE 1 (bases 1 to 9257)
AUTHORS Slesarev,A.I., Mezheva,K.V., Makarova,K.S., Polushin,N.N., Shcherbinina,O.V., Shakhova,V.V., Belova,G.I., Aravind,L., Natile,D.A., Rogozin,I.B., Tatusov,R.L., Wolf,Y.I., Stetter,K.O., Malykh,A.G., Koonin,E.V. and Kozhavkin,S.A.
TITLE The Complete Genome of the Hyperthermophile Methanopyrus kandleri AV19 and Monophyly of Archaeal Methanogens
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9257)
AUTHORS Slesarev,A.I., Mezheva,K.V., Makarova,K.S., Polushin,N.N., Shcherbinina,O.V., Shakhova,V.V., Belova,G.I., Aravind,L., Natile,D.A., Rogozin,I.B., Tatusov,R.L., Wolf,Y.I., Stetter,K.O., Malykh,A.G., Koonin,E.V. and Kozhavkin,S.A.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2002) Fidelity Systems, Inc., Gaithersburg, MD 20879
FEATURES
source 1..9257
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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(without alignments)
11568.794 Million cell updates/sec

Title: US-09-697-089-3
Perfect score: 3072
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 12

Total number of hits satisfying chosen parameters: 375039

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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2	2919	95.0	3545	22	AAH98254	Murine EST-derived			
3	2918	95.0	3213	22	AAH78219	Nucleotide sequenc			
4	2868	93.4	3396	24	ABK22731	Human cDNA encodin			
5	2634	85.7	3615	22	AA503946	Human caspase recr			
6	2082	67.1	2215	22	AAH78218	Nucleotide sequenc			
7	1781	58.0	2950	22	AAH99581	Human protein enco			
8	840	27.3	891	24	ABK22766	Human cDNA encodin			
9	815	26.5	1395	24	ABK22732	Human cDNA encodin			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	618	20.1	618	24	ABK22767	Human cDNA encodin
11	489	15.9	2735	22	AAH34171	Human colon cancer
12	461	15.0	768	24	ABK22734	Human cDNA encodin
13	420	13.7	608	22	AA526160	Human cDNA encodin
14	304	9.9	522	22	AA526575	Human cDNA encodin
15	269	8.8	578	24	ABK22733	Human cDNA encodin
16	261	8.5	261	24	ABK22765	Human cDNA encodin
17	242	7.9	421	22	ABA45612	Human breast cell
18	242	7.9	421	22	ABA56119	Human foetal liver
19	242	7.9	421	22	ABA25770	Probe #4236 for ge
20	242	7.9	421	22	AAK04305	Human brain expres
21	242	7.9	421	22	AAK29801	Human bone marrow
22	242	7.9	421	22	AAI14389	Probe #4322 for ge
23	242	7.9	421	22	AAI35764	Probe #4450 used t
24	242	7.9	421	22	AAI04213	Probe #4204 used t
25	242	7.9	421	24	ABS04362	Human genome-deriv
26	220	7.2	220	22	ABA50734	Human breast cell
27	220	7.2	220	22	ABA68704	Human foetal liver
28	220	7.2	220	22	ABA35668	Probe #14134 for g
29	220	7.2	220	22	AAK17044	Human brain expres
30	220	7.2	220	22	AAK42828	Human bone marrow
31	220	7.2	220	22	AAI23590	Probe #13523 for g
32	220	7.2	220	22	AAI48904	Probe #17590 used
33	220	7.2	220	22	AAI09206	Probe #9197 used t
34	220	7.2	220	24	ABS16884	Human genome-deriv
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36	60	2.0	60	24	ABNA0447	Human spliced tran
37	29	0.9	29	24	ABK22753	Human CLAN A PCR p
38	25	0.8	25	24	ABK22754	Human CLAN B PCR p
39	25	0.8	25	24	ABK22755	Human CLAN D PCR p
40	25	0.8	25	24	ABK22752	Human CLAN A PCR p
41	24	0.8	24	24	ABK22758	Human CLAN CARD do
42	24	0.8	23	24	ABK22750	Human CLAN CDNA PC
43	23	0.7	23	24	ABK22746	Human CLAN CDNA PC
44	23	0.7	23	24	ABK22756	Human CLAN C PCR p
45	21	0.7	21	24	ABK22749	Human CLAN CDNA PC
46	21	0.7	30	24	ABK22751	Human CLAN CARD do
47	21	0.7	7067	24	AA595269	Long terminal repe
48	20	0.7	431	23	ABV46663	Human prostate exp
49	20	0.7	475	24	ABK78972	Bacillus clausili g
50	20	0.7	768	24	ABK22734	Human cDNA encodin
51	20	0.7	3811	23	ABL25908	Drosophila melanog
52	20	0.7	4737	23	ABL04194	Drosophila melanog
53	19	0.6	431	22	ABA12901	Human nervous syst
54	19	0.6	451	23	AS74824	DNA encoding novel
55	19	0.6	549	22	AAH11452	Human cDNA clone (
56	19	0.6	579	19	AAK30828	H. pylori cell env
57	19	0.6	649	19	AAK14445	H. pylori GHPO 875
58	19	0.6	1034	23	AA570584	DNA encoding novel
59	19	0.6	1780	22	AA545200	cDNA encoding nove
60	19	0.6	1908	21	AAF13098	Aspergillus oryzae
61	19	0.6	2379	24	ABL56644	Nucleotide sequenc
62	19	0.6	2825	22	AAH16202	Human cDNA sequenc
63	19	0.6	3217	23	ABL09400	Drosophila melanog
64	19	0.6	8632	23	AA595627	Propionibacterium
65	19	0.6	10917	24	ABA97708	Wild-type mouse Wo
66	19	0.6	14346	22	AA532551	Human genomic DNA
67	19	0.6	30310	24	ABK38253	Genomic DNA from t
68	18	0.6	21	24	ABK22748	Human CLAN CDNA PC
69	18	0.6	116	21	AAK14986	Human secreted pro
70	18	0.6	147	22	AAK68570	Human immune/haema
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76	18	0.6	377	21	AAA31325	Plant microsatelli
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78	18	0.6	434	23	ABV00662	Human prostate exp
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c 84	18	0.6	454	22	AAK30303	Human bone marrow	c 157	18	0.6	2832	23	ABL29982	Drosophila melanog
c 85	18	0.6	454	22	AAI14905	Probe #4838 for ge	c 158	18	0.6	2861	23	AAK79745	Human immune/haema
c 86	18	0.6	454	22	AAI36257	Probe #4943 used t	c 159	18	0.6	2869	23	ABL07056	Drosophila melanog
c 87	18	0.6	454	22	AAI04685	Probe #4676 used t	c 160	18	0.6	3000	20	AAK84399	S. capsulata IF012
c 88	18	0.6	454	24	ABS04888	Human genome-deriv	c 161	18	0.6	3001	21	AAH51776	Chromosome 13q31-q
c 89	18	0.6	466	21	AAK01809	Human secreted pro	c 162	18	0.6	3001	21	AAH51787	Chromosome 13q31-q
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c 101	18	0.6	503	23	ABV39973	Human prostate exp	c 174	18	0.6	3958	20	AAV80604	Kidney injury asso
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c 103	18	0.6	594	11	AAQ05868	DNA encoding novel	c 176	18	0.6	3999	24	AB199451	DNA encoding an as
c 104	18	0.6	652	21	AAQ05868	Sequence encoding	c 177	18	0.6	4168	23	ABL30172	Mouse ischaemic co
c 105	18	0.6	682	21	AAQ07589	Fusarium venenatum	c 178	18	0.6	4199	23	ABL30188	Drosophila melanog
c 106	18	0.6	682	21	AAK44321	Arabidopsis thalia	c 179	18	0.6	4215	22	AAI58415	Drosophila melanog
c 107	18	0.6	763	23	ABL29983	Drosophila melanog	c 180	18	0.6	4871	22	AAI60201	Human polynucleoti
c 108	18	0.6	814	22	AAH05406	Human cDNA clone (c 181	18	0.6	4911	23	ABL13032	Drosophila melanog
c 109	18	0.6	863	23	ABL114985	Drosophila melanog	c 182	18	0.6	4951	20	AAI13198	Drosophila melanog
c 110	18	0.6	864	23	ABL11737	Drosophila melanog	c 183	18	0.6	4951	20	AAI13198	Enterococcus faeca
c 111	18	0.6	873	23	ABV09831	Human prostate exp	c 184	18	0.6	4982	18	AAH85267	HMG-CoA reductase
c 112	18	0.6	873	23	ABV11991	Human prostate exp	c 185	18	0.6	4986	23	AAH88902	DNA encoding novel
c 113	18	0.6	888	20	AAK20212	Enterococcus faeca	c 186	18	0.6	5031	23	ABL11822	Drosophila melanog
c 114	18	0.6	888	20	AAK20212	Enterococcus faeca	c 187	18	0.6	5120	23	AAK84984	DNA encoding novel
c 115	18	0.6	960	22	AAH67086	E faecalis EF10 g	c 188	18	0.6	5121	22	AAK84984	DNA encoding novel
c 116	18	0.6	992	11	AAQ05870	C glutamicum codin	c 189	18	0.6	5173	24	AAK33333	Human immune/haema
c 117	18	0.6	1034	21	AAQ05870	Sequence encoding	c 190	18	0.6	5212	9	AAH80317	Proliferation pote
c 118	18	0.6	1083	23	AAH71387	Human secreted pro	c 191	18	0.6	5292	21	AAH21374	Transcription cont
c 119	18	0.6	1092	22	AAK82524	Corynebacterium gl	c 192	18	0.6	5292	21	AAH21374	Human low adenosin
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c 121	18	0.6	1163	22	AAK37592	Human prostate exp	c 194	18	0.6	5511	17	AAK35252	CDNA encoding plas
c 122	18	0.6	1205	20	AAK242236	Human musculoskele	c 195	18	0.6	5890	22	AAK05680	Human reproductive
c 123	18	0.6	1243	24	ABL89619	Human normal blad	c 196	18	0.6	6108	22	AAK39728	Genomic sequence #
c 124	18	0.6	1250	9	AAH80316	Human polynucleoti	c 197	18	0.6	6108	22	AAK65557	Human immune/haema
c 125	18	0.6	1343	22	AAK86733	Human polynucleoti	c 198	18	0.6	6108	22	AAK90069	Human digestive sy
c 126	18	0.6	1473	21	AAK40012	Human polynucleoti	c 199	18	0.6	6111	22	AAK39727	Genomic sequence #
c 127	18	0.6	1491	21	AAK47150	Arabidopsis thalia	c 200	18	0.6	6212	21	AAK90068	Human digestive sy
c 128	18	0.6	1515	19	AAV40738	DNA encoding a ser	c 201	18	0.6	6212	21	AAK35253	Human low adenosin
c 129	18	0.6	1561	21	AAK21032	C. felis esterase,	c 202	18	0.6	6231	23	ABL09308	Human adenosine re
c 130	18	0.6	1561	21	AAK34910	C. felis esterase,	c 203	18	0.6	6276	23	ABL26815	Drosophila melanog
c 131	18	0.6	1579	22	AAH13702	Human low adenosin	c 204	18	0.6	6689	23	ABL11814	Drosophila melanog
c 132	18	0.6	1595	24	ABQ91965	Human adenosine re	c 205	18	0.6	7380	20	AAK84028	MMP9 promoter beta
c 133	18	0.6	1611	12	AAQ12528	Human cDNA sequenc	c 206	18	0.6	7383	22	AAK00153	Matrix metalloprot
c 134	18	0.6	1611	21	AAK47151	Human NF-KB activa	c 207	18	0.6	7386	22	AAK90294	Human digestive sy
c 135	18	0.6	1618	23	ABL11537	Thymidylate phosph	c 208	18	0.6	7897	23	AAI57671	Human colorectal c
c 136	18	0.6	1619	21	AAK15908	DNA encoding a ser	c 209	18	0.6	7897	23	ABL05564	Drosophila melanog
c 137	18	0.6	1650	19	AAV40760	Drosophila melanog	c 210	18	0.6	8873	24	ABL70173	Chemically treated
c 138	18	0.6	1650	19	AAV40761	Human protein clon	c 211	18	0.6	8873	24	AAK61124	Human gene regulat
c 139	18	0.6	1723	20	AAV71287	C. felis esterase,	c 212	18	0.6	8873	24	ABK31210	Signal transductio
c 140	18	0.6	1761	24	AAK33265	C. felis esterase,	c 213	18	0.6	9084	22	AAK33604	Human immune syste
c 141	18	0.6	1800	15	AAQ67601	Human vesicular bi	c 214	18	0.6	9805	22	AAK34718	Human for a no
c 142	18	0.6	1878	22	AAK25374	Human secreted pro	c 215	18	0.6	9805	22	AAK05681	Human reproductive
c 143	18	0.6	1926	20	AAV82522	Retinoblastoma pro	c 216	18	0.6	11968	23	ABL26814	Human immune syste
c 144	18	0.6	1962	20	AAK77504	Nucleotide sequenc	c 217	18	0.6	13732	24	ABL33820	Drosophila melanog
c 145	18	0.6	1982	19	AAV40735	Sphingomonas capsu	c 218	18	0.6	15915	23	ABL04550	Human immune syste
c 146	18	0.6	1982	19	AAV40736	Human ovarian tumo	c 219	18	0.6	17252	22	AAK28668	Drosophila melanog
c 147	18	0.6	1982	22	AAK21167	C. felis esterase,	c 220	18	0.6	17509	24	ABN95599	Genomic sequence #
c 148	18	0.6	1986	23	ABL30173	Ctenocephalides fe	c 221	18	0.6	19040	22	ABN95599	Gene #2097 used to
c 149	18	0.6	1996	24	ABA04431	Drosophila melanog	c 222	18	0.6	23044	23	ABL11536	Human nervous syst
c 150	18	0.6	2144	19	AAV40758	Human p1744 prote	c 223	18	0.6	32205	22	AAK08217	Drosophila melanog
c 151	18	0.6	2144	19	AAV40759	C. felis esterase,	c 224	18	0.6	32205	22	AAK08217	Human ovarian and
c 152	18	0.6	2144	22	AAK21182	C. felis esterase,	c 225	18	0.6	32986	22	AAK69758	Human reproductive
c 153	18	0.6	2299	19	AAK296326	Ctenocephalides fe	c 226	18	0.6	32986	22	AAK69758	Human immune/haema
c 154	18	0.6	2299	19	AAK296326	S. pneumoniae deri	c 227	18	0.6	39746	23	ABL33398	Drosophila melanog
c 155	18	0.6	2619	22	AAK26680	Streptococcus pneu	c 228	18	0.6	45186	22	AAK60478	Wild-type human CT
						Human genomic DNA				236303	22	AAK11614	Human genomic DNA

229	18	0.6	325791	22	AAS43104	Human Oestrogen re	302	17	0.6	541	24	ABS17367	Human genome-deriv
230	18	0.6	349980	22	AAH68530	C glutamicum codin	303	17	0.6	542	22	AAD14988	Human NOV9 DNA. H
231	18	0.6	1503900	22	AAK95240	Human neuregulin-1	c 304	17	0.6	551	24	ABK62815	Rat sequence diffe
232	18	0.6	1503900	22	AAK96733	Human neuregulin-1	c 305	17	0.6	552	22	ABA63892	Human foetal liver
233	18	0.6	1664976	19	AAV21209	Methanococcus jann	c 306	17	0.6	575	22	ABA31072	Probe #9538 for ge
234	17	0.6	21	20	AAZ18259	P450 enzyme gene s	c 307	17	0.6	575	22	AAI18893	Probe #8826 for ge
235	17	0.6	32	24	ABK53200	Lipase (tliA) 5' p	c 308	17	0.6	576	20	AAZ22765	Human SOCS16 cDNA.
236	17	0.6	47	21	AAZ67938	Human map-related	c 309	17	0.6	583	22	AAI90506	Human excretory re
237	17	0.6	51	21	AAZ99916	Sequence of the st	c 310	17	0.6	583	22	AAI63406	Human kidney relat
238	17	0.6	60	24	AAZ39012	Human spliced tran	c 311	17	0.6	587	22	AAK63165	Human immune/haema
239	17	0.6	121	21	AAI10211	Human secreted pro	c 312	17	0.6	588	22	AAZ27307	cDNA encoding nove
240	17	0.6	167	23	ABL57927	Human VG51 exon 8.	c 313	17	0.6	588	23	AAK54335	Rat pseudomonas aerugi
241	17	0.6	212	21	AAI13747	Human secreted pro	c 314	17	0.6	590	24	ABK63068	Rat sequence diffe
242	17	0.6	243	22	AAI01773	Human reproductive	c 315	17	0.6	591	22	AAK46907	Human G protein-co
243	17	0.6	243	23	ABL97066	Human testicular a	c 316	17	0.6	591	23	ABV35313	Human prostate exp
244	17	0.6	276	20	AAV88937	EST clone HW846..	c 317	17	0.6	591	23	ABV44145	Human prostate exp
245	17	0.6	290	20	AAZ22458	Internal Transcrib	c 318	17	0.6	591	24	ABK1685	cDNA encoding nove
246	17	0.6	296	22	AAK53772	Murine transport a	c 319	17	0.6	604	23	ABV22637	Human prostate exp
247	17	0.6	308	23	ABV07396	Human prostate exp	c 320	17	0.6	604	23	ABV28460	Human prostate exp
248	17	0.6	312	22	AAH66827	C glutamicum codin	c 321	17	0.6	609	22	AAK89375	Human digestive sy
249	17	0.6	324	22	AAI188588	Human polynucleoti	c 322	17	0.6	619	21	AAAO1611	Human colon cancer
250	17	0.6	333	21	AAK22687	Human secreted pro	c 323	17	0.6	621	24	ABQ25194	Oligonucleotide fo
251	17	0.6	354	24	ABN68875	Streptococcus poly	c 324	17	0.6	621	24	ABQ25195	Oligonucleotide fo
252	17	0.6	355	24	ABL85192	Human ovarian canc	c 325	17	0.6	636	21	AAA30448	Human brain cDNA c
253	17	0.6	359	21	AAA44118	Human secreted exp	c 326	17	0.6	644	23	ABV14219	Human prostate exp
254	17	0.6	375	22	AAK59068	Human cancer relat	c 327	17	0.6	644	23	ABV14219	Human prostate exp
255	17	0.6	383	18	AAK83360	Breast cancer tumo	c 328	17	0.6	653	21	AAF08204	Human digestive sy
256	17	0.6	383	19	AAV68900	DNA molecule encod	c 329	17	0.6	653	24	ABQ58440	Human colon cancer
257	17	0.6	383	21	AAK80883	Human breast tumou	c 330	17	0.6	656	21	AAF13116	Fusarium venenatum
258	17	0.6	383	24	ABK46773	Human breast tumou	c 331	17	0.6	661	20	AAZ22439	Human colon cancer
259	17	0.6	387	24	AAK59729	Breast tumour-spec	c 332	17	0.6	702	23	ABL96431	Aspergillus oryzae
260	17	0.6	387	21	AAK29487	Human secreted pro	c 333	17	0.6	702	23	ABL96431	Internal Transcrib
261	17	0.6	390	23	ABV18991	Human prostate exp	c 334	17	0.6	714	22	AAI95590	Human reproductive
262	17	0.6	397	22	AAK59060	Human cancer relat	c 335	17	0.6	729	23	ABL06067	Human testicular a
263	17	0.6	399	23	AAK54509	Human cancer relat	c 336	17	0.6	734	22	AAH36020	Human neuroblastom
264	17	0.6	403	22	AAK59048	DNA encoding novel	c 337	17	0.6	739	21	AAK34392	Drosophila melanog
265	17	0.6	406	23	AAK57082	Human cancer relat	c 338	17	0.6	739	23	AAK590653	Human colon cancer
266	17	0.6	413	22	AAI92244	DNA encoding novel	c 339	17	0.6	745	21	AAK45988	Arabidopsis thalia
267	17	0.6	418	23	ABK41834	Human polynucleoti	c 340	17	0.6	759	23	ABV05050	Human prostate exp
268	17	0.6	422	23	ABV13941	cDNA encoding nove	c 341	17	0.6	762	22	AAI97375	Human neuroblastom
269	17	0.6	427	23	AAK74078	Human prostate exp	c 342	17	0.6	772	22	AAK22707	Human gastric canc
270	17	0.6	428	22	ABK41470	DNA encoding novel	c 343	17	0.6	804	21	AAK90125	Cytokine receptor-
271	17	0.6	432	21	AAK16337	Human nervous syst	c 344	17	0.6	816	24	ABQ88847	Human prostate exp
272	17	0.6	435	22	ABK46068	Human prostate can	c 345	17	0.6	816	24	ABQ88847	Arabidopsis thalia
273	17	0.6	435	22	ABA56606	Human breast cell	c 346	17	0.6	818	24	ABN98971	Arabidopsis thalia
274	17	0.6	435	22	ABA56606	Human foetal liver	c 347	17	0.6	832	23	ABL15671	Drosophila melanog
275	17	0.6	435	22	ABA26221	Probe #4867 for ge	c 348	17	0.6	840	22	AAH04154	Human cDNA clone (
276	17	0.6	435	22	AAK04750	Human brain expres	c 349	17	0.6	843	20	AAK00643	Human secreted pro
277	17	0.6	435	22	AAI14872	Human bone marrow	c 350	17	0.6	859	23	AAK84155	DNA encoding novel
278	17	0.6	435	22	AAI136228	Probe #4805 for ge	c 351	17	0.6	878	22	AAO2587	Human ovarian and
279	17	0.6	435	22	AAI04659	Probe #4914 used t	c 352	17	0.6	884	22	AAH06551	Human CDNA clone (
280	17	0.6	435	22	ABK04855	Probe #4850 used t	c 353	17	0.6	918	23	ABV11455	Human prostate exp
281	17	0.6	437	22	AAK59365	Human genome-deriv	c 354	17	0.6	927	21	AAZ53603	Neisseria meningit
282	17	0.6	439	23	ABV04772	Human immune/haema	c 355	17	0.6	927	22	AAH53526	S. epidermidis ope
283	17	0.6	442	23	ABV48770	Human prostate exp	c 356	17	0.6	931	22	AAI01836	Human reproductive
284	17	0.6	460	23	ABV35050	Human prostate exp	c 357	17	0.6	931	23	ABL97129	Human testicular a
285	17	0.6	460	23	ABV43897	Human prostate exp	c 358	17	0.6	939	24	ABN91158	Staphylococcus epi
286	17	0.6	478	24	ABN63353	Human prostate exp	c 359	17	0.6	945	21	AAK50863	Arabidopsis thalia
287	17	0.6	484	22	AAH13621	Human cancer relat	c 360	17	0.6	947	23	ABV29088	Human prostate exp
288	17	0.6	510	21	AAK38101	Human cDNA clone (c 361	17	0.6	947	23	ABV29088	Human prostate exp
289	17	0.6	522	22	AAH09564	DNA encoding novel	c 362	17	0.6	979	22	AAH32025	Human olfactory re
290	17	0.6	522	22	ABN94816	Human CDNA clone (c 363	17	0.6	996	24	ABN67399	Streptococcus poly
291	17	0.6	534	23	ABV18243	Gene #1314 used to	c 364	17	0.6	1001	22	AAH75151	Nucleotide sequenc
292	17	0.6	539	22	AAI90518	Human prostate exp	c 365	17	0.6	1013	22	AAI17919	G-protein coupled
293	17	0.6	541	22	ABA51181	Human polynucleoti	c 366	17	0.6	1076	22	AAH29941	c albicans apoptos
294	17	0.6	541	22	ABA51181	Human breast cell	c 367	17	0.6	1094	22	AAK41250	cDNA encoding nove
295	17	0.6	541	22	ABA69181	Human foetal liver	c 368	17	0.6	1094	22	AAK34981	cDNA encoding nove
296	17	0.6	541	22	ABA36107	Probe #14573 for g	c 369	17	0.6	1125	21	AAK43347	Arabidopsis thalia
297	17	0.6	541	22	AAK17482	Human brain expres	c 370	17	0.6	1132	22	AAI68145	Human aggreganase-
298	17	0.6	541	22	AAK43293	Human bone marrow	c 371	17	0.6	1147	22	AAK91200	Human digestive sy
299	17	0.6	541	22	AAI24061	Probe #13994 for g	c 372	17	0.6	1149	22	AAK91197	Human digestive sy
300	17	0.6	541	22	AAI49358	Probe #18044 used	c 373	17	0.6	1173	21	AAK83110	DNA encoding a pro
301	17	0.6	541	22	AAI09644	Probe #9635 used t	c 374	17	0.6	1179	23	AAK564921	DNA encoding novel

375	17	0.6	1185	22	AAK53293	Human polynucleoti	448	17	0.6	2073	24	ABL68820	Kidney cancer rela
376	17	0.6	1188	22	AAK52309	Human polynucleoti	c 449	17	0.6	2095	20	AAK27331	Human secreted pro
c 377	17	0.6	1229	22	AAI92643	Human polynucleoti	450	17	0.6	2115	20	AAK44723	Novel protein kina
c 378	17	0.6	1232	21	AAI12158	Murine X5L DNA fra	451	17	0.6	2124	24	AAI45611	Human ATP dependen
379	17	0.6	1245	22	ABA08870	Human Fas-associat	452	17	0.6	2175	24	ABN68111	Streptococcus poly
c 380	17	0.6	1261	21	AAK44835	Arabidopsis thalia	c 453	17	0.6	2180	22	AAH24225	Human oxidoreducta
c 381	17	0.6	1263	21	AAI93369	Mammalian interleu	454	17	0.6	2180	22	AAH14968	Human cDNA sequenc
382	17	0.6	1278	22	AAK90124	Murine cytokine re	c 455	17	0.6	2188	22	AAK34842	cDNA encoding nove
383	17	0.6	1284	23	ABV21452	Human prostate exp	456	17	0.6	2190	23	ABL05961	Drosophila melanog
384	17	0.6	1284	23	ABV27270	Human prostate exp	c 457	17	0.6	2191	22	AAK45025	cDNA encoding nove
385	17	0.6	1302	24	ABN91365	Staphylococcus epi	c 458	17	0.6	2192	24	AAK94879	Human DNA sequenc
386	17	0.6	1306	22	AAK54477	Zcytor 10 cytokine	c 459	17	0.6	2210	21	AAK62077	Hydrophobic domain
387	17	0.6	1318	21	AAK47883	Arabidopsis thalia	c 460	17	0.6	2224	19	AAV35472	Rat RSK3 coding se
c 388	17	0.6	1332	24	ABO78009	Chlamydia polynucl	c 461	17	0.6	2309	23	ABL05325	Human polynucleoti
389	17	0.6	1343	23	ABL12475	Drosophila melanog	462	17	0.6	2322	23	ABL05435	Drosophila melanog
390	17	0.6	1359	22	AAK65491	C glutamic codin	463	17	0.6	2328	23	ABL19593	Drosophila melanog
391	17	0.6	1360	23	ABV23029	Human prostate exp	464	17	0.6	2330	22	AAH14498	Human cDNA sequenc
392	17	0.6	1360	23	ABV28865	Human prostate exp	465	17	0.6	2375	23	ABL07241	Drosophila melanog
c 393	17	0.6	1371	24	ABN66153	Streptococcus poly	c 466	17	0.6	2447	23	AAK83213	DNA encoding novel
c 394	17	0.6	1381	21	AAK36170	Arabidopsis thalia	467	17	0.6	2450	23	ABL11997	Drosophila melanog
395	17	0.6	1404	20	AAK611424	DNA encoding a hum	468	17	0.6	2451	22	AAK26984	cDNA encoding nove
396	17	0.6	1409	24	ABK11149	Murine TSLPR (thym	469	17	0.6	2460	21	AAK98006	Human T gene cDNA
397	17	0.6	1409	24	ABK11530	Mouse thymic strom	c 470	17	0.6	2462	19	AAV35473	Human hSK3 coding
398	17	0.6	1410	23	ABL12471	Drosophila melanog	c 471	17	0.6	2464	22	AAK45213	cDNA encoding nove
399	17	0.6	1425	22	AAK54451	Zcytor 10 cytokine	c 472	17	0.6	2465	20	AAK23681	Human DKC1 cDNA
400	17	0.6	1428	23	ABL57930	Human VG51 coding	c 473	17	0.6	2466	23	AAK69887	DNA encoding novel
401	17	0.6	1452	13	AAQ29383	Mouse perforin C-t	474	17	0.6	2469	22	AAK78832	Human immune/haema
c 402	17	0.6	1456	22	AAK62706	Human DAPPI cDNA	475	17	0.6	2471	24	AAI72320	ISIGP-3 cDNA. Hom
403	17	0.6	1504	22	AAH15476	Human cDNA sequenc	476	17	0.6	2479	23	ABL23280	Drosophila melanog
404	17	0.6	1530	20	AAK22768	Human IUPAC versio	477	17	0.6	2488	23	ABL17627	Drosophila melanog
405	17	0.6	1530	20	AAK22766	Human refined SOCS	478	17	0.6	2504	22	AAK55869	Rat GLUTX2 coding
406	17	0.6	1532	20	AAK22767	Human IUPAC versio	c 479	17	0.6	2521	20	AAK08414	Human small conduc
c 407	17	0.6	1536	22	AAK20195	Human translation	480	17	0.6	2521	21	AAK16086	Human prostate can
c 408	17	0.6	1536	22	AAK86071	Human translation	481	17	0.6	2565	23	ABL14698	Drosophila melanog
409	17	0.6	1546	23	ABL20043	Drosophila melanog	c 482	17	0.6	2571	22	AAK52271	Human polynucleoti
410	17	0.6	1590	21	AAK48082	Zea mays DNA fragm	c 483	17	0.6	2658	12	AAQ14772	SP6DNA polymerase
c 411	17	0.6	1604	22	AAH15435	Human cDNA sequenc	484	17	0.6	2675	23	ABL12171	Drosophila melanog
412	17	0.6	1635	23	AAK80572	DNA encoding novel	c 485	17	0.6	2698	22	AAH18540	Human cDNA sequenc
c 413	17	0.6	1638	21	AAK43024	Arabidopsis thalia	486	17	0.6	2729	23	ABL06066	Drosophila melanog
414	17	0.6	1653	21	AAK63457	Human secreted pro	487	17	0.6	2785	24	AAK59856	Novel human coding
c 415	17	0.6	1659	22	ABA21325	Human nervous syst	c 488	17	0.6	2849	24	ABK34712	Human cDNA for nov
c 416	17	0.6	1665	21	AAK62067	Hydrophobic domain	c 489	17	0.6	2852	24	ABQ70918	Listeria monocytog
417	17	0.6	1680	24	ABK05623	Human protein tyro	c 490	17	0.6	2886	21	AAK70575	Antisense DRE Anta
418	17	0.6	1681	23	ABL10139	Drosophila melanog	491	17	0.6	2887	24	AAK93762	Human nucleic acid
c 419	17	0.6	1682	22	AAK20196	Human translation	c 492	17	0.6	2909	23	ABL26884	Drosophila melanog
c 420	17	0.6	1682	22	AAK86072	Human translation	493	17	0.6	2911	22	AAK25925	Human cDNA encodin
c 421	17	0.6	1682	24	ABK83618	Human cDNA differe	c 494	17	0.6	2925	23	ABL20028	Drosophila melanog
422	17	0.6	1700	24	ABK94908	Human novel polynu	c 495	17	0.6	2936	23	ABL15670	Drosophila melanog
423	17	0.6	1742	23	ABL09139	Drosophila melanog	496	17	0.6	2937	22	AAH18341	Human cDNA sequenc
c 424	17	0.6	1771	23	AAK90655	DNA encoding novel	c 497	17	0.6	2986	22	AAH55032	S. epidermidis gen
c 425	17	0.6	1779	23	AAK92315	DNA encoding novel	c 498	17	0.6	3005	24	ABL53693	Human ubiquitin de
426	17	0.6	1782	23	ABL12479	Drosophila melanog	499	17	0.6	3080	24	AAK37604	Human intracellula
c 427	17	0.6	1786	22	AAH02945	Human shear stress	c 500	17	0.6	3102	23	ABV25452	Human prostate exp
428	17	0.6	1857	24	AAK62551	cDNA sequence #338	c 501	17	0.6	3103	24	ABL55454	Human BAF57 protei
429	17	0.6	1879	21	AAK44557	Zea mays DNA fragm	502	17	0.6	3114	24	AAI44674	Human transporter
c 430	17	0.6	1911	22	AAK52679	Human polynucleoti	c 503	17	0.6	3180	24	ABN79868	Fungal ZBC gene se
c 431	17	0.6	1923	22	AAK05489	Human reproductive	c 504	17	0.6	3214	23	ABL22286	Drosophila melanog
c 432	17	0.6	1923	23	ABL98342	Human testicular a	c 505	17	0.6	3224	23	AAK82583	DNA encoding novel
c 433	17	0.6	1939	19	AAK32415	Homo sapiens clone	c 506	17	0.6	3224	23	AAK89304	DNA encoding novel
c 434	17	0.6	1939	22	AAK98431	Human cDNA clone B	c 507	17	0.6	3236	21	AAK98888	Human pancreatic c
c 435	17	0.6	1942	22	AAK51695	Human polynucleoti	c 508	17	0.6	3280	20	AAK23684	Human DKC1 DNA fra
c 436	17	0.6	1948	19	AAV26612	Homo sapiens gluta	509	17	0.6	3331	23	ABL20044	Drosophila melanog
437	17	0.6	1950	24	AAK24027	Human protein phos	c 510	17	0.6	3339	19	AAV61096	Mouse membrane typ
438	17	0.6	1955	22	AAK34915	Human colon cancer	511	17	0.6	3372	22	AAI59730	Human polynucleoti
439	17	0.6	1965	20	AAK60621	Polynucleotide seq	512	17	0.6	3378	24	AAK99410	DNA of APP related
c 440	17	0.6	1986	24	ABQ69092	Listeria monocytog	513	17	0.6	3406	24	ABN95130	Gene #1628 used to
441	17	0.6	1991	24	ABJ58952	Human tumour marke	514	17	0.6	3406	24	ABK64397	Human benign prost
442	17	0.6	2035	19	AAV30292	Bacillus thuringie	515	17	0.6	3406	24	ABL66479	Lung cancer relate
c 443	17	0.6	2050	22	AAH15461	Human cDNA sequenc	516	17	0.6	3458	24	AAK95018	Human DNA sequenc
444	17	0.6	2066	22	AAH15865	Human cDNA sequenc	c 517	17	0.6	3572	21	AAK18261	Lung cancer associ
445	17	0.6	2073	24	ABK83594	Human cDNA differe	518	17	0.6	3582	23	ABL17962	Drosophila melanog
446	17	0.6	2073	24	ABK95103	Gene #1601 used to	519	17	0.6	3600	21	AAK98971	S. xylosus mprF DN
447	17	0.6	2073	24	ABL68352	Kidney cancer rela	520	17	0.6	3626	22	AAH17757	Human cDNA sequenc

c 521	17	0.6	3635	22	AAS32830	Human genomic DNA	c 594	17	0.6	7387	21	AAA97914	L. mesenteroides a
c 522	17	0.6	3638	23	ABV23199	Human prostate exp	595	17	0.6	7465	21	ABN96860	Gene #3358 used to
c 523	17	0.6	3638	23	ABV29036	Human prostate exp	596	17	0.6	7655	24	AAA07847	HS-UNC-53/1 fragm
c 524	17	0.6	3643	24	ABK84074	Human cDNA differe	c 597	17	0.6	7669	22	AAS46597	Tumour suppressor
c 525	17	0.6	3715	23	ABL20042	Drosophila melanog	c 598	17	0.6	7669	24	ABL33846	Human immune syste
c 526	17	0.6	3717	21	AAC48934	Arabidopsis thalia	c 599	17	0.6	8032	24	ABL70448	Chemically treated
c 527	17	0.6	3791	24	ABK52289	cDNA encoding memb	c 600	17	0.6	8032	24	AAS61409	Human gene regulat
c 528	17	0.6	3970	21	AAA97911	L. mesenteroides a	c 601	17	0.6	8032	24	ABK31479	Signal transductio
c 529	17	0.6	4003	23	ABL12470	Drosophila melanog	c 602	17	0.6	8052	23	ABL26661	Drosophila melanog
c 530	17	0.6	4071	23	ABL08828	Drosophila melanog	c 603	17	0.6	8316	23	ABL18094	Drosophila melanog
c 531	17	0.6	4099	22	ABL26637	Human breast cance	c 604	17	0.6	8395	24	ABL32175	Human immune syste
c 532	17	0.6	4126	22	AAK80162	Human immune/haema	c 605	17	0.6	8605	23	ABL06307	Drosophila melanog
c 533	17	0.6	4126	22	AAK89461	Human digestive sy	c 606	17	0.6	8705	22	ABA82624	Human HBM gene reg
c 534	17	0.6	4134	23	AAS89154	DNA encoding novel	c 607	17	0.6	8805	20	AAZ23193	Mouse mammary tumo
c 535	17	0.6	4150	23	ABL07491	Drosophila melanog	c 608	17	0.6	9057	24	AAD26665	Human G-protein co
c 536	17	0.6	4157	24	ABL57463	Human protein phos	c 609	17	0.6	9057	24	AAD26722	Human G-protein co
c 537	17	0.6	4165	17	AAIT16483	cDNA encoding huma	c 610	17	0.6	9321	21	AAK97904	L. mesenteroides a
c 538	17	0.6	4165	19	AAV13998	Human eps15 protei	c 611	17	0.6	9840	22	AAC85482	Murine neuropeptid
c 539	17	0.6	4165	20	AAK04191	Human eps15 encodi	c 612	17	0.6	9862	24	ABA92593	Human kinase prote
c 540	17	0.6	4182	23	ABL26592	Drosophila melanog	c 613	17	0.6	10026	24	ABL33876	Human immune syste
c 541	17	0.6	4192	20	AAK00725	Human aggregan deg	c 614	17	0.6	10195	22	AAS26626	Human genomic DNA
c 542	17	0.6	4226	22	ABA21324	Human nervous syst	c 615	17	0.6	10438	23	ABL14372	Drosophila melanog
c 543	17	0.6	4257	24	ABK84770	Human cDNA differe	c 616	17	0.6	10634	22	AAK05488	Human reproductive
c 544	17	0.6	4275	23	ABL09776	Drosophila melanog	c 617	17	0.6	10634	23	ABL98341	Human testicular a
c 545	17	0.6	4277	23	ABL11776	Drosophila melanog	c 618	17	0.6	10710	24	ABL32893	Human immune syste
c 546	17	0.6	4301	22	AAI68146	Human aggreganase-	c 619	17	0.6	10736	22	AAK80161	Human immune/haema
c 547	17	0.6	4303	21	AAK95826	Human metalloprote	c 620	17	0.6	10736	22	AAK89460	Human digestive sy
c 548	17	0.6	4355	21	AAK75582	Human ORFX ORF1137	c 621	17	0.6	10769	23	ABL26660	Drosophila melanog
c 549	17	0.6	4359	23	ABL10138	Drosophila melanog	c 622	17	0.6	11500	23	ABL26680	Drosophila melanog
c 550	17	0.6	4364	24	AAD23658	Human 16051a cDNA	c 623	17	0.6	11964	24	ABQ67025	Human anglogenesis
c 551	17	0.6	4406	22	AAK46100	Human DNA encoding	c 624	17	0.6	11976	24	ABL32595	Human immune syste
c 552	17	0.6	4407	21	AAK37111	Human PRO1563 (UNQ	c 625	17	0.6	12144	22	AAS46260	DNA encoding novel
c 553	17	0.6	4407	22	AAF54426	Probe #46 used in	c 626	17	0.6	13273	22	AAS36849	Human cardiovascul
c 554	17	0.6	4432	23	ABL12478	Drosophila melanog	c 627	17	0.6	13563	23	ABL06306	Drosophila melanog
c 555	17	0.6	4434	18	AAK93389	Bloom's syndrome B	c 628	17	0.6	14209	22	ABK89137	Human digestive sy
c 556	17	0.6	4437	18	AAK67013	Bloom syndrome act	c 629	17	0.6	14307	24	ABL32728	Human immune syste
c 557	17	0.6	4437	18	AAK93390	Bloom's syndrome B	c 630	17	0.6	14551	24	ABL34585	Human metastasis a
c 558	17	0.6	4437	18	AAK93392	Bloom's syndrome B	c 631	17	0.6	14598	22	AAS27769	DNA encoding novel
c 559	17	0.6	4437	18	AAK93394	Bloom's syndrome B	c 632	17	0.6	15054	22	AAS40425	DNA encoding human
c 560	17	0.6	4437	18	AAK93395	Bloom's syndrome B	c 633	17	0.6	15054	22	AAK04033	Human reproductive
c 561	17	0.6	4437	24	ABL67661	Oesophagus cancer	c 634	17	0.6	15372	23	ABL12192	Drosophila melanog
c 562	17	0.6	4438	18	AAK93391	Bloom's syndrome B	c 635	17	0.6	15424	23	ABL27214	Drosophila melanog
c 563	17	0.6	4438	18	AAK93393	Bloom's syndrome B	c 636	17	0.6	16869	21	ABN97976	Human retroviral s
c 564	17	0.6	4516	23	ABL09198	Drosophila melanog	c 637	17	0.6	16941	21	AAZ34737	Drosophila dissati
c 565	17	0.6	4551	23	AAS87023	DNA encoding novel	c 638	17	0.6	17047	22	AAK81251	Human immune/haema
c 566	17	0.6	4569	24	AAD23659	Human 16051b cDNA	c 639	17	0.6	17534	24	ABK40026	Human chemically p
c 567	17	0.6	4708	23	ABL17626	Drosophila melanog	c 640	17	0.6	17965	22	AAK05510	Human reproductive
c 568	17	0.6	4893	23	ABL07240	Drosophila melanog	c 641	17	0.6	18559	23	ABL14336	Drosophila melanog
c 569	17	0.6	5319	23	ABL05960	Drosophila melanog	c 642	17	0.6	18559	23	ABL121012	Drosophila melanog
c 570	17	0.6	5388	24	ABL32245	Human immune syste	c 643	17	0.6	19142	20	AAK20580	Polynucleotide seq
c 571	17	0.6	5429	23	ABL12170	Drosophila melanog	c 644	17	0.6	19385	23	ABL21130	Drosophila melanog
c 572	17	0.6	5491	23	AAS85968	DNA encoding novel	c 645	17	0.6	20184	23	ABL12118	Drosophila melanog
c 573	17	0.6	5598	22	AAS32873	Human genomic DNA	c 646	17	0.6	20184	23	ABL18276	Drosophila melanog
c 574	17	0.6	5703	22	AAS32874	Human genomic DNA	c 647	17	0.6	24053	22	AAD12308	Toxoplasma gondii
c 575	17	0.6	6004	21	AAK07835	Human homologue of	c 648	17	0.6	24110	22	AAK16628	Human novel protei
c 576	17	0.6	6065	24	ABL32504	Human immune syste	c 649	17	0.6	26329	22	AAS42041	Genomic sequence #
c 577	17	0.6	6079	24	ABL32258	Human immune syste	c 650	17	0.6	27884	22	AAK77781	Human immune/haema
c 578	17	0.6	6204	21	AAK97917	L. mesenteroides a	c 651	17	0.6	28344	23	ABL21640	Drosophila melanog
c 579	17	0.6	6300	23	ABL12474	Drosophila melanog	c 652	17	0.6	31129	24	AAD36229	Human transporter
c 580	17	0.6	6242	22	AAS27776	DNA encoding novel	c 653	17	0.6	31474	22	AAK05461	Human reproductive
c 581	17	0.6	6283	24	ABK39991	Human chemically p	c 654	17	0.6	31474	23	ABL98314	Human testicular a
c 582	17	0.6	6283	24	ABL32834	Human immune syste	c 655	17	0.6	31949	22	ABL05410	Human reproductive
c 583	17	0.6	6328	23	ABL02594	Drosophila melanog	c 656	17	0.6	31949	22	ABL98269	Human testicular a
c 584	17	0.6	6468	23	ABL09816	Drosophila melanog	c 657	17	0.6	32186	22	AAK05411	Human reproductive
c 585	17	0.6	6545	23	ABL14373	Drosophila melanog	c 658	17	0.6	32186	23	ABL98270	Human testicular a
c 586	17	0.6	6596	23	ABL08072	Drosophila melanog	c 659	17	0.6	32190	22	AAK36479	Human musculoskele
c 587	17	0.6	6754	20	AAK20602	Polynucleotide seq	c 660	17	0.6	32195	22	AAK04180	Human reproductive
c 588	17	0.6	6754	24	ABL70346	Chemically treated	c 661	17	0.6	32780	22	AAK24652	Nucleotide sequenc
c 589	17	0.6	6754	24	AAK61305	Human gene regulat	c 662	17	0.6	36305	24	ABK22783	Human high bone ma
c 590	17	0.6	6810	20	AAK20267	Borrelia burgdorfe	c 663	17	0.6	38374	24	ABK96966	Gene #3464 used to
c 591	17	0.6	7117	23	ABL05434	Drosophila melanog	c 664	17	0.6	38374	24	ABL68363	Kidney cancer rela
c 592	17	0.6	7198	23	ABL19592	Drosophila melanog	c 665	17	0.6	38374	24	ABL68364	Kidney cancer rela
c 593	17	0.6	7273	23	ABL11996	Drosophila melanog	c 666	17	0.6	38374	24	ABL68824	Kidney cancer rela

c 667	17	0.6	44602	22	AAK77611	Human immune/haema	740	16	0.5	189	22	AAK47454	Human bone marrow
c 668	17	0.6	48727	22	AAK67375	Human immune/haema	741	16	0.5	189	22	AAI53288	Probe #21974 used
c 669	17	0.6	50849	24	ABN87883	Human glutathione	c 742	16	0.5	189	24	ABQ91274	M. capsulatus gene
c 670	17	0.6	56093	24	ABL61744	Colon adenocarcino	c 743	16	0.5	189	24	ABQ91492	M. capsulatus gene
c 671	17	0.6	73465	24	ABQ98161	Human osteoblast d	c 744	16	0.5	192	24	AAQ90518	M. capsulatus gene
c 672	17	0.6	99960	21	AAZ50905	Human TBC-1 partia	c 745	16	0.5	199	22	AAH45193	Murine oligonucleo
c 673	17	0.6	114793	22	AAAD08215	Human genome from	c 746	16	0.5	202	21	AAC08465	Human colon cancer
c 674	17	0.6	129021	21	AAF22296	BAC containing rep	c 747	16	0.5	208	21	AAC98716	Human prostate exp
c 675	17	0.6	149671	24	ABK84797	Human cDNA differe	c 748	16	0.5	209	21	AAC35717	Arabidopsis thalia
c 676	17	0.6	155074	24	ABN85735	Human genomic regi	c 749	16	0.5	216	19	AAI12202	Human biallelic po
c 677	17	0.6	183999	22	AAF92831	Human ABC1 genomic	c 750	16	0.5	216	19	AAI12203	Human biallelic po
c 678	17	0.6	249487	24	ABN85733	Mouse genomic regi	c 751	16	0.5	220	22	ABA49663	Human breast cell
c 679	17	0.6	349980	22	AAH68525	C glutamic codin	c 752	16	0.5	220	22	ABA67566	Human foetal liver
c 680	17	0.6	349980	22	AAH68529	C glutamic codin	c 753	16	0.5	220	22	ABA34644	Probe #13110 for g
c 681	17	0.6	640681	24	ABA92787	Buchnera sp. genom	c 754	16	0.5	220	22	AAK15988	Human brain expres
c 682	17	0.6	1038602	20	AAZ01425	Complete genome se	c 755	16	0.5	220	22	AAK41734	Human bone marrow
c 683	17	0.6	2365589	24	ABA90521	Genomic sequence o	c 756	16	0.5	220	22	AAI22490	Probe #12423 for g
c 684	17	0.6	4411529	22	AAI99682	Mycobacterium tube	c 757	16	0.5	220	22	AAI47782	Probe #16468 used
c 685	16	0.5	17	23	ABK03548	Human CD20 DNzyme	c 758	16	0.5	220	22	AAI08176	Probe #8167 used t
c 686	16	0.5	20	22	AAF24978	Nucleotide sequenc	c 759	16	0.5	220	24	ABSI15743	Human genome-deriv
c 687	16	0.5	33	24	ABQ77511	Human cytokine rec	c 760	16	0.5	222	24	ABQ91649	M. capsulatus gene
c 688	16	0.5	36	13	AAQ31346	IL-6R antibody pri	c 761	16	0.5	223	22	AAQ43332	DNA encoding novel
c 689	16	0.5	40	20	AAZ25261	M-Raf mitochondria	c 762	16	0.5	227	23	ABV21387	Human prostate exp
c 690	16	0.5	50	22	AAI31666	Human SNP oligonuc	c 763	16	0.5	227	23	ABV27205	Human prostate exp
c 691	16	0.5	65	24	ABN27831	Rat spliced transc	c 764	16	0.5	247	21	AAC30920	Human secreted pro
c 692	16	0.5	65	24	ABN50981	Mouse spliced tran	c 765	16	0.5	251	19	AAI11014	Human biallelic po
c 693	16	0.5	65	24	ABN51063	Mouse spliced tran	c 766	16	0.5	251	23	ABV06336	Human prostate exp
c 694	16	0.5	84	22	AAI21921	Human collagen gen	c 767	16	0.5	252	22	ABA49012	Human breast cell
c 695	16	0.5	109	22	ABA72173	Human foetal liver	c 768	16	0.5	252	22	ABA66925	Human foetal liver
c 696	16	0.5	109	22	AAK20597	Human brain expres	c 769	16	0.5	252	22	ABA34011	Probe #12477 for g
c 697	16	0.5	109	22	AAK46739	Human bone marrow	c 770	16	0.5	252	22	AAK15371	Human brain expres
c 698	16	0.5	112	22	AAI49206	Probe #17892 used	c 771	16	0.5	252	22	AAK41094	Human bone marrow
c 699	16	0.5	112	24	ABSI7203	Human genome-deriv	c 772	16	0.5	252	22	AAI21859	Probe #11792 for g
c 700	16	0.5	113	24	ABL74122	Corn tassell-derive	c 773	16	0.5	252	22	AAI47143	Probe #15829 used
c 701	16	0.5	132	15	AAQ53915	Partial sequence o	c 774	16	0.5	252	22	AAI07546	Probe #7537 used t
c 702	16	0.5	132	18	AAV03166	Partial RNA-2 sequ	c 775	16	0.5	252	24	ABSI5087	Human genome-deriv
c 703	16	0.5	132	20	AAV99299	Partial nucleotide	c 776	16	0.5	254	21	AAC70683	Single nucleotide
c 704	16	0.5	133	24	ABL69090	Kidney cancer rela	c 777	16	0.5	254	21	AAC70701	Single nucleotide
c 705	16	0.5	141	22	ABM49960	Human breast cell	c 778	16	0.5	255	22	AH821601	Rat differential t
c 706	16	0.5	141	22	ABA67879	Human foetal liver	c 779	16	0.5	257	20	AAZ20003	Spider venom parti
c 707	16	0.5	141	22	ABA34933	Probe #13399 for g	c 780	16	0.5	260	20	AAZ20004	Human secreted parti
c 708	16	0.5	141	22	AAK16283	Human brain expres	c 781	16	0.5	260	21	AAC03558	Human secreted pro
c 709	16	0.5	141	22	AAI22792	Probe #12725 for g	c 782	16	0.5	261	16	AAI20840	Human gene signatu
c 710	16	0.5	141	22	AAI48094	Probe #16780 used	c 783	16	0.5	261	24	ABN25398	Human ORFX polynuc
c 711	16	0.5	141	22	AAI08466	Probe #8457 used t	c 784	16	0.5	262	23	ABV02197	Human prostate exp
c 712	16	0.5	141	24	ABSI16061	Human genome-deriv	c 785	16	0.5	268	20	AAH87257	Human single nucle
c 713	16	0.5	143	23	AAI42527	Exon 2 from a gene	c 786	16	0.5	269	23	ABV32511	Human prostate exp
c 714	16	0.5	143	24	ABA01108	Human DNA sequence	c 787	16	0.5	269	23	ABV41436	Human prostate exp
c 715	16	0.5	143	24	AAI99833	Human chromosome 2	c 788	16	0.5	270	24	ABL85716	Human ovarian canc
c 716	16	0.5	145	22	ABA73137	Human foetal liver	c 789	16	0.5	271	22	ABA48166	Human breast cell
c 717	16	0.5	145	22	AAK21573	Human brain expres	c 790	16	0.5	271	22	ABA66043	Human foetal liver
c 718	16	0.5	145	22	AAK47733	Human bone marrow	c 791	16	0.5	271	22	ABA33126	Probe #11592 for g
c 719	16	0.5	145	22	AAI53566	Probe #22252 used	c 792	16	0.5	271	22	AAK14466	Human brain expres
c 720	16	0.5	145	24	ABSI21764	Human genome-deriv	c 793	16	0.5	271	22	AAK40206	Human bone marrow
c 721	16	0.5	150	22	AAH21878	Mouse digital sequ	c 794	16	0.5	271	22	AAI20974	Probe #10907 for g
c 722	16	0.5	150	24	ABK71456	Central nervous sy	c 795	16	0.5	271	22	AAI46221	Probe #14907 used
c 723	16	0.5	152	22	AAC99210	Human brain T calc	c 796	16	0.5	271	22	AAI06687	Probe #6678 used t
c 724	16	0.5	163	22	AAC91735	Streptococcus pneu	c 797	16	0.5	271	24	ABSI4254	Human genome-deriv
c 725	16	0.5	165	22	AAI29052	Colon tumour relat	c 798	16	0.5	273	22	AAK56129	Human immune/haema
c 726	16	0.5	175	22	ABA76018	Human foetal liver	c 799	16	0.5	276	24	ABQ69697	Listeria innocua D
c 727	16	0.5	175	22	ABM40581	Probe #19047 for g	c 800	16	0.5	277	22	AAD02662	Human Wtl antisens
c 728	16	0.5	175	22	AAK24696	Human brain expres	c 801	16	0.5	277	22	ABV09136	Human prostate exp
c 729	16	0.5	175	22	AAK50695	Human bone marrow	c 802	16	0.5	277	23	ABV33726	Cellubrevin-1 part
c 730	16	0.5	175	22	AAI27708	Probe #17641 for g	c 803	16	0.5	284	17	AAI339872	Human cellubrevin
c 731	16	0.5	175	22	AAI56673	Probe #25359 used	c 804	16	0.5	284	21	AAI339872	M. capsulatus gene
c 732	16	0.5	175	24	ABSI24165	Human genome-deriv	c 805	16	0.5	285	24	ABQ91398	EST clone DF266.
c 733	16	0.5	181	16	AAI25078	Human gene signatu	c 806	16	0.5	286	20	AAI98083	Human cancer cell
c 734	16	0.5	183	24	ABQ91838	M. capsulatus gene	c 807	16	0.5	288	20	AAI98389	Listeria innocua D
c 735	16	0.5	186	24	ABQ90654	M. capsulatus gene	c 808	16	0.5	288	24	ABQ67341	Listeria innocua D
c 736	16	0.5	186	24	ABQ91050	M. capsulatus gene	c 809	16	0.5	288	24	ABQ69760	Human pancreatic c
c 737	16	0.5	187	20	AAZ20001	Spider venom parti	c 810	16	0.5	290	22	ABA07185	Human pancreatic c
c 738	16	0.5	187	22	ABA72865	Human foetal liver	c 811	16	0.5	290	22	ABA07188	Human pancreatic c
c 739	16	0.5	189	22	AAK21299	Human brain expres	c 812	16	0.5	290	22	AAK89817	Human digestive sy

813	16	0.5	290	22	AAK89818	Human digestive sy	c 886	16	0.5	376	23	ABV36296	Human prostate exp
814	16	0.5	290	22	AAK89820	Human digestive sy	c 887	16	0.5	376	23	ABV43117	Human prostate exp
815	16	0.5	291	23	ABL23291	Drosophila melanog	888	16	0.5	381	14	AAQ60422	Human brain expres
816	16	0.5	291	24	ABQ67351	Listeria innocua D	889	16	0.5	383	22	ABA09434	Human tumour suppr
817	16	0.5	293	24	ABL72419	Corn tassell-derive	890	16	0.5	383	22	AA43407	DNA encoding novel
818	16	0.5	296	23	ABV34256	Human prostate exp	891	16	0.5	383	22	AA188246	Human polynucleoti
819	16	0.5	298	24	ABL73833	Corn tassell-derive	c 892	16	0.5	383	22	AA192187	Human polynucleoti
820	16	0.5	300	16	AAQ99392	Rat allograft infl	893	16	0.5	384	22	AAH53482	S. epidermidis ope
821	16	0.5	300	20	AAZ14620	Human gene express	894	16	0.5	384	23	ABV32066	Human prostate exp
822	16	0.5	300	20	AAZ12854	Human gene express	895	16	0.5	384	23	ABV41004	Human prostate exp
823	16	0.5	300	20	AAZ98454	Human cancer cell	c 896	16	0.5	385	22	AA191147	Human polynucleoti
824	16	0.5	300	21	AAZ65612	Rat allograft infl	c 897	16	0.5	386	23	AA191081	DNA encoding novel
825	16	0.5	300	21	AAA00860	Human colon cancer	c 898	16	0.5	388	22	AA110681	Human breast cancer
826	16	0.5	300	22	AAH70472	Human cervical can	c 899	16	0.5	390	21	AAC41195	Arabidopsis thalia
827	16	0.5	300	22	AAH73162	Human cervical can	c 900	16	0.5	390	22	AA109561	Human breast cancer
828	16	0.5	300	24	ABQ58483	Human colon cancer	c 901	16	0.5	391	20	AAV90050	EST clone CW922.
829	16	0.5	306	21	AAC23134	Human secreted pro	c 902	16	0.5	393	24	ABL78819	Human ovarian cnc
830	16	0.5	311	19	AAV19193	Human XAG growth f	903	16	0.5	394	21	AAZ30052	Human secreted pro
831	16	0.5	311	22	AAFG3352	HUXAG-3 related ES	904	16	0.5	394	21	AAZ42778	Human 5' EST isola
832	16	0.5	311	24	ABK09495	Human ovarian tumo	c 905	16	0.5	395	22	AA123555	Human breast cancer
833	16	0.5	313	23	ABV15929	Human prostate exp	c 906	16	0.5	396	23	ABV00134	Human prostate exp
834	16	0.5	317	21	AAF10835	Fusarium venenatum	c 907	16	0.5	396	23	ABV01577	Human prostate exp
835	16	0.5	319	23	ABV01504	Human prostate exp	c 908	16	0.5	400	22	ABL7690	Human polynucleoti
836	16	0.5	320	22	ABA06885	Human pancreatic c	c 909	16	0.5	400	24	ABL83521	Human ovarian cnc
837	16	0.5	320	22	AAK87864	Human digestive sy	c 910	16	0.5	401	22	AAK95957	Human neuregulin g
838	16	0.5	321	22	ABAL12027	Human nervous syst	c 911	16	0.5	401	22	AAK95958	Human neuregulin g
839	16	0.5	322	22	AA121198	Human breast cancer	c 912	16	0.5	401	22	AAK97450	Human neuregulin g
840	16	0.5	324	24	ABQ91632	M. capsulatus gene	c 913	16	0.5	401	22	AAK97451	Human neuregulin g
841	16	0.5	326	22	AAH69732	Human cervical can	c 914	16	0.5	401	24	ABL79404	Human ovarian cnc
842	16	0.5	330	24	ABL63443	Breast cancer rela	915	16	0.5	403	22	AAH99000	Human EST-derived
843	16	0.5	335	18	AAV78569	Staphylococcus aur	c 916	16	0.5	403	23	ABV04958	Human prostate exp
844	16	0.5	338	22	AAC84611	Human zfp13 protein	c 917	16	0.5	405	22	AA37351	Novel human diagno
845	16	0.5	341	22	AAK28015	Novel cDNA encodin	c 918	16	0.5	405	22	AA191149	Human polynucleoti
846	16	0.5	343	22	AAK60878	Human immune/haema	c 919	16	0.5	409	22	AA124693	Human breast cancer
847	16	0.5	344	23	ABV01656	Human prostate exp	c 920	16	0.5	411	21	AAZ27825	Human secreted pro
848	16	0.5	345	22	ABA74317	Human foetal liver	c 921	16	0.5	412	22	AA13797	Human breast cancer
849	16	0.5	345	22	AAK22784	Human brain expres	922	16	0.5	412	23	ABV48088	Human prostate exp
850	16	0.5	345	22	AAK48953	Human bone marrow	c 923	16	0.5	413	21	AAH30495	Human colon cancer
851	16	0.5	345	22	AA154781	Probe #23467 used	c 924	16	0.5	413	23	ABV15505	Human prostate exp
852	16	0.5	345	24	ABS22606	Human genome-deriv	925	16	0.5	413	24	ABL67631	Oesophagus cancer
853	16	0.5	346	23	ABV01745	Human prostate exp	926	16	0.5	413	24	ABL67913	Ovary cancer relat
854	16	0.5	347	23	ABV10914	Human prostate exp	c 927	16	0.5	415	20	AAZ20912	Polynucleotide seq
855	16	0.5	351	22	AA109307	Human breast cancer	928	16	0.5	415	22	ABA44512	Human breast cell
856	16	0.5	351	22	AA117196	Human breast cancer	929	16	0.5	415	22	ABA54954	Human foetal liver
857	16	0.5	352	24	ABN26569	Human ORFX polynuc	930	16	0.5	415	22	ABA24719	Probe #3185 for ge
858	16	0.5	353	22	AAH12322	Human breast cancer	931	16	0.5	415	22	AAK03225	Human brain expres
859	16	0.5	355	18	AAH83277	Breast cancer tumo	932	16	0.5	415	22	AAK28679	Human bone marrow
860	16	0.5	355	19	AAV69023	DNA molecule encod	933	16	0.5	415	22	AAK87305	Human immune/haema
861	16	0.5	355	19	AAV68999	DNA molecule encod	934	16	0.5	415	22	AAK87307	Human immune/haema
862	16	0.5	355	21	AAC80800	Human breast tumou	935	16	0.5	415	22	AAK87309	Human immune/haema
863	16	0.5	355	21	AAC80960	Human breast tumou	936	16	0.5	415	22	AA113255	Probe #3188 for ge
864	16	0.5	355	24	ABN16600	Human ORFX polynuc	937	16	0.5	415	22	AA134608	Probe #3294 used t
865	16	0.5	355	24	ABK46690	Human breast tumou	938	16	0.5	415	22	AA103160	Probe #3151 used t
866	16	0.5	355	24	ABK46690	Human breast tumou	939	16	0.5	415	24	ABS03190	Human genome-deriv
867	16	0.5	355	24	AA599646	Human breast tumou	c 940	16	0.5	415	24	AAAC01953	Human secreted pro
868	16	0.5	355	24	AA599806	Breast tumour-spec	c 941	16	0.5	417	21	AAAC01953	Human colon cancer
869	16	0.5	356	18	AAV77300	Staphylococcus aur	942	16	0.5	418	21	AAC98493	Human colon cancer
870	16	0.5	356	24	ABN18021	Human ORFX polynuc	943	16	0.5	420	21	AAZ27071	Rat pPARalpha liga
871	16	0.5	357	21	AAK67422	Eucalyptus grandis	c 944	16	0.5	420	22	AAH81518	Genomic sequence #
872	16	0.5	360	22	AAK64881	Novel human polynu	c 945	16	0.5	421	23	ABV31983	Human prostate exp
873	16	0.5	360	24	AAH77407	Human ovarian cnc	946	16	0.5	423	21	AAC08059	Human secreted pro
874	16	0.5	362	24	ABK45352	cDNA encoding colo	c 947	16	0.5	423	23	ABV10825	Human prostate exp
875	16	0.5	366	21	AAA31622	Plant microsateili	c 948	16	0.5	425	21	AAC74755	Human ORFX ORF310
876	16	0.5	367	18	AAV78420	Staphylococcus aur	c 949	16	0.5	425	23	ABV10673	Human prostate exp
877	16	0.5	367	23	ABV31457	Human prostate exp	c 950	16	0.5	425	24	ABN25491	Human ORFX polynuc
878	16	0.5	367	23	ABV40436	Human prostate exp	c 951	16	0.5	426	22	AA528019	Novel cDNA encodin
879	16	0.5	370	21	AAH82128	N. meningitidis pa	c 952	16	0.5	427	24	ABL80950	Human ovarian cnc
880	16	0.5	371	22	AAH81429	Human polynucleoti	c 953	16	0.5	429	23	ABL21719	Drosophila melanog
881	16	0.5	372	21	AAH30196	Human colon cancer	954	16	0.5	431	22	AA102285	Human reproductive
882	16	0.5	372	23	AA570696	DNA encoding novel	c 955	16	0.5	432	24	ABL78814	Human ovarian cnc
883	16	0.5	374	22	AA174553	Human breast cancer	956	16	0.5	434	22	AA521895	Human collagen gen
884	16	0.5	374	22	AA186024	Human polynucleoti	957	16	0.5	434	24	ABK35449	Human cDNA encodin
885	16	0.5	374	22	AA191055	Human polynucleoti	c 958	16	0.5	435	23	ABV03967	Human prostate exp

Db 2556 GCTCAGAACTCTCAAAATTTGGTCAAACTGAGCATTTCTTGATTATCAGAAAAATTACCTG 2615
Qy 2581 GAAAAAGATGAAATGAAGCTCTTCATGAACATGATCGACAGATCAAGTCTCAGACAG 2640
Db 2616 GAAAAAGATGAAATGAAGCTCTTCATGAACATGATCGACAGATCAAGTCTCAGACAG 2675
Qy 2641 CTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGAGCAGCTCAGCAGCTGTG 2700
Db 2676 CTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGAGCAGCTCAGCAGCTGTG 2735
Qy 2701 AAACATTTGGAGAGGTCCTCCCAACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACA 2760
Db 2736 AAACATTTGGAGAGGTCCTCCCAACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACA 2795
Qy 2761 GATACAGAGATAGAAATTTTAGTGCCATTTTGTGGAAGAACCCTCTGAAAACTTCCAG 2820
Db 2796 GATACAGAGATAGAAATTTTAGTGCCATTTTGTGGAAGAACCCTCTGAAAACTTCCAG 2855
Qy 2821 CAGTTGAATTTGGCGGGAATCGTGTGACGAGTGTGATGGCTTGCCTTCATGGTGTA 2880
Db 2856 CAGTTGAATTTGGCGGGAATCGTGTGACGAGTGTGATGGCTTGCCTTCATGGTGTA 2915
Qy 2881 TTTGAGAACTTAAGCAATTAAGTCTTTTTCGACTTAAAGAAATTTCTACCTGAT 2940
Db 2916 TTTGAGAACTTAAGCAATTAAGTCTTTTTCGACTTAAAGAAATTTCTACCTGAT 2975
Qy 2941 CCAGCATTAAGCAAACTTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTCAAGAGCT 3000
Db 2976 CCAGCATTAAGCAAACTTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTCAAGAGCT 3035
Qy 3001 AGGCTTGTGGGTGCAATTTGATGATGATGATCTCAGTGTATTACAGAGTCTTTTAAA 3060
Db 3036 AGGCTTGTGGGTGCAATTTGATGATGATGATCTCAGTGTATTACAGAGTCTTTTAAA 3095
Qy 3061 CTAGTAAGTCT 3072
Db 3096 CTAGTAAGTCT 3107
RESULT 2
AAH98254
ID AAH98254 standard; cDNA; 3545 BP.
XX AC AAH98254;
XX DT 12-OCT-2001 (first entry)
XX DE Murine EST-derived coding sequence SEQ ID NO: 111.
XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX OS Mus musculus.
XX PN WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US02687.
XX PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werlman T;
XX WPI; 2001-476164/51.
DR

DR P-PSDB; AAM23595.
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX Claim 1; Page 250-251; 1275pp; English.
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX Sequence 3545 BP; 1038 A; 755 C; 816 G; 936 T; 0 other;
SQ
Query Match 95.0%; Score 2919; DB 22; Length 3545;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3069; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ATGAATTTCAATAAGGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTTATA 60
Db 232 ATGAATTTCAATAAGGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTGTTATA 291
Qy 61 AAGCAATCAGATGACCTATTGTTATGGAATGTTCTGAATCGGAAGTAACATC 120
Db 292 AAGCAATCAGATGACCTATTGTTATGGAATGTTCTGAATCGGAAGTAACATC 351
Qy 121 ATTTGCTCGAGAAGGTGGAGCAGATGCTGCTAGAGGATCATTCACATGATTTTGA 180
Db 352 ATTTGCTCGAGAAGGTGGAGCAGATGCTGCTAGAGGATCATTCACATGATTTTGA 411
Qy 181 AAGGTTTCAGAGTCTCTGTAACCTCTTCTTAAATCCCTTAAAGAGTGAATCCTCTA 240
Db 412 AAGGTTTCAGAGTCTCTGTAACCTCTTCTTAAATCCCTTAAAGAGTGAATCCTCTA 471
Qy 241 TTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGATCAGAGGAGACTTGGACAT 300
Db 472 TTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGATCAGAGGAGACTTGGACAT 531
Qy 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACCTTTATCCCTT 360
Db 532 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACCTTTATCCCTT 591
Qy 361 GGTGAAGATATGACATTTATTTAACTTGAAGACACCTTCACAGAACCTGTCTGTGG 420
Db 592 GGTGAAGATATGACATTTATTTAACTTGAAGACACCTTCACAGAACCTGTCTGTGG 651
Qy 421 AGAAGGACCAACACCATCACCGGTGGAGCAGCTGACCCCTGAATGGCTCTCGAGGCT 480
Db 652 AGAAGGACCAACACCATCACCGGTGGAGCAGCTGACCCCTGAATGGCTCTCGAGGCT 711
Qy 481 CTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGAAGGCAAGTCCACACTCTGTCGAG 540
Db 712 CTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGAAGGCAAGTCCACACTCTGTCGAG 771
Qy 541 CGCATTTGCCATGCTCTGGGGCTCCGGAAGTGAAGGCTCTGACCAAGTTCAAATTCGTC 600
Db 772 CGCATTTGCCATGCTCTGGGGCTCCGGAAGTGAAGGCTCTGACCAAGTTCAAATTCGTC 831
Qy 601 TTTCTTCCTCCGCTCAGCAGGCCCCAGGCTGAGCTTTTGAACCCCTCTGTGATCAACTC 660
Db 832 TTTCTTCCTCCGCTCAGCAGGCCCCAGGCTGAGCTTTTGAACCCCTCTGTGATCAACTC 891
Qy 661 CTGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGTGGGG 720
Db 892 CTGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGTGGGG 951
Qy 721 CAGAGGTTCTTTTCTCTTGTGATGGCTTACAAATGAATCAAGCCCCAGAACTGCCAGAA 780
Db 952 CAGAGGTTCTTTTCTCTTGTGATGGCTTACAAATGAATCAAGCCCCAGAACTGCCAGAA 1011

Db 980 CTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATATGA 1039
QY 902 CAGAAGACAGCGCCCGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGCTGAAGGCT 961
Db 1040 CAGAAGACAGCGCCCGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGCTGAAGGCT 1099
QY 962 TGTGTCTCCAAATTCAGAAATTCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTG 1021
Db 1100 TGTGTCTCCAAATTCAGAAATTCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTG 1159
QY 1022 TGTGTATCACTTGTGCAATCCAGATGGGTGAAGTGAAGTTCCTACTCTCACACACAACAA 1081
Db 1160 TGTGTATCACTTGTGCAATCCAGATGGGTGAAGTGAAGTTCCTACTCTCACACACAACAA 1219
QY 1082 CGCTGTTCATACCTTCTATGATCTGTGATACAGAAAAACAACAACAATAAAGGTG 1141
Db 1220 CGCTGTTCATACCTTCTATGATCTGTGATACAGAAAAACAACAACAATAAAGGTG 1279
QY 1142 TGGCTGCAAGTGACTTCATTCGAGGCTTGGACCACCTGTGGAGACCTAGCTCTGGAGGGTG 1201
Db 1280 TGGCTGCAAGTGACTTCATTCGAGGCTTGGACCACCTGTGGAGACCTAGCTCTGGAGGGTG 1339
QY 1202 TGTCTCCCAACAGTTTGATTTCCAACTGCAGGATGTGCCAGCGTGAATGAGGATGTCC 1361
Db 1340 TGTCTCCCAACAGTTTGATTTCCAACTGCAGGATGTGCCAGCGTGAATGAGGATGTCC 1399
QY 1262 TGTGCACAACCTGGCTCCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAAT 1321
Db 1400 TGTGCACAACCTGGCTCCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAAT 1459
QY 1322 TCTTTCCAAAGTCATTCAGGAGTACACAGCAGGAGGAAGACTCAGCAGTTTATTGACGT 1381
Db 1460 TCTTTCCAAAGTCATTCAGGAGTACACAGCAGGAGGAAGACTCAGCAGTTTATTGACGT 1519
QY 1382 CTATGAGCCAGAGGAGTGACCAAGGGAAATGGTTACTTGCAGAAAAATGGTTTCCATTT 1441
Db 1520 CTATGAGCCAGAGGAGTGACCAAGGGAAATGGTTACTTGCAGAAAAATGGTTTCCATTT 1579
QY 1442 CGGACATTTACATCCACTTATFAGCAGCTGCTCCGGTACACCTCTGGGTCAATCTGTGGAAG 1501
Db 1580 CGGACATTTACATCCACTTATFAGCAGCTGCTCCGGTACACCTCTGGGTCAATCTGTGGAAG 1639
QY 1502 CCACCAGGGCTGTATGAAGCAGCTCGCAGCAGTGTATCAACACGGCTGCTTCTCGGAC 1561
Db 1640 CCACCAGGGCTGTATGAAGCAGCTCGCAGCAGTGTATCAACACGGCTGCTTCTCGGAC 1699
QY 1562 TTTCCATCGCCAGAGCCCTCTCTGAGACAGGAATCTTTGCAAGTGTGAAAAACCA 1621
Db 1700 TTTCCATCGCCAGAGCCCTCTCTGAGACAGGAATCTTTGCAAGTGTGAAAAACCA 1759
QY 1622 CTGAGCAAGAAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATT 1681
Db 1760 CTGAGCAAGAAATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATT 1819
QY 1682 TATATCAAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAAG 1741
Db 1820 TATATCAAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAAG 1879
QY 1742 GFAAAGCTTATATCAACTCAGGGAACATCCCCGATTAATTTGACTTCTTTGAAAC 1801
Db 1880 GFAAAGCTTATATCAACTCAGGGAACATCCCCGATTAATTTGACTTCTTTGAAAC 1939
QY 1802 ATTTGCCCAATTTGCAAGTGTCTGAGCTTCATTAACCTGGAATTTATGGGGGAGCTA 1861
Db 1940 ATTTGCCCAATTTGCAAGTGTCTGAGCTTCATTAACCTGGAATTTATGGGGGAGCTA 1999
QY 1862 TGGCTTTCATGGGAAAAGGCTGCAAGAGACACAGGTGGAATCCACATGGAAGAGGCCCCAG 1921
Db 2000 TGGCTTTCATGGGAAAAGGCTGCAAGAGACACAGGTGGAATCCACATGGAAGAGGCCCCAG 2059
QY 1922 AAACCTTACATTCACAGAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGGA 1981
Db 2060 AAACCTTACATTCACAGAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGGA 2119

QY 1982 CTCTGGAGGTCACACCTCCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCACATATCTGG 2041
Db 2120 CTCTGGAGGTCACACCTCCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCACATATCTGG 2179
QY 2042 GGAATAATFATCAGCTCTGCCACAAGCCTCAGGCTGCAATAAAGAGATGTCTGGTGTGG 2101
Db 2180 GGAATAATFATCAGCTCTGCCACAAGCCTCAGGCTGCAATAAAGAGATGTCTGGTGTGG 2239
QY 2102 CTGGAAGCCTCAGCTTTGGTCTCAGCACCTGTGAAGCAATTTATCTCTCATGGTGAAG 2161
Db 2240 CTGGAAGCCTCAGCTTTGGTCTCAGCACCTGTGAAGCAATTTATCTCTCATGGTGAAG 2299
QY 2162 CCAGTCCCTCACCATAGAAGATGAGAGGCACATCACATCTGTAACAACACCTGAAAACCT 2221
Db 2300 CCAGTCCCTCACCATAGAAGATGAGAGGCACATCACATCTGTAACAACACCTGAAAACCT 2359
QY 2222 TGAGTATTCATGACCTACAGAAATCAACGGCTGCCGGTGTCTGACTGACAGCTTGGGTA 2281
Db 2360 TGAGTATTCATGACCTACAGAAATCAACGGCTGCCGGTGTCTGACTGACAGCTTGGGTA 2419
QY 2282 ACTTGAAGAACCTTACAAAGCTCATATATGATTAACATAAAGATGAATGAAGAGATGCTA 2341
Db 2420 ACTTGAAGAACCTTACAAAGCTCATATATGATTAACATAAAGATGAATGAAGAGATGCTA 2479
QY 2342 TAAACCTAGCTGAAGGCTGAAAAACCTGAAGAAGATGTGTTTATTTTCATTTGACCCACT 2401
Db 2480 TAAACCTAGCTGAAGGCTGAAAAACCTGAAGAAGATGTGTTTATTTTCATTTGACCCACT 2539
QY 2402 TGCTGACATTTGAGAGGGAATGGATTACATAGTCAAGTCTCTGCAAGTGAACCCCTGTG 2461
Db 2540 TGCTGACATTTGAGAGGGAATGGATTACATAGTCAAGTCTCTGCAAGTGAACCCCTGTG 2599
QY 2462 ACCTTGAAGAAATTCAAATTAGTCTCCTGCTGCTGTGCTGCAAAATGCAGTCAAAATCCTAG 2521
Db 2600 ACCTTGAAGAAATTCAAATTAGTCTCCTGCTGCTGTGCTGCAAAATGCAGTCAAAATCCTAG 2659
QY 2522 CTCAGAAATCTTCAAAATTTGGTCAAACTGAGCATCTCTTGATTTTATCAGAAAAATTTACCTGG 2581
Db 2660 CTCAGAAATCTTCAAAATTTGGTCAAACTGAGCATCTCTTGATTTTATCAGAAAAATTTACCTGG 2719
QY 2582 AAAAAGATGGAATGAAGCTCTTCATGAATGATGACAGGATGAACGTGCTAGAACAAG 2641
Db 2720 AAAAAGATGGAATGAAGCTCTTCATGAATGATGACAGGATGAACGTGCTAGAACAAG 2779
QY 2642 TCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGCAGCCCTGAGCAGCTGTGTA 2701
Db 2780 TCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGCAGCCCTGAGCAGCTGTGTA 2839
QY 2702 AACATTTGGAGGAGTCCCAACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACAG 2761
Db 2840 AACATTTGGAGGAGTCCCAACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACAG 2899
QY 2762 ATACAGAGATTAGAATTTTAGGTGCATTTTTTGAAGAAGAACCCCTGAAAAAATTCACAG 2821
Db 2900 ATACAGAGATTAGAATTTTAGGTGCATTTTTTGAAGAAGAACCCCTGAAAAAATTCACAG 2959
QY 2822 AGTTGAATTTGGCGGGAATTCGTGTGAGCAGTGTGATGGTGGCTTGCCTTCATGGGTGTAT 2881
Db 2960 AGTTGAATTTGGCGGGAATTCGTGTGAGCAGTGTGATGGTGGCTTGCCTTCATGGGTGTAT 3019
QY 2882 TTGAGAAATCTTAAGCAATTAGTGTTTTTTGCATTTTAGTACTAAAGAAATTTCTACCTGTATC 2941
Db 3020 TTGAGAAATCTTAAGCAATTAGTGTTTTTTGCATTTTAGTACTAAAGAAATTTCTACCTGTATC 3079
QY 2942 CAGCATTTAGTCAGAAAACTTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTCACAAGAGCTA 3001
Db 3080 CAGCATTTAGTCAGAAAACTTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTCACAAGAGCTA 3139
QY 3002 GGCTTGTGGGTGGCAATTTGATGATGATCTCAGTGTGTTTATACAGGTGCTTTTAAAC 3061
Db 3140 GGCTTGTGGGTGGCAATTTGATGATGATCTCAGTGTGTTTATACAGGTGCTTTTAAAC 3199

Qy 3062 TAGTAACGTCT 3072
|||||
Db 3200 TAGTAACGTCT 3210

RESULT 4

ABK22731
ID ABK22731 standard; cDNA; 3396 BP.

XX AC ABK22731;

XX DT 26-MAR-2002 (first entry)

XX DE Human cDNA encoding CLAN A.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; cancer; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.

XX OS Homo sapiens.

XX PN WO200190156-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US17158.

XX PR 24-MAY-2000; 2000US-0579240.

XX PR 10-OCT-2000; 2000US-0686347.

XX PR 14-MAR-2001; 2001US-275980P.

XX PR 23-MAY-2001; 2001US-0864921.

XX PA (BURN-) BURNHAM INST.

XX PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

XX PI Oliveira VM, Hayashi H, Pawlowski K;

XX DR WPI; 2002-083086/11.

XX DR P-PSDB; AAU80861.

XX PT New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -

XX PS Claim 1; Page 166-171; 216pp; English.

XX CC The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a

CC cDNA encoding a CARD domain containing protein.

XX Sequence 3396 BP; 992 A; 737 C; 793 G; 874 T; 0 other;
SQ Matches 3068; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Query Match 93.48; Score 2868; DB 24; Length 3396;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3068; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGAATTTTATAAAGGACAATAGCGAGCCCTTATTCAAAGAAATGGGAATGACTCTTTATA 60
|||||

Db 277 ATGAATTTTATAAAGGACAATAGCGAGCCCTTATTCAAAGAAATGGGAATGACTCTTTATA 336
|||||

Qy 61 AAGCAAAATCACAGATGACCTATTCTTATGGAATCTTCTGAATCGCGAAGAAAGTAACATC 120
|||||

Db 337 AAGCAAAATCACAGATGACCTATTCTTATGGAATCTTCTGAATCGCGAAGAAAGTAACATC 396
|||||

Qy 121 ATTTGCTCGAGAGAGGTGGAGCAGGATGCTGCTAGAGGGATCAITTCACATGATTTTGAA 180
|||||

Db 397 ATTTGCTCGAGAGAGGTGGAGCAGGATGCTGCTAGAGGGATCAITTCACATGATTTTGAA 456
|||||

Qy 181 AAGGTTTCAGAGTCTCTTAACCTCTTTTAAATCCCTTAAGGAGTGAACATATCTCTTA 240
|||||

Db 457 AAGGTTTCAGAGTCTCTTAACCTCTTTTAAATCCCTTAAGGAGTGAACATATCTCTTA 516
|||||

Qy 241 TTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAAAGAGACTTGGACAT 300
|||||

Db 517 TTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAAAGAGACTTGGACAT 576
|||||

Qy 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTCAACTTTTATCCCTT 360
|||||

Db 577 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTCAACTTTTATCCCTT 636
|||||

Qy 361 GGTGAAGATATTGACATTTATTTTAACTTGAAGGACCTTTCACAGAACTGTCTGTGG 420
|||||

Db 637 GGTGAAGATATTGACATTTATTTTAACTTGAAGGACCTTTCACAGAACTGTCTGTGG 696
|||||

Qy 421 AGGAAGGACCAACACCATCACCCTGGAGCAGCTGACCCCTGAATGGCTCTCTGACAGCT 480
|||||

Db 697 AGGAAGGACCAACACCATCACCCTGGAGCAGCTGACCCCTGAATGGCTCTCTGACAGCT 756
|||||

Qy 481 CTTCAGAGCCCTTGACATTTGAAGGGAATCTGCCAAGGCAAGTCCACTCTGCTGAG 540
|||||

Db 757 CTTCAGAGCCCTTGACATTTGAAGGGAATCTGCCAAGGCAAGTCCACTCTGCTGAG 816
|||||

Qy 541 CGCATTTGCCATGCTCTGGGGCTCCGAAAGTCAAGGCTCTGACCAAGTTCAAATTCGTC 600
|||||

Db 817 CGCATTTGCCATGCTCTGGGGCTCCGAAAGTCAAGGCTCTGACCAAGTTCAAATTCGTC 876
|||||

Qy 601 TTTCTCTCCCTCTCAGCAGGGCCCGAGGTGGACTTTTGAACCCCTCTGTGATCAACTC 660
|||||

Db 877 TTTCTCTCCCTCTCAGCAGGGCCCGAGGTGGACTTTTGAACCCCTCTGTGATCAACTC 936
|||||

Qy 661 CTGATATACCTGGCACAAATCAGNAAGCAGACATTCATGGCCATGCTCTGAGCTGCGG 720
|||||

Db 937 CTGATATACCTGGCACAAATCAGNAAGCAGACATTCATGGCCATGCTCTGAGCTGCGG 996
|||||

Qy 721 CAGAGGTTCTTTCTCTTTGAGGCTTACAATGAATTCAGCCGCCAGAACTGCCAGAA 780
|||||

Db 997 CAGAGGTTCTTTCTCTTTGAGGCTTACAATGAATTCAGCCGCCAGAACTGCCAGAA 1056
|||||

Qy 781 ATCGAAGCCCTGATAAAGAAACACCGCTTCAAGAACATGGTCTGTCACCACTACC 840
|||||

Db 1057 ATCGAAGCCCTGATAAAGAAACACCGCTTCAAGAACATGGTCTGTCACCACTACC 1116
|||||

Qy 841 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCTTGACTGTGAGGTGGGGATATG 900
|||||

Db 1117 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCTTGACTGTGAGGTGGGGATATG 1176
|||||

Qy 901 ACAGAAACACGCGCCAGGCTCTATCCGAAAGTGTGATCAAGGAGCTTGTCTGAAGGC 960
|||||

Db 1177 ACAGAAACACGCGCCAGGCTCTATCCGAAAGTGTGATCAAGGAGCTTGTCTGAAGGC 1236
|||||

Qy 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020
|||||

ID AAS03946 standard; DNA; 3615 BP.
 XX AC AAS03946;
 XX DT 12-SEP-2001 (first entry)
 XX DE Human caspase recruitment domain 12 (CARD-12) genomic DNA.
 XX
 KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;
 KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
 KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;
 KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;
 KW aplastic anaemia; myocardial infarction; inflammatory disorder;
 KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;
 KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;
 KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ds;
 KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;
 KW excitotoxic brain damage; liver disease.
 XX OS Homo sapiens.
 XX
 XX FH Key Location/Qualifiers
 XX CDS 1..3615
 XX FT /**tag= a
 XX FT /product= "Human CARD-12"
 XX
 XX PN W0200130971-A2.
 XX
 XX PD 03-MAY-2001.
 XX
 XX PF 26-OCT-2000; 2000WO-US99643.
 XX
 XX PR 27-OCT-1999; 99US-0161822.
 XX
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX
 XX PI Bertin J, Robison KE;
 XX WPI; 2001-308628/32.
 XX P-PSDB; AAU02881.
 XX
 XX PT Isolated caspase recruitment domain-12 polypeptide and nucleic acids
 XX encoding them, useful for treating and diagnosing disorders associated
 XX with abnormal apoptosis such as cancer, arthritis and Alzheimer's
 XX disease -
 XX
 XX PS Disclosure; Fig 2; 93pp; English.
 XX
 XX CC The sequence represents a genomic DNA which encodes the human caspase
 XX recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a
 XX number of proteins that transmit signals that activate apoptosis and
 XX inflammatory pathways in response to stress and other stimuli. Therefore,
 XX CARD-12 and its corresponding nucleic acid may be used in treatment and
 XX diagnosis of patients suffering from disorders associated with an
 XX abnormal level (an increase or a decrease) of apoptotic cell death or
 XX abnormal activity of stress-related pathways. The disorders include
 XX cancer, viral infections (e.g. caused by poxviruses, adenoviruses),
 XX autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),
 XX neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral
 XX sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial
 XX infarction, stroke), inflammatory and immune system disorders (e.g.
 XX Crohn's disease, insulin-dependent diabetes, contact dermatitis,
 XX psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,
 XX lepromatous leprosy), ischaemic and hypoxic brain injury, kidney
 XX ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial
 XX meningitis and liver disease.
 XX
 XX SQ Sequence 3615 BP; 1041 A; 811 C; 845 G; 918 T; 0 other;
 Query Match 85.7%; Score 2634; DB 22; Length 3615;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 263 GTCCTTTTCATCAGACATCAGAGAGACTTGGAGGATTTGGCTCAGAGATTAAAGGACT 322
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 734 GTCCTTTTCATCAGACATCAGAGAGACTTGGAGGATTTGGCTCAGAGATTAAAGGACT 793
 QY 323 TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATTCACATATTAT 382
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 794 TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATTCACATATTAT 853
 QY 383 TTAACCTTGAAGAGACACCTTTCACAGAACCTGCTCTGTGGAGGAAGACCAACACCATCAC 442
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 854 TTAACCTTGAAGAGACACCTTTCACAGAACCTGCTCTGTGGAGGAAGACCAACACCATCAC 913
 QY 443 CGCTGGAGCAGCTGACCCCTGAATGGCTCTCTGCAGGCTCTTTTCAGAGCCCTGCATCAT 502
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 914 CGCTGGAGCAGCTGACCCCTGAATGGCTCTCTGCAGGCTCTTTTCAGAGCCCTGCATCAT 973
 QY 503 AAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCACGCGCATTCGCCATGCTCTGGGGCT 562
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 974 AAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCACGGAATTCGCCATGCTCTGGGGCT 1033
 QY 563 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGTTCTTCTCTCGCTCTCAGCAGGG 622
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1034 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGTTCTTCTCTCGCTCTCAGCAGGG 1093
 QY 623 CCCAGGGTGGACTTTTGTAAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACAATCA 682
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1094 CCCAGGGTGGACTTTTGTAAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACAATCA 1153
 QY 683 GGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGCGCAGAGGGTCTTTTCTCTTCTTG 742
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1154 GGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGCGCAGAGGGTCTTTTCTCTTCTTG 1213
 QY 743 ATGCTACAATGAATTCAAAGCCCGAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAA 802
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1214 ATGCTACAATGAATTCAGGCCCGAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAA 1273
 QY 803 ACCACCGCTTCAAGAACATGCTCATCGCTACCACTACCACTGAGTGCCTGAGGCACATAC 862
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1274 ACCACCGCTTCAAGAACATGCTCATCGCTACCACTACCACTGAGTGCCTGAGGCACATAC 1333
 QY 863 GGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGATATGACAGAGACAGCGCCAGGGCTC 922
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1334 GGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGATATGACAGAGACAGCGCCAGGGCTC 1393
 QY 923 TCATCCGAGAAAGTGTGATCAAGGAGCTGTCTGAAGGCTGTGTCTCCAAATTCAGAAAT 982
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1394 TCATCCGAGAAAGTGTGATCAAGGAGCTGTCTGAAGGCTGTGTCTCCAAATTCAGAAAT 1453
 QY 983 CCAGTGCTTGAAGAAATCTCATGAAGACCCCTCTCTTTTGGTTCATCATCTTGTGCAATCC 1042
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1454 CCAGTGCTTGAAGAAATCTCATGAAGACCCCTCTCTTTTGGTTCATCATCTTGTGCAATCC 1513
 QY 1043 AGATGGGTGAAGTGTGAGTTCACACTCTCACACACAAACGCTGTTCATACCTTCTATG 1102
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1514 AGATGGGTGAAGTGTGAGTTCACACTCTCACACACAAACGCTGTTCATACCTTCTATG 1573
 QY 1103 ATCTGTTGATACAGAAAAACAAACACAAACATAAAGTGTGGCTGCAAGTGAATTCATTC 1162
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1574 ATCTGTTGATACAGAAAAACAAACACAAACATAAAGTGTGGCTGCAAGTGAATTCATTC 1633
 QY 1163 GGAGCCTGGACCATGTGGAGACCTAGCTCTGGAGGGTGTGTTCTTCCACAAAGTTTGATT 1222
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1634 GGAGCCTGGACCATGTGGAGACCTAGCTCTGGAGGGTGTGTTCTTCCACAAAGTTTGATT 1693
 QY 1223 TCGAAGTGCAGGATGTGCCAGCGTGAATGAGATGTCCTGCTGACAACTGGGCTCCCTCT 1282
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1694 TCGAAGTGCAGGATGTGCCAGCGTGAATGAGATGTCCTGCTGACAACTGGGCTCCCTCT 1753
 QY 1283 GTAATATACAGCTCAAAGTTCAAGCCAAAGTATAAATTTCTTTCACAAAGTATTCACAGG 1342
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 1754 GTAATATACAGCTCAAAGTTCAAGCCAAAGTATAAATTTCTTTCACAAAGTATTCACAGG 1813
 QY 1343 AGTACAGCAGGAGGAGAACTACGAGTTTATTGACGCTCTCATGAGCCAGGAGGTGA 1402

|||||
Db 1814 AGTACAGCAGGACGAGAACTCAGCAGTTTATTGAGCTCTCATGAGCCAGAGAGGTGA 1873
QY 1403 CCAAGGGGAATGTTACTTCGACAAAATGGTTTCATTTTCGGACATTACATCCACTATA 1462
Db 1874 CCAAGGGGAATGTTACTTCGACAAAATGGTTTCATTTTCGGACATTACATCCACTATA 1933
QY 1463 GCAGCTGCTCCGGTACACCTGTGGGTCACTCTGTGAAGCCACCAGGGCTGTTATGAAGC 1522
Db 1934 GCAGCTGCTCCGGTACACCTGTGGGTCACTCTGTGAAGCCACCAGGGCTGTTATGAAGC 1993
QY 1523 ACCTCGACAGAGTATCAACACGGCTGCTTCCTCGGACTTTCCATCGCCAAAGAGGCCCTC 1582
Db 1994 ACCTCGACAGAGTATCAACACGGCTGCTTCCTCGGACTTTCCATCGCCAAAGAGGCCCTC 2053
QY 1583 TCTGGGACAGAGAACTCTTGCAAAAGTGTGAAAACACCACTGAGCAGAAATTTCTGAAG 1642
Db 2054 TCTGGGACAGAGAACTCTTGCAAAAGTGTGAAAACACCACTGAGCAGAAATTTCTGAAG 2113
QY 1643 CCATAAACATCAATCTCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 1702
Db 2114 CCATAAACATCAATCTCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 2173
QY 1703 AATCAGCCCTGAGCCAGAAATTTGAAGCTTTCTTCAAGGTAAAGCTTATATATCAACT 1762
Db 2174 AATCAGCCCTGAGCCAGAAATTTGAAGCTTTCTTCAAGGTAAAGCTTATATATCAACT 2233
QY 1763 CAGGGAACATCCCGATTACTTATTTGACTTCTTTGACATTTGCCCAATTTGCGAAGTG 1822
Db 2234 CAGGGAACATCCCGATTACTTATTTGACTTCTTTGACATTTGCCCAATTTGCGAAGTG 2293
QY 1823 CTCTGGACTTCATTAACCTGGACTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1882
Db 2294 CCCTGGACTTCATTAACCTGGACTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 2353
QY 1883 CAGAAGACAGAGTGGAAATCCACATGGAAGAGGCCCCAGAAACCTACATTTCCAGCAGGG 1942
Db 2354 CAGAAGACACAGTGGAAATCCACATGGAAGAGGCCCCAGAAACCTACATTTCCAGCAGGG 2413
QY 1943 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGAGCTCGAGGTCACACTCCGG 2002
Db 2414 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGAGCTCGAGGTCACACTCCGG 2473
QY 2003 ATTTACAGCAAGTTGAATAAGCAAGATATCACATATCTGGGAAAATATTCAGCTCTGCCA 2062
Db 2474 ATTTACAGCAAGTTGAATAAGCAAGATATCAGATATCTGGGAAAATATTCAGCTCTGCCA 2533
QY 2063 CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGGCTGGAAGCCTCAGTTTGGTCC 2122
Db 2534 CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGGCTGGAAGCCTCAGTTTGGTCC 2593
QY 2123 TCAGCAGCTCTAAGAACATTTATCTCTCATGTGTGAAGCCAGTCCCTCACCATTAGAG 2182
Db 2594 TCAGCAGCTCTAAGAACATTTATCTCTCATGTGTGAAGCCAGTCCCTCACCATTAGAG 2653
QY 2183 ATGAGGGCACATCACATCTGTAAACAACTGAAACCTTTGAGTATTCATGACCTACAGA 2242
Db 2654 ATGAGGGCACATCACATCTGTAAACAACTGAAACCTTTGAGTATTCATGACCTACAGA 2713
QY 2243 ATCAAGGGCTGCGGGTGTCTGACTGACACAGCTTGGGTAACTTGAAGAACCTTTACAAAGC 2302
Db 2714 ATCAAGGGCTGCGGGTGTCTGACTGACACAGCTTGGGTAACTTGAAGAACCTTTACAAAGC 2773
QY 2303 TCATAATGGATAACATAAAGATCAATGAAGATCTATAAACTAGCTGAAGGGCTGA 2362
Db 2774 TCATAATGGATAACATAAAGATCAATGAAGATCTATAAACTAGCTGAAGGGCTGA 2833
QY 2363 AAAACCTGAAGAGATGTGTTTATTTTCACTTGACCCACATTTGCTGACATTGGAGAGGGA 2422
Db 2834 AAAACCTGAAGAGATGTGTTTATTTTCACTTGACCCACATTTGCTGACATTGGAGAGGGA 2893
QY 2423 TGGATTACATAGTCAAGTCTCTGCTCAAGTGAACCCCTGTGACCTTGAAGAAATTTCAATTAG 2482
|||||

Db 2894 TGGATTACATAGTCAAGTCTCTCTCAAGTGAACCCCTGTGACCTTGAAGAAATTTCAATTAG 2953
QY 2483 TCTCCTGCTGCTTGTCTGCAAAATGCGAGTGAAATCTTAGCTCAGAATCTTCAAAATTTGG 2542
Db 2954 TCTCCTGCTGCTTGTCTGCAAAATGCGAGTGAAATCTTAGCTCAGAATCTTCAAAATTTGG 3013
QY 2543 TCAAACTGAGCATCTCTTGTATTATCAGAAATTTACCTGGAAAAAGATGGAATGAAGCTC 2602
Db 3014 TCAAACTGAGCATCTCTTGTATTATCAGAAATTTACCTGGAAAAAGATGGAATGAAGCTC 3073
QY 2603 TTCAATGAACCTGATGACAGAGATGAACGTGTAGAACAGCTCACCGCAGTATGCTGCCCT 2662
Db 3074 TTCAATGAACCTGATGACAGAGATGAACGTGTAGAACAGCTCACCGCAGTATGCTGCCCT 3133
QY 2663 GGGGCTGTGACGTGCAAGGAGCCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTCCAC 2722
Db 3134 GGGGCTGTGACGTGCAAGGAGCCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTCCAC 3193
QY 2723 AACTCGTCAAGCTTTGGGTTGAAAACTGGAGACTCACAGATACAGAGATTTAGAAATTTTAG 2782
Db 3194 AACTCGTCAAGCTTTGGGTTGAAAACTGGAGACTCACAGATACAGAGATTTAGAAATTTTAG 3253
QY 2783 GTGCATTTTTTGGAAAGAACCCCTCTGAAAACTTCCAGCAGTTGAATTTGGCGGGAAATC 2842
Db 3254 GTGCATTTTTTGGAAAGAACCCCTCTGAAAACTTCCAGCAGTTGAATTTGGCGGGAAATC 3313
QY 2843 GTGTGAGCAGTGTGATGGCTTGCCCTTCATGGTGTATTTGAGAAATCTTAAGCAATTTAG 2902
Db 3314 GTGTGAGCAGTGTGATGGCTTGCCCTTCATGGTGTATTTGAGAAATCTTAAGCAATTTAG 3373
QY 2903 TGTGTTTTTGTACCTTTAGTACTATAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTA 2962
Db 3374 TGTGTTTTTGTACCTTTAGTACTATAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTA 3433
QY 2963 GCCAAGTGTATCCAAAGTAACTTTTCTGCAAGAACAGTGGCTTGTGGTGGCAATTTG 3022
Db 3434 GCCAAGTGTATCCAAAGTAACTTTTCTGCAAGAACAGTGGCTTGTGGTGGCAATTTG 3493
QY 3023 ATCATGATGATCTCAGTGTATTATACAG 3049
Db 3494 ATGATGATGATCTCAGTGTATTATACAG 3520

RESULT 6
AAH78218
ID AAH78218 standard; DNA; 2215 Bp.
XX
AC AAH78218;
XX
DT 26-NOV-2001 (first entry)
XX Nucleotide sequence of a human secreted polypeptide.
DE
XX Human; secreted polypeptide; nervous disease; muscular disease; tumour;
KW gastrointestinal ulceration; spinal cord disease; trachea disease;
KW thyroid gland disease; ovary disease; prostate disease; heart disease;
KW renal gland disease; small intestine disease; thymus disease;
KW lymph node disease; muscular system disease; colon disease;
KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
KW myocardial infarction; angioplasty; liver disease; coagulation disorder;
KW microbial disease; immune disorder; inflammation; transplant rejection;
KW bone thickness; bone density; ferroxidase loss; apoptosis;
KW vascular smooth cell proliferation; vaccine; ss.
XX Homo sapiens.
OS
XX
FH Key
FT CDS
FT 1..2214
FT /tag- a
FT /product= "secreted polypeptide"
FT /note= "no termination codon given"
XX
PN WO200166690-A2.

XX 13-SEP-2001.
XX 05-MAR-2001; 2001WO-US07143.
XX 06-MAR-2000; 2000US-0187107.
XX 03-MAR-2000; 2000US-0188916.
XX 03-OCT-2000; 2000US-0236874.
XX 03-OCT-2000; 2000US-0237846.
XX (SMK) SMITHKLINE BEECHAM CORP.
XX (SMK) SMITHKLINE BEECHAM PLC.
XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX WPI: 2001-570768/64.
XX P-PSDB; AAG67526.
XX Novel isolated secreted polypeptide useful for treating nervous and
XX muscular diseases, gastrointestinal ulceration, coagulation and immune
XX disorders, microbial diseases, inflammation and transplant rejection -
XX Claim 2; Page 52-53; 102pp; English.
XX The present sequence encodes a human secreted polypeptide. The
XX secreted polypeptides and polynucleotides are useful for treating
XX nervous and muscular diseases, for inhibiting tumour formation and
XX metastasis, for treating gastrointestinal ulceration, for preventing
XX and treating diseases in spinal cord, thyroid gland, ovary, prostate,
XX renal gland, small intestine, heart, trachea, thymus, lymph node,
XX muscular system and colon, for treating lipase deficiency in cystic
XX fibrosis and pancreatitis, for treating undesirable clot formation
XX such as myocardial infarction, during angioplasty and all surgical
XX procedures that require decreased blood clot formation, for treating
XX liver diseases, coagulation disorders and microbial diseases, for
XX treating immune disorders, for treating inflammation and transplant
XX rejection, for enhancing bone thickness and increasing bone density,
XX for reducing the loss of essential ferroxidases, for suppressing
XX apoptosis, and for regulating vascular smooth cell proliferation. They
XX may also be used as vaccines.
XX Sequence 2215 BP; 621 A; 522 C; 519 G; 553 T; 0 other;
Query Match 67.1%; Score 2062; DB 22; Length 2215;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2212; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 43 ATGGGAATGACTGTATTAAGCAATACAGATGACCTATTGTATGAATGTTCTGAAT 102
DB 1 ATGGGAATGACTGTATTAAGCAATACAGATGACCTATTGTATGAATGTTCTGAAT 60
QY 103 CGCGAAGAAGTAACATCATTTGCTCGAGAAGGTGGAGCAGGATGCTGTAGAGGGATC 162
DB 61 CGCGAAGAAGTAACATCATTTGCTCGAGAAGGTGGAGCAGGATGCTGTAGAGGGATC 120
QY 163 ATTCACATGATTTTGAAGAGGTTTCAGAGTCCTGTAACTCTTTCTTTAAATCCCTTAAG 222
DB 121 ATTCACATGATTTTGAAGAGGTTTCAGAGTCCTGTAACTCTTTCTTTAAATCCCTTAAG 180
QY 223 GAGTGGAACTATCCCTATTTTCAGACTTGAATGACAAAGTCTTTTTCATCAGACATCA 282
DB 181 GAGTGGAACTATCCCTATTTTCAGACTTGAATGACAAAGTCTTTTTCATCAGACATCA 240
QY 283 GAAGGAGACTTGGAGATTTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTT 342
DB 241 GAAGGAGACTTGGAGATTTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTT 300
QY 343 CTGAACATTTTATCCCTTGGTGAAGATATTGACATTTATTTTAACTTGAAGACACCTTC 402
DB 301 CTGAACATTTTATCCCTTGGTGAAGATATTGACATTTATTTTAACTTGAAGACACCTTC 360
QY 403 ACAGAACCTGTCTGTGGAGGAGGACCAACACCATCACCGGTGAGCAGCTGACCTG 462
DB 1441 TGTGGGTATCTGTGGAGGACCCAGGGCTGTATTAAGACACCTTCGACAGCTGATCA 1500

DB 361 ACAGAACCTGTCTGTGGAGGAGGACCAACACCATACCGCGTGGAGCAGCTGACCCCTG 420
QY 463 AATGGCCTCTGCAGGCTCTTTTCAGAGCCCTGCATCATTTAAGGGGAATCTCGCAAGGC 522
DB 421 AATGGCCTCTGCAGGCTCTTTTCAGAGCCCTGCATCATTTAAGGGGAATCTGGCAAGGC 480
QY 523 AAGTCCACTCTGCTGCAGCGCATTCGCCATGTCTCGGGCTCCGGAAAGTGCAGGCTCTG 582
DB 481 AAGTCCACTCTGCTGCAGCGCAATTCGCCATGTCTCGGGCTCCGGAAAGTGCAGGCTCTG 540
QY 583 ACCAAGTTCAATTCGCTCTTCTCTCGTCTCAGCAGGGCCAGGGTGGACTTTTGA 642
DB 541 ACCAAGTTCAATTCGCTCTTCTCTCGTCTCAGCAGGGCCAGGGTGGACTTTTGA 600
QY 643 ACCCTCTGTGATCAACTCTCGATATACCTGSCAATCAGGAAGCAGACATTCATGACC 702
DB 601 ACCCTCTGTGATCAACTCTCGATATACCTGSCAATCAGGAAGCAGACATTCATGACC 660
QY 703 ATGCTGCTGAAGCTCGCGCAGAGGGTCTTTTCTCTTCTTGTATGGCTACAATGAATCAAG 762
DB 661 ATGCTGCTGAAGCTCGCGCAGAGGGTCTTTTCTCTTCTTGTATGGCTACAATGAATCAAG 720
QY 763 CCCAGAACTGCCAGAAATCGAAGCCCTGATAAGGAAAAACCCCGCTTCAGAAACATG 822
DB 721 CCCAGAACTGCCAGAAATCGAAGCCCTGATAAGGAAAAACCCCGCTTCAGAAACATG 780
QY 823 GTCATCGTCACACTACCACTGAGTGCTGAGGACATACGCGACTTTGGTCCCTGACT 882
DB 781 GTCATCGTCACACTACCACTGAGTGCTGAGGACATACGCGACTTTGGTCCCTGACT 840
QY 883 GCTGAGTGGGGATATGACAGAAGACGCGCCAGGCTCTCATCCGAAAGTGTGATC 942
DB 841 GCTGAGTGGGGATATGACAGAAGACGCGCCAGGCTCTCATCCGAAAGTGTGATC 900
QY 943 AAGAGCTGTGCTGAAGGCTTGTGCTCAAAATCAGAAATCCAGTGTCTGAGGAACTC 1002
DB 901 AAGAGCTGTGCTGAAGGCTTGTGCTCAAAATCAGAAATCCAGTGTCTGAGGAACTC 960
QY 1003 ATGAAGACCCCTCTCTTTGCTGATCATCTGTGCAATCCAGATGGGTGAAAGTCACTC 1062
DB 961 ATGAAGACCCCTCTCTTTGCTGATCATCTGTGCAATCCAGATGGGTGAAAGTCACTC 1020
QY 1063 CACTCTCACACACAAACACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAAC 1122
DB 1021 CACTCTCACACACAAACACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAAC 1080
QY 1123 AAACACAAACATAAAGGTGTGCTGCAAGTGTGCTGCAAGTGTGCTGCAAGTGTGCTGCA 1182
DB 1081 AAACACAAACATAAAGGTGTGCTGCAAGTGTGCTGCAAGTGTGCTGCAAGTGTGCTGCA 1140
QY 1183 GACCTAGCTCTGGAGGGTGTGTTCTCCCAAGTTTGAATTTTCAAGTGTGCTGCAAGTGTGCTC 1242
DB 1141 GACCTAGCTCTGGAGGGTGTGTTCTCCCAAGTGTGTTCTCCCAAGTGTGCTGCAAGTGTGCTC 1200
QY 1243 AGCGTGAATGAGGATGCTCTGCTGACAACTGGGCTCTCTGTAATATATACAGCTCAAGG 1302
DB 1201 AGCGTGAATGAGGATGCTCTGCTGACAACTGGGCTCTCTGTAATATATACAGCTCAAGG 1260
QY 1303 TTCAGGCCAAAGTATAAATTTCTTTCACAAGTCAATTCAGAGGATACACAGCAGGAGGAAGA 1362
DB 1261 TTCAGGCCAAAGTATAAATTTCTTTCACAAGTCAATTCAGAGGATACACAGCAGGAGGAAGA 1320
QY 1363 CTCAGCAGTTTATTCACGCTCTCATGAGCAGAGGAGGTGACCAAGGGGAATGGTTACTTGG 1422
DB 1321 CTCAGCAGTTTATTCACGCTCTCATGAGCAGAGGAGGTGACCAAGGGGAATGGTTACTTGG 1380
QY 1423 CAGAAATGGTTTCCATTTCCGACATTTACATCCACTTATAGAGCCTGCTCCGGTACACC 1482
DB 1381 CAGAAATGGTTTCCATTTCCGACATTTACATCCACTTATAGAGCCTGCTCCGGTACACC 1440
QY 1483 TGTGGGTATCTGTGGAGGACCCAGGGCTGTATTAAGACACCTTCGACAGCTGATCA 1542
DB 1441 TGTGGGTATCTGTGGAGGACCCAGGGCTGTATTAAGACACCTTCGACAGCTGATCA 1500

QY 1543 CACGGCTGCTTCGGACTTTCCATGCCAAGAGGCTCTCTGGAGACAGGAATCTTTG 1602
DB 1501 CACGGCTGCTTCGGACTTTCCATGCCAAGAGGCTCTCTGGAGACAGGAATCTTTG 1560
QY 1603 CAAAGTGTGAAAAACACCACCTGAGCAAGAAATCTGAAAGCCATAAATCAATTCCTTT 1662
DB 1561 CAAAGTGTGAAAAACACCACCTGAGCAAGAAATCTGAAAGCCATAAATCAATTCCTTT 1620
QY 1663 GTAGAGTGTGCATCCATTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAGAA 1722
DB 1621 GTAGAGTGTGCATCCATTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAGAA 1680
QY 1723 TTTCAAGCTTCTTCTCAAGGTAAAAGCTTATATCAACTCAGGGAACATCCCGATTAC 1782
DB 1681 TTTCAAGCTTCTTCTCAAGGTAAAAGCTTATATCAACTCAGGGAACATCCCGATTAC 1740
QY 1783 TTATTTGACTTCTTTGAAATTTGCCAAATTTGCAAGTGTCTTGACTTCATTTAAACTG 1842
DB 1741 TTATTTGACTTCTTTGAAATTTGCCAAATTTGCAAGTGTCTTGACTTCATTTAAACTG 1800
QY 1843 GACTTTTATGGGAGCTATGGCTTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGATC 1902
DB 1801 GACTTTTATGGGAGCTATGGCTTTCATGGGAAAAGGCTGCAGAAGACACAGGTGGATC 1860
QY 1903 CACATGGAAGAGGCCCCAGAAACCTACATTCGCCAGGAGGCTGTATCTTTGTTCTTCAAC 1962
DB 1861 CACATGGAAGAGGCCCCAGAAACCTACATTCGCCAGGAGGCTGTATCTTTGTTCTTCAAC 1920
QY 1963 TGGAGCAGGAATTCAGGACTCTGGAGGTCACTCTCGGGATTTCAGCAAGTTGAATAAG 2022
DB 1921 TGGAGCAGGAATTCAGGACTCTGGAGGTCACTCTCGGGATTTCAGCAAGTTGAATAAG 1980
QY 2023 CAAGATATCATATCTTGGGAAAATATTGAGTCTGCCACAAGCCTCAGGCTCAATA 2082
DB 1981 CAAGATATCATATCTTGGGAAAATATTGAGTCTGCCACAAGCCTCAGGCTCAATA 2040
QY 2083 AAGAGATGTGTGGTGGCTGGAAGGCTCAGTTTGTGCTCAGCACCTGTGAAGAACATT 2142
DB 2041 AAGAGATGTGTGGTGGCTGGAAGGCTCAGTTTGTGCTCAGCACCTGTGAAGAACATT 2100
QY 2143 TATTCTCTATGTGGAGCCAGTCCCTCACCATAGAAGATGAGAGGCACATCACATCT 2202
DB 2101 TATTCTCTATGTGGAGCCAGTCCCTCACCATAGAAGATGAGAGGCACATCACATCT 2160
QY 2203 GTACAAACCTGAAACCTTGAGTATTCAATGACCTCAGAAATCAAGGCTGCCGG 2257
DB 2161 GTACAAACCTGAAACCTTGAGTATTCAATGACCTCAGAAATCAAGGCTGCCGG 2215

RESULT 7
AAH9581
ID AAH9581 standard; cDNA; 2950 BP.
XX
AC AAH9581;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human protein encoding cDNA sequence SEQ ID NO:416.
XX
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiac; central nervous system; virucide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW antiaggregant; haemostatic; vulnery; antiulcer; osteopathic; eczema;
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmune;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;

KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.
XX Homo sapiens.
XX WO200153455-A2.
XX 26-JUL-2001.
XX 22-DEC-2000; 2000WO-US35017.
XX 23-DEC-1999; 99US-04711275.
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-457603/49.
DR P-PSDB; AAM25640.
XX Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
PT Claim 1; Page 511-512; 1217pp; English.
XX
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery;
CC antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.
XX
SQ Sequence 2950 BP; 915 A; 592 C; 628 G; 815 T; 0 other;

Query Match 58.0%; Score 1781; DB 22; Length 2950;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1881; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1190 CTCTGGAGGGTGTCTTCTCCACAAAGTTTGATTTTCCGAACTCAGAGTGTGCCAGCTGA 1249
DB 45 CTCTGGAGGGTGTCTTCTCCACAAAGTTTGATTTTCCGAACTCAGAGTGTGCCAGCTGA 104
QY 1250 ATGAGGATGTCTCTGACAACTGGGCTCTCTGTAATAATACAGCTCAAAGGTTTCAAGC 1309
DB 105 ATGAGGATGTCTCTGACAACTGGGCTCTCTGTAATAATACAGCTCAAAGGTTTCAAGC 164
QY 1310 CAAAGTATAAATTTCTTTCACAAAGTATTCACAGGAGTACACAGAGGAGAACTCAGCA 1369
DB 165 CAAAGTATAAATTTCTTTCACAAAGTATTCACAGGAGTACACAGAGGAGAACTCAGCA 224
QY 1370 GTTTATTGACGTCTCATGAGCCAGGAGGTGACCAAGGGAATGGTTACTTGCAGAAA 1429
DB 225 GTTTATTGACGTCTCATGAGCCAGAGGAGGTGACCAAGGGAATGGTTACTTGCAGAAA 284
QY 1430 TGGTTTCCATTTCGAGACATTACCTTATACAGGCTCTCCGGTACACCTGTGGGT 1489

Db	285	TGGTTTCCATTTCGGACATTACATCCACATTATAGCAGCCTGCTCCGGTACACCTGTGGGT	344
Qy	1490	CATCTGTGGAAGCCACCAGGGCTGTTTATGAAGCACTCGCAGCAGTGTATCAACACGGCT	1549
Db	345	CATCTGTGGAAGCCACCAGGGCTGTTTATGAAGCACTCGCAGCAGTGTATCAACACGGCT	404
Qy	1550	GCCTTCTCGGACTTTCATCGCCAAGAGGCCCTCTGGAGACAGGAATCTTTTGCAAAAGT	1609
Db	405	GCCTTCTCGGACTTTCATCGCCAAGAGGCCCTCTGGAGACAGGAATCTTTTGCAAAAGT	464
Qy	1610	TGAANAACACCCTGACGACAGAANAATCTCGAAGCCATAAACAATCAATTCCTTTGAGAGT	1669
Db	465	TGAANAACACCCTGACGACAGAANAATCTCGAAGCCATAAACAATCAATTCCTTTGAGAGT	524
Qy	1670	GTGGCATCCATTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAATTTGAAG	1729
Db	525	GTGGCATCCATTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAATTTGAAG	584
Qy	1730	CTTTCTTTTCAAGTAAAGCTTATATATCAACTCAGGGAACATCCCCGATTACTTATTTG	1789
Db	585	CTTTCTTTTCAAGTAAAGCTTATATCAACTCAGGGAACATCCCCGATTACTTATTTG	644
Qy	1790	ACTTCTTTTGAACATTTGCCCAATTGTGCAAGTGCCTCTGGACTTCATTTAACTGGACATTTT	1849
Db	645	ACTTCTTTTGAACATTTGCCCAATTGTGCAAGTGCCTCTGGACTTCATTTAACTGGCGCTTTT	704
Qy	1850	ATGGGGGAGCTATGTGGCTTCATGGGAAAAGGCTGCAGAGACACACAGTGGGAATCCACATGG	1909
Db	705	ATGGGGGAGCTATGTGGCTTCATGGGAAAAGGCTGCAGAGACACACAGTGGGAATCCACATGG	764
Qy	1910	AAGAGGCCCGAGAAACCTACATTCOCAGAGGGCTGTATCTTTGTCTTCAACTGGAAGC	1969
Db	765	AAGAGGCCCGAGAAACCTACATTCOCAGAGGGCTGTATCTTTGTCTTCAACTGGAAGC	824
Qy	1970	AGGAATTCAGGACTCTGGAGGTCACACTCCGGGATTTAGCAAGTTGAATTAAGCAAGATA	2029
Db	825	AGGAATTCAGGACTCTGGAGGTCACACTCCGGGATTTAGCAAGTTGAATTAAGCAAGATA	884
Qy	2030	TCACATATCTGGGGAAAATATTTCAGCTCTGCCACAAGGCTCAGGCTGCAAAATAAGAGAT	2089
Db	885	TCAGATATCTGGGGAAAATATTTCAGCTCTGCCACAAGGCTCAGGCTGCAAAATAAGAGAT	944
Qy	2090	GTGCTGTGTGGCTGGAAGCCTCAGTTTGGTCCCTCAGCACCTGTGAAGCAACATTTATTTCTC	2149
Db	945	GTGCTGTGTGGCTGGAAGCCTCAGTTTGGTCCCTCAGCACCTGTGAAGCAACATTTATTTCTC	1004
Qy	2150	TCATGGTGGGAAGCCAGCTCCCTCACCATAGAGAGATGAGAGGCACATCACATCTGTACAA	2209
Db	1005	TCATGGTGGGAAGCCAGCTCCCTCACCATAGAGAGATGAGAGGCACATCACATCTGTACAA	1064
Qy	2210	ACCTGAAAACCTTGAGTATTTCATGACTACAGAAATCAAGGCTGCCGGTGGCTCTGACTG	2269
Db	1065	ACCTGAAAACCTTGAGTATTTCATGACTACAGAAATCAAGGCTGCCGGTGGCTCTGACTG	1124
Qy	2270	ACAGCTTGGTAACTTTGAAGAACCTTACAAAGCTCATATGGAATAACATAAAGATGAATG	2329
Db	1125	ACAGCTTGGTAACTTTGAAGAACCTTACAAAGCTCATATGGAATAACATAAAGATGAATG	1184
Qy	2330	AAGAAGATGCTATAAACAATGCTGAAGGCCCTGAAAACCTGAAGAAGATGTTTTTATTTTC	2389
Db	1185	AAGAAGATGCTATAAACAATGCTGAAGGCCCTGAAAACCTGAAGAAGATGTTTTTATTTTC	1244
Qy	2390	ATTTGACCCACTTGTCTGACATTTGGAGAGGAATGGAATACATAGTCAAGTCTCTGTCAAA	2449
Db	1245	ATTTGACCCACTTGTCTGACATTTGGAGAGGAATGGAATACATAGTCAAGTCTCTGTCAAA	1304
Qy	2450	GTGAACCCCTGTGACCTTGAAGAAATTCAAATTAGTCTCCTGCTGCTGTCTGTCAAAATCGAG	2509
Db	1305	GTGAACCCCTGTGACCTTGAAGAAATTCAAATTAGTCTCCTGCTGCTGTCTGTCAAAATCGAG	1364
Qy	2510	TGAANAATCTAGCTCAGAAATCTTCAAAATTTGGTCAAACTCAGCATTTCTTGATTTATTCAG	2569
Db	1365	TGAANAATCTAGCTCAGAAATCTTCAAAATTTGGTCAAACTCAGCATTTCTTGATTTATTCAG	1424

QY	2570	AAATTAACCTGGAAAAAGATGGAATTAAGAGCTCTTCATGAACCTGATCGACAGGATGAACG	2629
Db	1425	AAATTAACCTGGAAAAAGATGGAATTAAGAGCTCTTCATGAACCTGATCGACAGGATGAACG	1484
QY	2630	TGCTAGAACAGCTCACCGCAGCTGATGCTGCCCTGGGGCTGTGACGTGCAAGGCGAGCCTGA	2689
Db	1485	TGCTAGAACAGCTCACCGCAGCTGATGCTGCCCTGGGGCTGTGACGTGCAAGGCGAGCCTGA	1544
QY	2690	GCAGCCTGTTGAAACATTTGGAGGAGGTCCCAACAACCTCGTCAAGCTTGGGTTGAAAAA	2749
Db	1545	GCAGCCTGTTGAAACATTTGGAGGAGGTCCCAACAACCTCGTCAAGCTTGGGTTGAAAAA	1604
QY	2750	GGAGACTCAGATACAGAGATTAGAAATTTTAGTGTCATTTTGGGAAAGAACCCCTCTGA	2809
Db	1605	GGAGACTCAGATACAGAGATTAGAAATTTTAGTGTCATTTTGGGAAAGAACCCCTCTGA	1664
QY	2810	AAAACTTCCAGCAGTTGAATTTGGCGGGAATCGTGTGACAGTGATGGATGCTTGCCT	2869
Db	1665	AAAACTTCCAGCAGTTGAATTTGGCGGGAATCGTGTGACAGTGATGGATGCTTGCCT	1724
QY	2870	TCATGGGTGTATTGAGAATCTTTAAGCAATTAGTGTTTTTGTAGCTTTAGTACTAAAGAAT	2929
Db	1725	TCATGGGTGTATTGAGAATCTTTAAGCAATTAGTGTTTTTGTAGCTTTAGTACTAAAGAAT	1784
QY	2930	TTCTACTGATCCAGCATTTAGTCAGAAAACCTTAGCCAAAGTGTTATCCAAAGTTAACTTTTC	2989
Db	1785	TTCTACTGATCCAGCATTTAGTCAGAAAACCTTAGCCAAAGTGTTATCCAAAGTTAACTTTTC	1844
QY	2990	TGCAAGAACTAGGCTTGTTGGGTGGCAATTTTCATGATGATGATCTCAGTGTTATTACAG	3049
Db	1845	TGCAAGAACTAGGCTTGTTGGGTGGCAATTTTCATGATGATGATCTCAGTGTTATTACAG	1904
QY	3050	GTGCTTTTAACTAGTAACCTGCT 3072	
Db	1905	GTGCTTTTAACTAGTAACCTGCT 1927	
RESULT 8			
ABK22766			
ID	ABK22766	standard; cdNA; 891 BP.	
XX	AC	ABK22766;	
XX	AC	ABK22766;	
DT	26-MAR-2002	(first entry)	
XX	Human	cdNA encoding CLAN NACHT.	
XX	Caspase	recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;	
KW	abnormal	cell proliferation; cancer; abnormal cell death; apoptosis;	
KW	autoimmune	disease; inflammation; keratinocyte hyperplasia;	
KW	inflammatory	hyperplasia; fibrosis; smooth muscle cell proliferation;	
KW	leukon	angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;	
KW	leukemia;	allergy; arthritis; lupus; Schrogen's syndrome;	
KW	Crohn's	disease; graft-versus-host disease; stroke;	
KW	myocardial	infarction; heart failure; neurodegenerative disease;	
KW	Parkinson's	disease; Alzheimer's disease; HIV;	
KW	human	immunodeficiency virus infection.	
OS	Homo sapiens.		
XX	WO200190156-A2.		
PN	29-NOV-2001.		
PD	29-NOV-2001.		
XX	24-MAY-2001;	2001WO-US17158.	
XX	24-MAY-2000;	2000US-0579240.	
PR	10-OCT-2000;	2000US-0686347.	
PR	14-MAR-2001;	2001US-275980P.	
PR	23-MAY-2001;	2001US-0864921.	
PA	(BURN-)	BURNHAM INST.	

XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX WPI: 2002-083086/11.
DR P-PSDB; AAU80872.
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke
XX
PS Claim 1; Page 200-201; 216pp; English.
XX
CC The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.
XX
SQ Sequence 891 BP; 237 A; 228 C; 217 G; 209 T; 0 other;

Query Match 27.3%; Score 840; DB 24; Length 891;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 890; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 481 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCCAAGTCCACTCTGCTGCAG 540
DB 1 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCCAAGTCCACTCTGCTGCAG 60
QY 541 CGCATTGCCATGCTCTGGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAATTCGTC 600
DB 61 CGCATTGCCATGCTCTGGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAATTCGTC 120
QY 601 TTCTTCTCCGCTCTCAGCAGGGCCCGAGGTGGACTTTTGAACCCCTCTGTGATCAACTC 660
DB 121 TTCTTCTCCGCTCTCAGCAGGGCCCGAGGTGGACTTTTGAACCCCTCTGTGATCAACTC 180
QY 661 CTGGATATACCTGGCAATCAGAGAGCAGACATTCATGCGCCATGCTGCTGAAGCTGCGG 720
DB 181 CTGGATATACCTGGCAATCAGAGAGCAGACATTCATGCGCCATGCTGCTGAAGCTGCGG 240
QY 721 CAGAGGGTCTTTTCCCTCTTGTGCTTCAATGAATTCAGCCGCCAGAACTGCCAGAA 780
DB 241 CAGAGGGTCTTTTCCCTCTTGTGCTTCAATGAATTCAGCCGCCAGAACTGCCAGAA 300
QY 781 ATCGAAGCCCTGTATAAGGAAACCCACCGCTTCAAGAACATGGTCTATCGTCACCACTACC 840
DB 301 ATCGAAGCCCTGTATAAGGAAACCCACCGCTTCAAGAACATGGTCTATCGTCACCACTACC 360
QY 841 ACTGAGTGCCTGAGGCACATPACGGCAGTTTGGTCCCTGACTCTGAGGTGGGGATATG 900
DB 361 ACTGAGTGCCTGAGGCACATPACGGCAGTTTGGTCCCTGACTCTGAGGTGGGGATATG 420
QY 901 ACAGAGACAGCCGCCAGGCTCTCATCCGAGAAAGTCTGATCAAGGAGCTTGTGAGGC 960
DB 421 ACAGAGACAGCCGCCAGGCTCTCATCCGAGAAAGTCTGATCAAGGAGCTTGTGAGGC 480

QY 961 TTGTTGCTCCAAATTCAGAAATCCAGGTCGTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020
DB 481 TTGTTGCTCCAAATTCAGAAATCCAGGTCGTTGAGGAATCTCATGAAGACCCCTCTCTTT 540
QY 1021 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAGTCAGTTCCTCACTCTCACACAACA 1080
DB 541 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAGTCAGTTCCTCACTCTCACACAACA 600
QY 1081 ACGTGTTCATACCTCTCTATGATCTTGTATACAGAAAAACAACAACAATAAAGGT 1140
DB 601 ACGTGTTCATACCTCTCTATGATCTTGTATACAGAAAAACAACAACAATAAAGGT 660
QY 1141 GTGGTGCAGAGTCACTTCATTCGGAGCCTGGACACATGTCGAGACCTAGTCTGGAGGT 1200
DB 661 GTGGTGCAGAGTCACTTCATTCGGAGCCTGGACACCTAGTCTGGAGGT 720
QY 1201 GTGTTCTCCACAAAGTTTGAATTCGAACTCAGAGATGTCAGCGTGAATGAGGATGTC 1260
DB 721 GTGTTCTCCACAAAGTTTGAATTCGAACTCAGAGATGTCAGCGTGAATGAGGATGTC 780
QY 1261 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGGTTCAAGCCAAAGATATAA 1320
DB 781 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGGTTCAAGCCAAAGATATAA 840
QY 1321 TTCTTTTCAAGTCAATTCAGGAGTACACAGCAGGACGAAAGACTCAGCACT 1371
DB 841 TTCTTTTCAAGTCAATTCAGGAGTACACAGCAGGACGAAAGACTCAGCACT 891
RESULT 9
ABK22732
ID ABK22732 standard; cDNA; 1395 BP.
XX
AC ABK22732;
XX
DT 26-MAR-2002 (first entry)
XX Human cDNA encoding CLAN B.
XX
KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
XX
OS Homo sapiens.
XX
XX WO200190156-A2.
XX
PD 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US17158.
XX
XX 24-MAY-2000; 2000US-0579240.
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275980P.
PR 23-MAY-2001; 2001US-0864921.
XX
XX (BURN-) BURNHAM INST.
XX
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX
XX WPI: 2002-083086/11.
DR P-PSDB; AAU80872.
XX
PT New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation

PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
XX arthritis or stroke

PS Claim 1; Page 174-176; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.

XX Sequence 1395 BP; 436 A; 248 C; 327 G; 384 T; 0 other;

Query Match 26.5%; Score 815; DB 24; Length 1395;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 815; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2258 GTGGTCTGACTGACAGCTTGGTAACTTGAAGAACCCTTACAAGCTCAATAAGGATAACA 2317

DB 539 GTGGTCTGACTGACAGCTTGGTAACTTGAAGAACCCTTACAAGCTCAATAAGGATAACA 598

QY 2318 TAAAGATGAATGAAGAAGTGTATATAAACTAGCTGAAGGCTGAAAAACCTGAAGAAGA 2377

DB 599 TAAAGATGAATGAAGAAGTGTATATAAACTAGCTGAAGGCTGAAAAACCTGAAGAAGA 658

QY 2378 TGTGTTATTTTATTTGACCCACTTGTCTGACATTTGGAGAGGGGAATGATACATAGTCA 2437

DB 659 TGTGTTATTTTATTTGACCCACTTGTCTGACATTTGGAGAGGGGAATGATACATAGTCA 718

QY 2438 AGTCTCTGTCAAGTGAACCTGTGACCTTGAAGAATCAATTAGTCTCTCTCTGTGT 2497

DB 719 AGTCTCTGTCAAGTGAACCTGTGACCTTGAAGAATCAATTAGTCTCTCTCTGTGT 778

QY 2498 CTGCAAAATGACAGTGAATAATCTTAGCTCAGAAATCTTTCACAAATTTGGTCAAACTGAGCATTC 2557

DB 779 CTGCAAAATGACAGTGAATAATCTTAGCTCAGAAATCTTTCACAAATTTGGTCAAACTGAGCATTC 838

QY 2558 TTGATTTATCAGAAATTTACCTGGAAAAGATGGAATGAAGCTTCTCATGAACCTGATCG 2617

DB 839 TTGATTTATCAGAAATTTACCTGGAAAAGATGGAATGAAGCTTCTCATGAACCTGATCG 898

QY 2618 ACAGGATGAACCTGTAGAACAGCTCACGCACTGATCTGCCCTGGGGCTGTGACGTGC 2677

DB 899 ACAGGATGAACCTGTAGAACAGCTCACGCACTGATCTGCCCTGGGGCTGTGACGTGC 958

QY 2678 AAGGAGCCTGTAGCAGCCTGTTTGAACATTTTGGAGAGGTCCCAAACTCGTCAAGCTTG 2737

DB 959 AAGGAGCCTGTAGCAGCCTGTTTGAACATTTTGGAGAGGTCCCAAACTCGTCAAGCTTG 1018

QY 2738 GGTGAAAACCTGGAGACTCACAGATACAGAGATTAGATTTTAGTGTCATTTTGGAA 2797

DB 1019 GGTGAAAACCTGGAGACTCACAGATACAGAGATTAGATTTTAGTGTCATTTTGGAA 1078

QY 2798 AGAACCCCTGTGAACACTTCAGCAGTGAATTTGGCGGGGAATCGTGTGACCACTGATG 2857

DB 1079 AGAACCCCTGTGAACACTTCAGCAGTGAATTTGGCGGGGAATCGTGTGACCACTGATG 1138

QY 2858 GATGGCTTGCCTTTCATGGTGTATTGAGAAATCTTAAAGCAATTTAGTGTTTTGGACTTTA 2917

DB 1139 GATGGCTTGCCTTTCATGGTGTATTGAGAAATCTTAAAGCAATTTAGTGTTTTGGACTTTA 1198

QY 2918 GTACTAAAGAAATTTCTACCTGATCCAGCAATTTAGTCAGAAAACCTAGCCCAAGTGTATCCA 2977

DB 1199 GTACTAAAGAAATTTCTACCTGATCCAGCAATTTAGTCAGAAAACCTAGCCCAAGTGTATCCA 1258

QY 2978 AGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATTTGATGATGATGATCTCA 3037

DB 1259 AGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATTTGATGATGATGATCTCA 1318

QY 3038 GTGTTATTACAGGCTGCTTTTAAACTAGTAACCTGCT 3072

DB 1319 GTGTTATTACAGGCTGCTTTTAAACTAGTAACCTGCT 1353

RESULT 10

ABK22767

ID ABK22767 standard; cDNA; 618 BP.

XX AC ABK22767;

XX 26-MAR-2002 (first entry)

DE Human cDNA encoding CLAN LRR.

XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;

XX abnormal cell proliferation; cancer; abnormal cell death; apoptosis;

XX autoimmune disease; inflammation; keratinocyte hyperplasia;

XX inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;

XX balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;

XX leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;

XX Crohn's disease; graft-versus-host disease; stroke;

XX myocardial infarction; heart failure; neurodegenerative disease;

XX Parkinson's disease; Alzheimer's disease; HIV;

XX human immunodeficiency virus infection.

XX Homo sapiens.

XX WO200190156-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001WO-US17158.

XX 24-MAY-2000; 2000US-0579240.

XX 10-OCT-2000; 2000US-0686347.

XX 14-MAR-2001; 2001US-275980P.

XX 23-MAY-2001; 2001US-0864921.

XX (BURN-) BURNHAM INST.

XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

XX Oliveira VAM, Hayashi H, Pawlowski K;

XX WPI; 2002-083086/11.

XX P-PSDB; AU08073.

XX New caspase recruitment domain (CARD)-containing polypeptides and
XX encoding nucleic acids, useful for treating abnormal cell proliferation
XX or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
XX arthritis or stroke

PS Claim 1; Page 202-203; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)
XX -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
XX from it, and the polynucleotides encoding them. Also included are a
XX recombinant vector comprising the polynucleotide, recombinant cells
XX containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
XX and insect cells) and an anti-CARD antibody. The CARD-containing
XX polypeptide and CARD-encoding nucleic acid are useful for treating a
XX pathology characterised by abnormal cell proliferation (e.g. cancer),

XX Rosen CA, Barash SC, Ruben SM;
PI WPI: 2001-488783/53.
DR P-PSDB; AAU16173.
XX
XX New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -
XX
XX Claim 1: SEQ ID No 339; 980pp; English.
XX
XX The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. Antibodies to the proteins can also
CC be used in alleviating symptoms associated with the disorders and in
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence encodes a novel secreted protein of the invention.

Query Match 13.7%; Score 420; DB 22; Length 608;
Best Local Similarity 99.6%; Pred. No. 9.7e-198;
Matches 520; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1494 TGTGGAAGCCACCGGCTGTATGATGAAGACCTCGCAGCAGTGTATCAACACGGCTGCCT 1553
Db 87 TGTGGAAGCCACCGGCTGTATGATGAAGACCTCGCAGCAGTGTATCAACACGGCTGCCT 146
Qy 1534 TCTCGGACTTTCATCGCCAGAGGCTCTCTGGAGCAGCAATCTTTGCAAGTGTGAA 1613
Db 147 TCTCGGACTTTCATCGCCAGAGGCTCTCTGGAGCAGCAATCTTTGCAAGTGTGAA 206
Qy 1614 AAACACCACCTGAGCAAGAAATCTGAAAGCCATAAATCAATCTTTGTAGAGTGTGG 1673
Db 207 AAACACCACCTGAGCAAGAAATCTGAAAGCCATAAATCAATCTTTGTAGAGTGTGG 266
Qy 1674 CATCATTTATATCAAGAGATGATCATCAATATGACCTCGCAGCAAGATTTGAAGCTTT 1733
Db 267 CATCATTTATATCAAGAGATGATCATCAATATGACCTCGCAGCAAGATTTGAAGCTTT 326
Qy 1734 CTTTCAAGTAAAGCTTATATATCACTCAGGGAACATCCCGATCTATTATTGACTT 1793
Db 327 CTTTCAAGTAAAGCTTATATATCACTCAGGGAACATCCCGATCTATTATTGACTT 386
Qy 1794 CTTTGAACATTTGCCCAATTTGCAAGTGCCTGGACTTCATTAACTGGACTTTTATGG 1853
Db 387 CTTTGAACATTTGCCCAATTTGCAAGTGCCTGGACTTCATTAACTGGACTTTTATGG 446
Qy 1854 GGGAGCTATGCTTCATGGGAAAGGCTGAGAGACACAGCTGGATCCACATGGGAAGA 1913
Db 447 GGGAGCTATGCTTCATGGGAAAGGCTGAGAGACACAGCTGGATCCACATGGGAAGA 506
Qy 1914 GGCCCCAGAAACCTACATTCACAGAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGA 1973
Db 507 GGCCCCAGAAACCTACATTCACAGAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGA 566

Qy 1974

ATTGAGGACTCTGGAGGTCACTCCGGGATTTTCAGCAAGTT 2015

|||||

Db 567

ATTGAGGACTCTGGAGGTCACTCCGGGATTTTCAGCAAGTT 608

RESULT 14

AAS26575

ID AAS26575 standard; cDNA; 522 BP.

XX AAS26575;

XX AAS26575;

XX 07-NOV-2001 (first entry)

XX Human cDNA encoding a novel secreted protein, Seq ID 754.

DE Human; immunosuppressive; antiarthritic; ss; antirheumatic;

KW cytosolic; cardiac; vasotropic; cerebroprotective; nootropic;

KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;

KW vulnary; secreted protein; rheumatoid arthritis;

KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;

KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;

KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;

KW corneal infection; wound healing; epithelial cell proliferation;

KW skin ageing; food additive; preservative; antiproliferative.

XX Homo sapiens.

OS Homo sapiens.

PN W0200155322-A2.

XX 02-AUG-2001.

PD 17-JAN-2001; 2001WO-US01341.

XX 31-JAN-2000; 2000US-0179055.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0226868.

PR 22-AUG-2000; 2000US-0227182.

PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

PR 01-SEP-2000; 2000US-0229343.

PR 01-SEP-2000; 2000US-0229344.

PR 01-SEP-2000; 2000US-0229345.

Db 61 ACGATTGGCTCAGGATTAAAGGACTTGTACCATACCCATCTTTCTGAACCTTTATC 120

QY 356 CCCTTGGTGAAGATATGACATTATTTTAACTTCAAAGACACCTTCACAGAACCTGTCC 415
|||||
Db 121 CCCTTGGTGAAGATATGACATTATTTTAACTTCAAAGACACCTTCACAGAACCTGTCC 180
QY 416 TGTGGAGGAGGACCAACACCATCATCCCGTGGAGCAGCTGACCCCTGAATGCCCTTCCTGC 475
|||||
Db 181 TGTGGAGGAGGACCAACACCATCATCCCGTGGAGCAGCTGACCCCTGAATGCCCTTCCTGC 240
QY 476 AGGCTCTTCAGAGCCCTTCATCATTTGAAGGGAATCTGGCAAGCAAGTCCATCTCTGC 535
|||||
Db 241 AGGCTCTTCAGAGCCCTTCATCATTTGAAGGGAATCTGGCAAGCAAGTCCATCTCTGC 300
QY 536 TGCAGCGCATTCGCCATGCTCTGGGGCTCCGGAAGTGCAGAGGCTCTGACCAAGTT 590
|||||
Db 301 TGCAGCGCATTCGCCATGCTCTGGGGCTCCGGAAGTGCAGAGGCTCTGACCAAGTT 355

RESULT 15
ABK22733
ID ABK22733 standard; cDNA; 578 BP.
XX AC ABK22733;
XX DT 26-MAR-2002 (first entry)
XX DE Human cDNA encoding CLAN C.
XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.

OS Homo sapiens.
XX WO200190156-A2.
XX PN 29-NOV-2001.
XX PD 24-MAY-2001; 2001WO-US17158.
XX PF 24-MAY-2000; 2000US-0579240.
XX PR 10-OCT-2000; 2000US-0686347.
XX PR 14-MAR-2001; 2001US-275980P.
XX PR 23-MAY-2001; 2001US-0864921.
XX PA (BURN-) BURNHAM INST.
XX PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX WPI; 2002-083086/11.
XX DR P-PSDB; AAU80863.
XX DR New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -
XX Claim 1; Page 177; 216pp; English.
XX CC The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing

CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation.
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.

XX
SQ Sequence 578 BP; 172 A; 106 C; 143 G; 157 T; 0 other;

Query Match 8.8%; Score 269; DB 24; Length 578;

Best Local Similarity 100.0%; Pred. No. 8.8e-123;

Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTTTCATAAAGGACAATAGCGGAGCCCTTATTCAAAGAAATGGGAATGACTTTATA 60
|||||
Db 277 ATGATTTTCATAAAGGACAATAGCGGAGCCCTTATTCAAAGAAATGGGAATGACTTTATA 336
QY 61 AAGCAAAATCACAGATGACCTATTGTATGGAATGTCTGAATCGCGAAGAAAGTAAACATC 120
|||||
Db 337 AAGCAAAATCACAGATGACCTATTGTATGGAATGTCTGAATCGCGAAGAAAGTAAACATC 396
QY 131 ATTGTCTCGAAGAGGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGA 180
Db 397 ATTTGCTCGAAGAGGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGA 456
QY 181 AAGGTTTCAGAGTCTGTAACCTCTTCTTAATCCCTTAAGGAGTGGAACTATCTCTA 240
|||||
Db 457 AAGGTTTCAGAGTCTGTAACCTCTTCTTAATCCCTTAAGGAGTGGAACTATCTCTA 516
QY 241 TTTCAGGACTTGAATGGACAAGTCTTTT 269
|||||
Db 517 TTTCAGGACTTGAATGGACAAGTCTTTT 545

RESULT 16

ABK22765

ID ABK22765 standard; cDNA; 261 BP.

XX AC ABK22765;

XX DT 26-MAR-2002 (first entry)

XX DE Human cDNA encoding CLAN CARD.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.

XX OS Homo sapiens.

XX PN WO200190156-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US17158.

XX PR 24-MAY-2000; 2000US-0579240.

PR 10-OCT-2000; 2000US-0686347.

```
PR 14-MAR-2001; 2001US-275980P.
XX 23-MAY-2001; 2001US-0864921.
PA (BURN-) BURNHAM INST.
XX Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX WPI; 2002-083086/11.
DR P-PSDB; AAU80871.
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -
XX
XX Claim 1; Page 199; 216pp; English.
XX
XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.
XX
SQ Sequence 261 BP; 86 A; 44 C; 59 G; 72 T; 0 other;

Query Match      8.5%; Score 261; DB 24; Length 261;
Best Local Similarity 100.0%; Pred. No. 8e-119;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTCTAAGGACATAGCCGAGCCCTTATTCAAAGATGGGAATGACTGTATA 60
DB 1 ATGAATTTCTAAGGACATAGCCGAGCCCTTATTCAAAGATGGGAATGACTGTATA 60
QY 61 AAGCAATATCACATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAGTAACATC 120
DB 61 AAGCAATATCACATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAGTAACATC 120
QY 121 ATTTGTCGAGAGGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTGAAA 180
DB 121 ATTTGTCGAGAGGTGGAGCAGGATGCTGCTAGAGGGATCATTCACATGATTTGAAA 180
QY 181 AAGGGTTCAGAGTCCTGTACCTCTTTCTTAATCCCTTAAGAGTGGAACTATCCTCTA 240
DB 181 AAGGGTTCAGAGTCCTGTACCTCTTTCTTAAATCCCTTAAGAGTGGAACTATCCTCTA 240
QY 241 TTTTCAGGACTTGAATGGACAA 261
DB 241 TTTTCAGGACTTGAATGGACAA 261

RESULT 17
ID ABA45612
XX ABA45612 standard; DNA; 421 BP.
AC ABA45612;
XX
XX 01-FEB-2002 (first entry)
```

```
XX Human breast cell single exon nucleic acid probe #4307.
XX
XX Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer; ss.
XX Homo sapiens.
OS
PN WO200157271-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US006662.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
XX Claim 1; SEQ ID NO 4307; 327pp + sequence listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Query Match      7.9%; Score 242; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.2e-109;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2781 AGGTGCATTTTGGAAAGAACCCCTCTGAAAAAATTCACAGCAGTTGAATTTGGCGGAAA 2840
DB 180 AGGTGCATTTTGGAAAGAACCCCTCTGAAAAAATTCACAGCAGTTGAATTTGGCGGAAA 239
QY 2841 TCCTGTGACGACGTGATGGATGGCTTGCCTTCATCGGGTGTATTGAGAACTTTAAGCAATT 2900
DB 240 TCCTGTGACGACGTGATGGATGGCTTGCCTTCATCGGGTGTATTGAGAACTTTAAGCAATT 299
QY 2901 AGTGTGTTTGTGACTTTAGTAGTAAAGAAATTTCTACCTGATCCAGCAGTACTAGCAAAACT 2960
DB 300 AGTGTGTTTGTGACTTTAGTAGTAAAGAAATTTCTACCTGATCCAGCAGTACTAGCAAAACT 359
QY 2961 TAGCCAAGTGTATTCCAAGTTAACTTTTCTGCAAGAGCTAGGCTGTTGTTGGGTGGCAATT 3020
DB 2961 TAGCCAAGTGTATTCCAAGTTAACTTTTCTGCAAGAGCTAGGCTGTTGTTGGGTGGCAATT 3020
```

Db 360 TAGCCAAGTGTATCAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGAAT 419
QY 3021 TG 3022
II
Db 420 TG 421

RESULT 18
ABA56119
ID ABA56119 standard; DNA; 421 BP.
XX ABA56119;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #4424.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
DR Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
XX
PS Claim 1; SEQ ID NO 4424; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Query Match 7.9%; Score 242; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.2e-109;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2781 AGGTGCATTTTGGAAAGAACCCCTCTGAAAACTCCAGCAGTTGAATTTGGCGGAAA 2840
Db 180 AGGTGCATTTTGGAAAGAACCCCTCTGAAAACTCCAGCAGTTGAATTTGGCGGAAA 239

QY 2841 TCGTGTGACAGTGTGATGGCTTCCCTCATGGTGTATTGAGAACTCTTAAGCAATT 2900
Db 240 TCGTGTGACAGTGTGATGGCTTCCCTCATGGTGTATTGAGAACTCTTAAGCAATT 299

QY 2901 AGTGTGTGTGACTTTAGTACTAAAGAAATTTCTACTGATCCAGCAGTTAGTCAGAAAACT 2960
Db 300 AGTGTGTGTGACTTTAGTACTAAAGAAATTTCTACTGATCCAGCAGTTAGTCAGAAAACT 359

QY 2961 TAGCCAAGTGTATCAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGAAT 3020
Db 360 TAGCCAAGTGTATCAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGAAT 419

QY 3021 TG 3022
II
Db 420 TG 421

RESULT 19
ABA25770
ID ABA25770 standard; DNA; 421 BP.
XX ABA25770;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #4236 for gene expression analysis in human heart cell sample.
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
DR Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
XX
PS Claim 1; SEQ ID No 4236; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Query Match 7.9%; Score 242; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.2e-109;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2781 AGGTGCATTTTGGAAAGAACCCCTCTGAAAACTCCAGCAGTTGAATTTGGCGGAAA 2840
Db 180 AGGTGCATTTTGGAAAGAACCCCTCTGAAAACTCCAGCAGTTGAATTTGGCGGAAA 239

```
QY 2841 TCGGTGAGCAGTGATGGATGGCTTGCCTTCATGGGTGTAATTGAGAACTCTTAAGCAATT 2900
    |||||||
Db 240 TCGGTGAGCAGTGATGGATGGCTTGCCTTCATGGGTGTAATTGAGAACTCTTAAGCAATT 299
QY 2901 AGTGTGTTTGGACCTTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACT 2960
    |||||||
Db 300 AGTGTGTTTGGACCTTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACT 359
QY 2961 TAGCCAAGTGTTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 3020
    |||||||
Db 360 TAGCCAAGTGTTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 419
QY 3021 TG 3022
    ||
Db 420 TG 421

RESULT 20
AAK04305
ID AAK04305 standard; DNA; 421 BP.
AC AAK04305;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 4296.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
XX Example 4; SEQ ID NO: 4296; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system,
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;
```

Query Match 7.9%; Score 242; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.2e-109;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 2781 AGGTGCATTTTGGAAAGAACCCCTCTGAAAAACTTCAGCAGTTGAATTTGGCGGGAAA 2840
    |||||||
Db 180 AGGTGCATTTTGGAAAGAACCCCTCTGAAAAACTTCAGCAGTTGAATTTGGCGGGAAA 239
QY 2841 TCGGTGAGCAGTGATGGATGGCTTGCCTTCATGGGTGTAATTGAGAACTCTTAAGCAATT 2900
    |||||||
Db 240 TCGGTGAGCAGTGATGGATGGCTTGCCTTCATGGGTGTAATTGAGAACTCTTAAGCAATT 299
QY 2901 AGTGTGTTTGGACCTTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACT 2960
    |||||||
Db 300 AGTGTGTTTGGACCTTACTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACT 359
QY 2961 TAGCCAAGTGTTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 3020
    |||||||
Db 360 TAGCCAAGTGTTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 419
QY 3021 TG 3022
    ||
Db 420 TG 421

RESULT 21
AAK29801
ID AAK29801 standard; DNA; 421 BP.
XX
AC AAK29801;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 4358.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
XX Example 4; SEQ ID NO: 4358; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;
```

Query Match 7.9%; Score 242; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.2e-109;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2781 AGTGCATTTTGGAAAGAACCCCTCTGAAAAAATTCAGCAGTTGAATTTGGCGGAAA 2840
|||||
Db 180 AGTGCATTTTGGAAAGAACCCCTCTGAAAAAATTCAGCAGTTGAATTTGGCGGAAA 239
|||||
QY 2841 TCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTTGAGATCTTAAGCAATT 2900
|||||
Db 240 TCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTTGAGATCTTAAGCAATT 299
|||||
QY 2901 AGTGTGTTTGTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACT 2960
|||||
Db 300 AGTGTGTTTGTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACT 359
|||||
QY 2961 TAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAACTAGGCTTGTGGTGGCAATT 3020
|||||
Db 360 TAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAACTAGGCTTGTGGTGGCAATT 419
|||||
QY 3021 TG 3022
||
Db 420 TG 421
||
RESULT 22
AAI14389
ID AAI14389 standard; DNA; 421 BP.
XX
AC AAI14389;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #4322 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PS WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 4322; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENPs). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;
Query Match 7.9%; Score 242; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.2e-109;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2781 AGTGCATTTTGGAAAGAACCCCTCTGAAAAAATTCAGCAGTTGAATTTGGCGGAAA 2840
|||||
Db 180 AGTGCATTTTGGAAAGAACCCCTCTGAAAAAATTCAGCAGTTGAATTTGGCGGAAA 239
|||||
QY 2841 TCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTTGAGATCTTAAGCAATT 2900
|||||
Db 240 TCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTTGAGATCTTAAGCAATT 299
|||||
QY 2901 AGTGTGTTTGTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACT 2960
|||||
Db 300 AGTGTGTTTGTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACT 359
|||||
QY 2961 TAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAACTAGGCTTGTGGTGGCAATT 3020
|||||
Db 360 TAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAACTAGGCTTGTGGTGGCAATT 419
|||||
QY 3021 TG 3022
||
Db 420 TG 421
||
RESULT 23
AAI35764
ID AAI35764 standard; DNA; 421 BP.
XX
AC AAI35764;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #4450 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PS WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID No 4450; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENPs).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX


```
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Query Match          7.9%; Score 242; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.2e-109;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2781 AGGTGCATTTTGGGAAGAACCCCTCTGAAAACTCCAGCAGTTGAATTTGGCGGGA 2840
      |||||||
DB 180 AGGTGCATTTTGGGAAGAACCCCTCTGAAAACTCCAGCAGTTGAATTTGGCGGGA 239

QY 2841 TCGTGTGAGCAGTGTATCCAAAGTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 2900
      |||||||
DB 240 TCGTGTGAGCAGTGTATCCAAAGTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 299

QY 2901 AGTGTGTTTGGACCTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAA 2960
      |||||||
DB 300 AGTGTGTTTGGACCTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAA 359

QY 2961 TAGCCAAGTGTATCCAAAGTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 3020
      |||||||
DB 360 TAGCCAAGTGTATCCAAAGTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 419

QY 3021 TG 3022
      ||
DB 420 TG 421

RESULT 24
AAI04213
ID AAI04213 standard; DNA; 421 BP.
XX AC AAI04213;
XX DT 09-OCT-2001 (first entry)
XX DE Probe #4204 used to measure gene expression in human breast sample.
XX KW Probe; human; breast disease; breast cancer; development disorder; ss;
XX KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX OS Homo sapiens.
XX PN WO200157270-A2.
XX PD 09-AUG-2001.
XX PF 29-JAN-2001; 2001WO-US00661.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2001-476286/51.
XX DR Novel single exon nucleic acid probe used to measuring gene expression
XX PT in a human breast -
XX PS Claim 25; SEQ ID No 4204; 322pp; English.
XX CC The present invention relates to novel single exon nucleic acid probes.
XX CC The present sequence is one such probe. The probes are useful for
XX CC measuring human gene expression in a human breast sample, where the probe
XX CC hybridises at high stringency to a nucleic acid expressed in the human
XX CC breast. The probes are useful for predicting, diagnosing, grading,
XX CC staging, monitoring and prognosing diseases of the human breast,
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CC particularly those diseases with polygenic aetiology. The diseases
CC include: breast cancer, disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and
CC non-carcinoma tumours.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Query Match          7.9%; Score 242; DB 22; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.2e-109;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2781 AGGTGCATTTTGGGAAGAACCCCTCTGAAAACTCCAGCAGTTGAATTTGGCGGGA 2840
      |||||||
DB 180 AGGTGCATTTTGGGAAGAACCCCTCTGAAAACTCCAGCAGTTGAATTTGGCGGGA 239

QY 2841 TCGTGTGAGCAGTGTATCCAAAGTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 2900
      |||||||
DB 240 TCGTGTGAGCAGTGTATCCAAAGTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 299

QY 2901 AGTGTGTTTGGACCTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAA 2960
      |||||||
DB 300 AGTGTGTTTGGACCTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAA 359

QY 2961 TAGCCAAGTGTATCCAAAGTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 3020
      |||||||
DB 360 TAGCCAAGTGTATCCAAAGTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATT 419

QY 3021 TG 3022
      ||
DB 420 TG 421

RESULT 25
ABS04362
ID ABS04362 standard; DNA; 421 BP.
XX AC ABS04362;
XX DT 19-AUG-2002 (first entry)
XX DE Human genome-derived single exon probe from lung SEQ ID No 4353.
XX KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
XX KW chronic obstructive pulmonary disease; interstitial lung disease;
XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
XX KW primary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX KW hyaline membrane disease.
XX OS Homo sapiens.
XX PN WO200186003-A2.
XX XX 15-NOV-2001.
XX PD 30-JAN-2001; 2001WO-US00665.
XX PF 04-FEB-2000; 2000US-180312P.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-234687P.
XX PR 27-SEP-2000; 2000US-236359P.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI
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PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX Claim 1; SEQ ID NO 4353; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of
CC probes; the novel set of probes which hybridise at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a single exon
CC probe of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Query Match 7.9%; Score 242; DB 24; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.2e-109;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2781 AGTGTCATTTTGGAGAAGCCCTCTGAAAACCTCCAGCAGTTCGAATTTGGCGGAAA 2840
DB 180 AGGTGCATTTTGGAGAAGCCCTCTGAAAACCTCCAGCAGTTCGAATTTGGCGGAAA 239
QY 2841 TCGTGTGACAGTGTGATGGCTTCCGCTTCATGGGTGATTTTGAGAAATCTTAAGCAATT 2900
DB 240 TCGTGTGACAGTGTGATGGCTTCCGCTTCATGGGTGATTTTGAGAAATCTTAAGCAATT 299
QY 2901 AGTGTGTTTGTACTTTAGTACTTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAAT 2960
DB 300 AGTGTGTTTGTACTTTAGTACTTAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAAT 359
QY 2961 TAGCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGGGTGGCAATT 3020
DB 360 TAGCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGGGTGGCAATT 419
QY 3021 TG 3022

DB 420 TG 421
II
RESULT 26
ABA50734
ID ABA50734 standard; DNA; 220 BP.
XX
XX ABA50734;
XX
XX 01-FEB-2002 (first entry)
XX Human breast cell single exon nucleic acid probe #9429.
XX Human; microarray; single exon probe; gene expression; breast;
XX disease; cancer; ss.
XX Homo sapiens.
XX WO200157271-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00662.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-SEP-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes,
XX useful for measuring gene expression in sample derived from human
XX breast, comprises number of single exon nucleic acid probes -
XX
XX Claim 4; SEQ ID NO 9429; 327pp + sequence listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human breast and BT 474 cells. The method involves contacting
XX the probes with a collection of detectably labelled nucleic acids
XX derived from mRNA of human breast, and then measuring the label
XX bound to each probe of the microarray. The probes are useful for
XX verifying the expression of regions of genomic DNA predicted to
XX encode proteins. They are useful for gene discovery, and for
XX determining predisposition and/or prognosing breast disease. Gene
XX expression analysis is useful for assessing the toxicity of chemical
XX agents on cells. The microarray of this invention presents a far greater
XX diversity of probes for measuring gene expression, with far less bias
XX than expressed sequence tag microarrays. The method is suitable for
XX rapid production of functional information from genomic sequence. The
XX present sequence is a single exon nucleic acid probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;

Query Match 7.2%; Score 220; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.8e-98;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 TTGGCGGGAAATCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTTGAGAAT 2889
DB 1 TTGGCGGGAAATCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTTGAGAAT 60

QY 2890 CTTAAGCAATTAGTGTGTTTTTTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 2949
|||||
Db 61 CTTAAGCAATTAGTGTGTTTTTTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 120
QY 2950 GTCAGAAACTTACCCAAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGT 3009
|||||
Db 121 GTCAGAAACTTACCCAAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGT 180
QY 3010 GGGTGGCAATTGATGATGATGATCTCAGTGTATTATACAG 3049
|||||
Db 181 GGGTGGCAATTGATGATGATGATCTCAGTGTATTATACAG 220

RESULT 27
ABA68704
ID ABA68704 standard; DNA; 220 BP.
XX ABA68704;
AC
XX
DT
XX
XX
DE
XX
DE Human foetal liver single exon nucleic acid probe #17009.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD
XX
PF
XX
PF 30-JAN-2001; 2001WO-US00669.
PR
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
XX
PS Claim 4; SEQ ID NO 17009; 639pp + sequence listing; English.
XX

CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC foetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX

XX Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;
Query Match 7.2%; Score 220; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.8e-98;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 TTGCGGGAATCGTGTGACAGTGTGATGGCTTCCCTTCATGGTGTATTGAGAA 2889
|||||
Db 1 TTGCGGGAATCGTGTGACAGTGTGATGGCTTCCCTTCATGGTGTATTGAGAA 60

QY 2890 CTTAAGCAATTAGTGTGTTTTTTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 2949
|||||
Db 61 CTTAAGCAATTAGTGTGTTTTTTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 120
QY 2950 GTCAGAAACTTACCCAAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGT 3009
|||||
Db 121 GTCAGAAACTTACCCAAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTGT 180
QY 3010 GGGTGGCAATTGATGATGATGATCTCAGTGTATTATACAG 3049
|||||
Db 181 GGGTGGCAATTGATGATGATGATCTCAGTGTATTATACAG 220

RESULT 28
ABA35668
ID ABA35668 standard; DNA; 220 BP.
XX ABA35668;
AC
XX
DT
XX
XX
DE
XX
DE Probe #14134 for gene expression analysis in human heart cell sample.
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD
XX
PF
XX
PF 30-JAN-2001; 2001WO-US00666.
PR
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 4; SEQ ID NO 14134; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX

XX Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;
Query Match 7.2%; Score 220; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.8e-98;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 2830 TTGGCGGGAATCGTGTGACAGTGTATCCAAAGTTAAGCTTTTCTGCAAGAAGCTAGGCTTGT 2889
Db 1 TTGGCGGGAATCGTGTGACAGTGTATCCAAAGTTAAGCTTTTCTGCAAGAAGCTAGGCTTGT 60
QY 2890 CTTAAGCAATTTAGTGTCTTGTGACCTTACTAAGAAATTTCTACCTGATCCAGCATTA 2949
Db 61 CTTAAGCAATTTAGTGTCTTGTGACCTTACTAAGAAATTTCTACCTGATCCAGCATTA 120
QY 2950 GTCCAGAAAACCTTAGCCAAAGTGTATCCAAAGTTAAGCTTTTCTGCAAGAAGCTAGGCTTGT 3009
Db 121 GTCCAGAAAACCTTAGCCAAAGTGTATCCAAAGTTAAGCTTTTCTGCAAGAAGCTAGGCTTGT 180
QY 3010 GGSTGSCAATTTGATGATGATGATCTCAGTGTATTATACAG 3049
Db 181 GGSTGSCAATTTGATGATGATGATCTCAGTGTATTATACAG 220

RESULT 29
AAK17044
ID AAK17044 standard; DNA; 220 BP.
XX
AC AAK17044;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 17035.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-483446/52.
XX
Single exon nucleic acid probes for analyzing gene expression in human
brains -
XX
Example 4; SEQ ID NO: 17035; 650pp + Sequence Listing; English.
XX
The present invention provides a number of single exon nucleic acid
probes which are derived from genomic sequences expressed in the human
brain. They can be used to measure gene expression in brain cell samples,
which may enable the diagnosis and improved treatment of nervous system
diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
epilepsy and cancers. The present sequence is one of the probes of the
invention.
XX
SQ Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;

Query Match 7.2%; Score 220; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.8e-98;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 TTGGCGGGAATCGTGTGACAGTGTATCCAAAGTTAAGCTTTTCTGCAAGAAGCTAGGCTTGT 2889
```

```
Db 1 TTGGCGGGAATCGTGTGACAGTGTATCCAAAGTTAAGCTTTTCTGCAAGAAGCTAGGCTTGT 60
QY 2890 CTTAAGCAATTTAGTGTCTTGTGACCTTACTAAGAAATTTCTACCTGATCCAGCATTA 2949
Db 61 CTTAAGCAATTTAGTGTCTTGTGACCTTACTAAGAAATTTCTACCTGATCCAGCATTA 120
QY 2950 GTCCAGAAAACCTTAGCCAAAGTGTATCCAAAGTTAAGCTTTTCTGCAAGAAGCTAGGCTTGT 3009
Db 121 GTCCAGAAAACCTTAGCCAAAGTGTATCCAAAGTTAAGCTTTTCTGCAAGAAGCTAGGCTTGT 180
QY 3010 GGSTGSCAATTTGATGATGATGATCTCAGTGTATTATACAG 3049
Db 181 GGSTGSCAATTTGATGATGATGATCTCAGTGTATTATACAG 220

RESULT 30
AAK42828
ID AAK42828 standard; DNA; 220 BP.
XX
AC AAK42828;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 17385.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488900/53.
XX
Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human bone marrow -
XX
Example 4; SEQ ID NO: 17385; 658pp + Sequence Listing; English.
XX
The present invention provides a number of single exon nucleic acid
probes which are derived from genomic sequences expressed in the human
bone marrow. They can be used to measure gene expression in bone marrow
samples, which may enable the improved diagnosis and treatment of cancers
such as lymphoma, leukaemia and myeloma. The present sequence is one of
the probes of the invention.
XX
SQ Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;

Query Match 7.2%; Score 220; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.8e-98;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 TTGGCGGGAATCGTGTGACAGTGTATCCAAAGTTAAGCTTTTCTGCAAGAAGCTAGGCTTGT 2889
Db 1 TTGGCGGGAATCGTGTGACAGTGTATCCAAAGTTAAGCTTTTCTGCAAGAAGCTAGGCTTGT 60
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```
QY 2890 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 2949
|||||
Db 61 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 120

QY 2950 GTCAGAAAACCTTAGCCAAAGTGTATCCAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTT 3009
|||||
Db 121 GTCAGAAAACCTTAGCCAAAGTGTATCCAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTT 180

QY 3010 GGGTGGCAATTTTCATGATGATGATCTCAGTGTATTATACAG 3049
|||||
Db 181 GGGTGGCAATTTTCATGATGATGATCTCAGTGTATTATACAG 220

RESULT 31
AAI23590
ID AAI23590 standard; DNA: 220 BP.
XX
AC AAI23590;
XX
DT 12-OCT-2001 (first entry)
DE
XX Probe #13523 for gene expression analysis in human cervical cell sample.
XX Probe: human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX Homo sapiens.
XX
XX WO200157278-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US006070.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human cervical epithelial cells -
XX
XX Claim 25; SEQ ID No 13523; 487pp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
XX (SENP). The present sequence is one such probe. The SENPs are derived
XX from human HeLa cells. The SENPs can be used to produce a single exon
XX microarray, which can be used for measuring human gene expression in a
XX sample derived from human cervical epithelial cells. By measuring gene
XX expression, the probes are therefore useful in grading and/or staging
XX of diseases of the cervix, notably cervical cancer.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;
XX
XX Query Match 7.2%; Score 220; DB 22; Length 220;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-98;
XX Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 TTGGCGGGAAATCGTGTGACGACGTGATGGCTTGCCTTCATGGGTGATTGAGAAAT 2889
|||||
Db 1 TTGGCGGGAAATCGTGTGACGACGTGATGGCTTGCCTTCATGGGTGATTGAGAAAT 60
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```
QY 2890 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 2949
|||||
Db 61 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 120

QY 2950 GTCAGAAAACCTTAGCCAAAGTGTATCCAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTT 3009
|||||
Db 121 GTCAGAAAACCTTAGCCAAAGTGTATCCAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTT 180

QY 3010 GGGTGGCAATTTTCATGATGATGATCTCAGTGTATTATACAG 3049
|||||
Db 181 GGGTGGCAATTTTCATGATGATGATCTCAGTGTATTATACAG 220

RESULT 32
AAI48904
ID AAI48904 standard; DNA: 220 BP.
XX
AC AAI48904;
XX
DT 17-OCT-2001 (first entry)
DE
XX Probe #17590 used to measure gene expression in human placenta sample.
XX Probe: human; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX Homo sapiens.
XX
XX WO200157272-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00663.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488997/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
XX
XX Claim 25; SEQ ID No 17590; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
XX The present sequence is one such probe. The probes are useful for
XX producing a microarray for predicting, measuring and displaying gene
XX expression in samples derived from human placenta. The probes are useful
XX for antenatal diagnosis of human genetic disorders.
XX
XX Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;
XX
XX Query Match 7.2%; Score 220; DB 22; Length 220;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-98;
XX Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 TTGGCGGGAAATCGTGTGACGACGTGATGGCTTGCCTTCATGGGTGATTGAGAAAT 2889
|||||
Db 1 TTGGCGGGAAATCGTGTGACGACGTGATGGCTTGCCTTCATGGGTGATTGAGAAAT 60

QY 2890 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 2949
|||||
Db 61 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTA 120
```

```
QY 2950 CTCAGAAACTTAGCCAAAGTCTTATCCAAAGTTAACTTTTCGCAAGAGCTAGGCTTGT 3009
|||||
Db 121 CTCAGAAACTTAGCCAAAGTCTTATCCAAAGTTAACTTTTCGCAAGAGCTAGGCTTGT 180
|||||

QY 3010 GGGTGGCAATTGATGATGATGATCTCAGTCTTATTACAG 3049
|||||
Db 181 GGGTGGCAATTGATGATGATGATCTCAGTCTTATTACAG 220
|||||

RESULT 33
AAI09206
ID AAI09206 standard; DNA; 220 BP.
XX
AC AAI09206;
XX
XX
DT 09-OCT-2001 (first entry)
XX
XX
DE Probe #9197 used to measure gene expression in human breast sample.
XX
XX
KW Probe; human; breast disease; breast cancer; development disorder; ss;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200157270-A2.
XX
XX
PD 09-AUG-2001.
XX
XX
PF 29-JAN-2001; 2001WO-US00661.
XX
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
DR WPI; 2001-476286/51.
XX
XX
PT Novel single exon nucleic acid probe used to measuring gene expression
PT in a human breast -
XX
XX
PS Claim 25; SEQ ID No 9197; 322pp; English.
XX
XX
CC The present invention relates to novel single exon nucleic acid probes.
CC The present sequence is one such probe. The probes are useful for
CC measuring human gene expression in a human breast sample, where the probe
CC hybridises at high stringency to a nucleic acid expressed in the human
CC breast. The probes are useful for predicting, diagnosing, grading,
CC staging, monitoring and prognosing diseases of the human breast,
CC particularly those diseases with polygenic aetiology. The diseases
CC include: breast cancer, disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and
CC non-carcinoma tumours.
CC
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;
Query Match 7.2%; Score 220; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.8e-98;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 TTGGCGGGAATCGTGTGAGCAGTGATGGCTTCATCGGGGTATTGAGAAAT 2889
|||||
Db 1 TTGGCGGGAATCGTGTGAGCAGTGATGGCTTCATCGGGGTATTGAGAAAT 60
|||||
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```
QY 2890 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAATTTTACCTGATCCAGCAATTA 2949
|||||
Db 61 CTTAAGCAATTAGTGTGTTTTTGGACTTTAGTACTAAAGAATTTTACCTGATCCAGCAATTA 120
|||||

QY 2950 GTCAGAAACTTAGCCAAAGTCTTATCCAAAGTTAACTTTTCGCAAGAGCTAGGCTTGT 3009
|||||
Db 121 GTCAGAAACTTAGCCAAAGTCTTATCCAAAGTTAACTTTTCGCAAGAGCTAGGCTTGT 180
|||||

QY 3010 GGGTGGCAATTGATGATGATGATCTCAGTCTTATTACAG 3049
|||||
Db 181 GGGTGGCAATTGATGATGATGATCTCAGTCTTATTACAG 220
|||||

RESULT 34
ABS16884
ID ABS16884 standard; DNA; 220 BP.
XX
AC ABS16884;
XX
XX
DT 19-AUG-2002 (first entry)
XX
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 16875.
XX
XX
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200186003-A2.
XX
XX
PD 15-NOV-2001.
XX
XX
PF 30-JAN-2001; 2001WO-US00665.
XX
XX
PR 04-FEB-2000; 2000US-180312P.
PR 26-MAY-2000; 2000US-207456P.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
DR WPI; 2002-114183/15.
XX
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
XX
PS Claim 4; SEQ ID No 16875; 634pp; English.
XX
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of
CC probes; the novel set of probes which hybridise at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
```

CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a single exon
CC probe open reading frame of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pt_sequences.

XX Sequence 220 BP; 58 A; 32 C; 54 G; 76 T; 0 other;

Query Match 7.2%; Score 220; DB 24; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.8e-98;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2830 TTGGCGGAAATCGTGTGACGATGATGGCTTGCCTTCAATGGTGTATTGAGAAAT 2889
Db 1 TTGGCGGAAATCGTGTGACGATGATGGCTTGCCTTCAATGGTGTATTGAGAAAT 60
QY 2890 CTTAAGCAATAGCTTTTGGACTTTAGTACTAAGAAATTTCTACTGATCCAGCATTA 2949
Db 61 CTTAAGCAATAGCTTTTGGACTTTAGTACTAAGAAATTTCTACTGATCCAGCATTA 120
QY 2950 GTCAGAAAACCTTACCAAGTGTATCAAGTTAACTTTTCGCAAGAAGCTAGGCTTGT 3009
Db 121 GTCAGAAAACCTTACCAAGTGTATCAAGTTAACTTTTCGCAAGAAGCTAGGCTTGT 180
QY 3010 GGGTGGCAATTTGATGATGATGATCATCTCAGTGTATTACAG 3049
Db 181 GGGTGGCAATTTGATGATGATGATCTCAGTGTATTACAG 220

RESULT 35
ABK22768
ID ABK22768 standard; cDNA; 165 BP.

XX ABK22768;

DT 26-MAR-2002 (first entry)

XX Human cDNA encoding CLAN SAM.

XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; cancer; smooth muscle cell proliferation;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Crohn's disease; stroke;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.

OS Homo sapiens.
XX WO200190156-A2.
PN 29-NOV-2001.
XX 24-MAY-2001; 2001WO-US17158.
XX 24-MAY-2000; 2000US-0579240.
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275980P.
PR 23-MAY-2001; 2001US-0864921.
XX (BURN-) BURNHAM INST.
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX WPI; 2002-083086/11.
DR P-PSDB; AAU0874.
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
arthritis or stroke -
XX Claim 1; Page 204; 216pp; English.
XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host diseases, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC cDNA encoding a CARD domain containing protein.
XX Sequence 165 BP; 51 A; 37 C; 38 G; 39 T; 0 other;
Query Match 3.7%; Score 114; DB 24; Length 165;
Best Local Similarity 99.4%; Pred. No. 7.3e-46;
Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1924 ACCTACATCCCGAGCGGCTGTATCTTTCTTCAACTGGAGCAGGATTCAGGACT 1983
Db 1 ACCTACATCCCGAGCGGCTGTATCTTTCTTCAACTGGAGCAGGATTCAGGACT 60
QY 1984 CTGGAGGTACACTCCCGGAGTTTCAGCAAGTTGAATAAGCAAGATATACATATCTCTGGG 2043
Db 61 CTGGAGGTACACTCCCGGAGTTTCAGCAAGTTGAATAAGCAAGATATACATATCTCTGGG 120
QY 2044 AAAATATTAGCTCTCCCAAGCCCTCAGGCTGCAATAAAGAGA 2088
Db 121 AAAATATTAGCTCTCCCAAGCCCTCAGGCTGCAATAAAGAGA 165
RESULT 36
ABN40447
ID ABN40447 standard; DNA; 60 BP.
XX ABN40447;
XX


```

XX 15-JUL-2002 (first entry)
XX Human spliced transcript detection oligonucleotide SEQ ID NO:13195.
DE Human; mouse; rat; splice transcript: detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss..
XX Homo sapiens.
OS WO200210449-A2.
PN WO200210449-A2.
XX
XX 07-FEB-2002.
PD
XX
XX 20-JUL-2001; 2001WO-IB01903.
PF
XX
XX 28-JUL-2000; 2000US-221607P.
PR
XX 02-MAY-2001; 2001US-287724P.
PR
XX (COMP-) COMPUGEN INC.
PA
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes.
XX
PS Example 1; SEQ ID 13195; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, and was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 12 A; 7 C; 22 G; 19 T; 0 other;

Query Match 2.0%; Score 60; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.5e-19;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2828 ATTTGGCGGGAATCGTGTGAGCACTGATGGATGCTTGCCTTCATGGTGTATTGTAGA 2887
Db 1 ATTTGGCGGGAATCGTGTGAGCACTGATGGATGCTTGCCTTCATGGTGTATTGTAGA 60

RESULT 37
ABK22753/c
ID ABK22753 standard; DNA; 29 BP.
XX
AC ABK22753;

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XX 26-MAR-2002 (first entry)
XX Human CLAN A PCR primer #2.
DE
XX
XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
XX
XX Homo sapiens.
OS
XX WO200190156-A2.
PN
XX
XX 29-NOV-2001.
PD
XX
XX 24-MAY-2001; 2001WO-US17158.
PF
XX
XX 24-MAY-2000; 2000US-0579240.
PR
XX 10-OCT-2000; 2000US-0686347.
PR
XX 14-MAR-2001; 2001US-275980P.
PR
XX 23-MAY-2001; 2001US-0864921.
PR
XX (BURN-) BURNHAM INST.
PA
XX
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX WPI; 2002-083086/11.
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke.
XX
XX Example 10; Page 115; 216pp; English.
PS
XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC PCR primer used to amplify a nucleic acid encoding a CARD-containing
CC protein.
XX
XX Sequence 29 BP; 8 A; 8 C; 8 G; 5 T; 0 other;

Query Match 0.9%; Score 29; DB 24; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 TGACTTCATTCGGAGCCCTGGACCCTGTG 1180
|||||

```

Db 29 TGACTTCATTCGGAGCCTGGACCACTGTG 1

RESULT 38
ABK22754

ID ABK22754 standard; DNA; 25 BP.

XX AC ABK22754;

XX DT 26-MAR-2002 (first entry)

XX DE Human CLAN B PCR primer #1.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
XX human immunodeficiency virus infection.

XX OS Homo sapiens.

XX PN W0200190156-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US17158.

XX PR 24-MAY-2000; 2000US-0579240.

XX PR 10-OCT-2000; 2000US-0686347.

XX PR 14-MAR-2001; 2001US-275980P.

XX PR 23-MAY-2001; 2001US-0864921.

XX PA (BURN-) BURNHAM INST.

XX PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;

XX WPI; 2002-083086/11.

XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -

XX Example 10; Page 115; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC a graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC PCR primer used to amplify a nucleic acid encoding a CARD-containing
XX protein.

SQ Sequence 25 BP; 6 A; 4 C; 9 G; 6 T; 0 other;

Query Match 0.88; Score 25; DB 24; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 CATCATTTGCTGGAGAGGTGGAG 141
|||||
DB 1 CATCATTTGCTGGAGAGGTGGAG 25

RESULT 39
ABK22755/c

ID ABK22755 standard; DNA; 25 BP.

XX AC ABK22755;

XX DT 26-MAR-2002 (first entry)

XX DE Human CLAN B PCR primer #2.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
XX human immunodeficiency virus infection.

XX OS Homo sapiens.

XX PN W0200190156-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US17158.

XX PR 24-MAY-2000; 2000US-0579240.

XX PR 10-OCT-2000; 2000US-0686347.

XX PR 14-MAR-2001; 2001US-275980P.

XX PR 23-MAY-2001; 2001US-0864921.

XX PA (BURN-) BURNHAM INST.

XX PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;

XX WPI; 2002-083086/11.

XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -

XX Example 10; Page 115; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC a graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC PCR primer used to amplify a nucleic acid encoding a CARD-containing
XX protein.

CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
 CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
 CC disease) or immunodeficiency associated disease (e.g. human
 CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
 CC in a variety of diagnostic applications. The present sequence is a
 CC PCR primer used to amplify a nucleic acid encoding a CARD-containing
 CC protein.
 XX
 SQ Sequence 25 BP; 8 A; 4 C; 5 G; 8 T; 0 other;
 Query Match 0.8%; Score 25; DB 24; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2959 CTTAGCCAAAGTGTATCCCAAGTTAA 2983
 Db 25 CTTAGCCAAAGTGTATCCCAAGTTAA 1
 RESULT 40
 ABK22758
 ID ABK22758 standard; DNA; 25 BP.
 XX
 AC ABK22758;
 XX
 DT 26-MAR-2002 (first entry)
 DE Human CLAN D PCR primer #1.
 XX
 KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
 KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;
 KW myocardial infarction; heart failure; neurodegenerative disease;
 KW Parkinson's disease; Alzheimer's disease; HIV;
 KW human immunodeficiency virus infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200190156-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 24-MAY-2001; 2001WO-US17158.
 XX
 PR 24-MAY-2000; 2000US-0579240.
 PR 10-OCT-2000; 2000US-0686347.
 PR 14-MAR-2001; 2001US-275980P.
 PR 23-MAY-2001; 2001US-0864921.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
 PI Oliveira VAM, Hayashi H, Pawlowski K;
 XX
 DR WPI; 2002-083086/11.
 XX
 PT New caspase recruitment domain (CARD)-containing polypeptides and
 PT encoding nucleic acids, useful for treating abnormal cell proliferation
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
 PT arthritis or stroke -
 XX
 PS Example 10; Page 116; 216pp; English.
 XX
 CC The invention relates to an isolated caspase recruitment domain (CARD)
 CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
 CC from it, and the polynucleotides encoding them. Also included are a
 CC recombinant vector comprising the polynucleotide, recombinant cells
 CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
 CC and insect cells) and an anti-CARD antibody. The CARD-containing

CC polypeptide and CARD-encoding nucleic acid are useful for treating a
 CC pathology characterised by abnormal cell proliferation (e.g. cancer),
 CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
 CC particular, the polypeptide and nucleic acid are useful for treating
 CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
 CC muscle cell proliferation in arteries following balloon angioplasty
 CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
 CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
 CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
 CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
 CC disease) or immunodeficiency associated disease (e.g. human
 CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
 CC in a variety of diagnostic applications. The present sequence is a
 CC PCR primer used to amplify a nucleic acid encoding a CARD-containing
 CC protein.
 XX
 SQ Sequence 25 BP; 11 A; 4 C; 5 G; 5 T; 0 other;
 Query Match 0.8%; Score 25; DB 24; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 AATTTTCATAAAGGACAAATAGCGGAG 28
 Db 1 AATTTTCATAAAGGACAAATAGCGGAG 25
 RESULT 41
 ABK22752
 ID ABK22752 standard; DNA; 24 BP.
 XX
 AC ABK22752;
 XX
 DT 26-MAR-2002 (first entry)
 DE Human CLAN A PCR primer #1.
 XX
 KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
 KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;
 KW myocardial infarction; heart failure; neurodegenerative disease;
 KW Parkinson's disease; Alzheimer's disease; HIV;
 KW human immunodeficiency virus infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200190156-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 24-MAY-2001; 2001WO-US17158.
 XX
 PR 24-MAY-2000; 2000US-0579240.
 PR 10-OCT-2000; 2000US-0686347.
 PR 14-MAR-2001; 2001US-275980P.
 PR 23-MAY-2001; 2001US-0864921.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
 PI Oliveira VAM, Hayashi H, Pawlowski K;
 XX
 DR WPI; 2002-083086/11.
 XX
 PT New caspase recruitment domain (CARD)-containing polypeptides and
 PT encoding nucleic acids, useful for treating abnormal cell proliferation
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
 PT arthritis or stroke -
 XX

PS Example 10; Page 115; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)
 CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
 CC from it, and the polynucleotides encoding them. Also included are a
 CC recombinant vector comprising the polynucleotide, recombinant cells
 CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
 CC and insect cells) and an anti-CARD antibody. The CARD-containing
 CC polypeptide and CARD-encoding nucleic acid are useful for treating a
 CC pathology characterised by abnormal cell proliferation (e.g. cancer),
 CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
 CC particular, the polypeptide and nucleic acid are useful for treating
 CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
 CC muscle cell proliferation in arteries following balloon angioplasty
 CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
 CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
 CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
 CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
 CC disease) or immunodeficiency associated disease (e.g. human
 CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
 CC in a variety of diagnostic applications. The present sequence is a
 CC PCR primer used to amplify a nucleic acid encoding a CARD-containing
 CC protein.

XX SQ Sequence 24 BP; 5 A; 3 C; 12 G; 4 T; 0 other;

Query Match 0.8%; Score 24; DB 24; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.32;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 135 GGTGAGCAGGATGCTGTAGAGG 158
 |||||

Db 1 GGTGAGCAGGATGCTGTAGAGG 24

RESULT 42

ABK22750

ID ABK22750 standard; DNA; 33 BP.

XX AC ABK22750;

XX DT 26-MAR-2002 (first entry)

XX DE Human CLAN CARD domain PCR primer #1.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
 KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;
 KW myocardial infarction; heart failure; neurodegenerative disease;
 KW Parkinson's disease; Alzheimer's disease; HIV;
 KW human immunodeficiency virus infection.

XX OS Homo sapiens.

XX PN WO200190156-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US17158.

XX PR 24-MAY-2000; 2000US-0579240.
 10-OCT-2000; 2000US-0686347.
 14-MAR-2001; 2001US-275980P.
 23-MAY-2001; 2001US-0864921.

XX (BURN-) BURNHAM INST.

XX PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
 PI Oliveira VAM, Hayashi H, Pawlowski K;

XX WPI; 2002-083086/11.

XX New caspase recruitment domain (CARD)-containing polypeptides and
 PT encoding nucleic acids, useful for treating abnormal cell proliferation
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
 PT arthritis or stroke

XX Example 10; Page 117; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)
 CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
 CC from it, and the polynucleotides encoding them. Also included are a
 CC recombinant vector comprising the polynucleotide, recombinant cells
 CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
 CC and insect cells) and an anti-CARD antibody. The CARD-containing
 CC polypeptide and CARD-encoding nucleic acid are useful for treating a
 CC pathology characterised by abnormal cell proliferation (e.g. cancer),
 CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
 CC particular, the polypeptide and nucleic acid are useful for treating
 CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
 CC muscle cell proliferation in arteries following balloon angioplasty
 CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
 CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
 CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
 CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
 CC disease) or immunodeficiency associated disease (e.g. human
 CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
 CC in a variety of diagnostic applications. The present sequence is a
 CC PCR primer used to amplify a nucleic acid encoding a CARD-containing
 CC protein.

XX SQ Sequence 33 BP; 12 A; 8 C; 6 G; 7 T; 0 other;

Query Match 0.8%; Score 24; DB 24; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATTCATTAAGGACAATAGC 24
 |||||

Db 10 ATGAATTCATTAAGGACAATAGC 33

RESULT 43

ABK22746/C

ID ABK22746 standard; DNA; 23 BP.

XX AC ABK22746;

XX DT 26-MAR-2002 (first entry)

XX DE Human CLAN CDNA PCR primer #1.

XX KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
 KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;
 KW myocardial infarction; heart failure; neurodegenerative disease;
 KW Parkinson's disease; Alzheimer's disease; HIV;
 KW human immunodeficiency virus infection.

XX OS Homo sapiens.

XX PN WO200190156-A2.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-US17158.

XX PR 24-MAY-2000; 2000US-0579240.

```
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275980P.
PR 23-MAY-2001; 2001US-0864921.
XX
XX (BURN-) BURNHAM INST.
XX
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX
XX WPI; 2002-083086/11.
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -
XX
XX Example 10; Page 111; 216pp; English.
XX
XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC PCR primer used to amplify a nucleic acid encoding a CARD-containing
CC protein.
XX
XX Sequence 23 BP; 6 A; 6 C; 5 G; 6 T; 0 other;
SQ
Query Match 0.7%; Score 23; DB 24; Length 23;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 149 CTGCTAGAGGGATCATTCACATG 171
Db 23 CTGCTAGAGGGATCATTCACATG 1
RESULT 44
ABK22756
ID ABK22756 standard; DNA; 23 BP.
XX
XX ABK22756;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human CLAN C PCR primer #1.
XX
XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke; PCR primer;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
XX
XX Homo sapiens.
```

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XX WO200190156-A2.
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US17158.
XX
XX 24-MAY-2000; 2000US-0579240.
PR 10-OCT-2000; 2000US-0686347.
PR 14-MAR-2001; 2001US-275980P.
PR 23-MAY-2001; 2001US-0864921.
XX
XX (BURN-) BURNHAM INST.
XX
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VAM, Hayashi H, Pawlowski K;
XX
XX WPI; 2002-083086/11.
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke -
XX
XX Example 10; Page 115; 216pp; English.
XX
XX The invention relates to an isolated caspase recruitment domain (CARD)
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
CC from it, and the polynucleotides encoding them. Also included are a
CC recombinant vector comprising the polynucleotide, recombinant cells
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
CC and insect cells) and an anti-CARD antibody. The CARD-containing
CC polypeptide and CARD-encoding nucleic acid are useful for treating a
CC pathology characterised by abnormal cell proliferation (e.g. cancer),
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
CC particular, the polypeptide and nucleic acid are useful for treating
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following balloon angioplasty
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
CC disease) or immunodeficiency associated disease (e.g. human
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful
CC in a variety of diagnostic applications. The present sequence is a
CC PCR primer used to amplify a nucleic acid encoding a CARD-containing
CC protein.
XX
XX Sequence 23 BP; 8 A; 4 C; 5 G; 6 T; 0 other;
SQ
Query Match 0.7%; Score 23; DB 24; Length 23;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 112 GTAAACATCATTTGCTGCGAGAA 134
Db 1 GTAAACATCATTTGCTGCGAGAA 23
RESULT 45
ABK22749
ID ABK22749 standard; DNA; 21 BP.
XX
XX ABK22749;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human CLAN cDNA PCR primer #4.
XX
XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
KW autoimmune disease; inflammation; keratinocyte hyperplasia;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
```



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RESULT 47
AAS95269
ID AAS95269 standard; DNA; 7067 BP.
XX
AC AAS95269;
XX
DT 14-FEB-2002 (first entry)
XX
DE Long terminal repeat (LTR) retrotransposon #20.
XX
KW Long terminal repeat transposon; LTR retrotransposon; ss; integrase;
KW transposable element; integration factor; POL region; pCal;
KW gene disruption system.
XX
OS Candida albicans.
XX
PN WO200181598-A2.
XX
PD 01-NOV-2001.
XX
PF 25-APR-2001; 2001WO-EP04649.
XX
PR 26-APR-2000; 2000WO-IB00729.
XX
PA (JANC ) JANSSEN PHARM NV.
XX
PI Nelissen BJM, De Backer MD, Luyten WHM;
XX
WPI; 2002-041412/05.
XX
XX
XX Novel long terminal repeat retrotransposon isolated from Candida
PT albicans, useful for introducing DNA into genome of a cell and to
PT assign a function to the nucleic acid sequence -
XX
XX Claim 1; Fig 7; 119pp; English.
XX
XX The invention relates to long terminal repeat (LTR) retrotransposons
CC isolated from Candida albicans. LTR retrotransposons are useful for
CC introducing DNA into the genome of a cell, which involves introducing a
CC transposable element comprising a nucleotide sequence encoding a desired
CC protein, located between LTR sequences. The element can insert into the
CC genome of the cell in the presence of an appropriate integration factor.
CC The integration factor comprises an integrase which preferably is itself
CC included in the transposable element, the integrase being derived from
CC the POL region of the pCal retrotransposon. This is useful for assigning
CC a function to a nucleotide sequence which involves inserting the sequence
CC between the long term repeats, introducing the element into the cell and
CC monitoring it for the presence of an altered phenotype of the cell. The
CC method is useful in a gene disruption system or a gene discovery system.
CC Sequences AAS95250-AAS95310 represent LTR retrotransposons of the
CC invention.
XX
SQ Sequence 7067 BP; 2540 A; 1197 C; 1057 G; 2273 T; 0 other;
Query Match 0.7%; Score 21; DB 24; Length 7067;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2002 GATTCAGCAAGTTGAATAAG 2022
|||||
Db 4763 GATTCAGCAAGTTGAATAAG 4783
RESULT 48
ABV46663
ID ABV46663 standard; cDNA; 431 BP.
XX
AC ABV46663;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 46654.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 9200-9201; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 431 BP; 141 A; 80 C; 89 G; 121 T; 0 other;
Query Match 0.7%; Score 20; DB 23; Length 431;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 317 AGGACTGTGACCATACCCCA 336
|||||
Db 243 AGGACTGTGACCATACCCCA 262
RESULT 49
ABK78972
ID ABK78972 standard; DNA; 475 BP.
XX
AC ABK78972;
XX
DT 13-AUG-2002 (first entry)
XX
DE Bacillus clausii genomic sequence tag (GST) #1815.
XX
KW Differential gene expression; genomic sequenced tag; GST;
KW altered culture condition; environmental stress;
KW physiological provocation; ds.
XX
```


OS Bacillus clausii.
XX WO200229113-A2.
XX 11-APR-2002.
XX 05-OCT-2001; 2001WO-US311437.
XX 06-OCT-2000; 2000US-0680598.
XX 27-MAR-2001; 2001US-279526P.
XX (NOVO) NOVOZYMES BIOTECH INC.
XX (NOVO) NOVOZYMES AS.
XX Berka R, Clausen IG;
XX WPI; 2002-416684/44.
XX
XX Monitoring differential expression of several genes in first Bacillus
XX cell relative to expression of same genes in one or more second
XX Bacillus cells, by using substrate containing Bacillus genomic
XX sequenced tag array -
XX
XX Claim 11; SEQ ID NO 6263; 200pp; English.
XX
XX The invention describes a method of monitoring differential expression of
XX genes in a first Bacillus cell relative to expression of the genes in
XX other Bacillus cells, comprising hybridising labelled nucleic acid probes
XX isolated from Bacillus cells to a substrate containing array of Bacillus
XX genomic sequenced tags (GST), examining the array, and determining
XX relative gene expression by an observed hybridisation reporter signal of
XX a spot in the array. The method is useful for measuring the expression of
XX genes in a first Bacillus cell relative to expression of the same genes
XX in one or more second Bacillus cells. The method is useful for monitoring
XX global expression of several genes from a Bacillus cell, discovering new
XX genes, identifying possible functions of unknown open reading frames and
XX monitoring gene copy number variation and stability. Monitoring changes
XX in expression of genes may be used to provide a representation of the way
XX in which Bacillus cells adapt to changes in culture conditions,
XX environmental stress or other physiological provocation. Extensive
XX follow-up characterisation is unnecessary, when one spot on an array
XX equals one gene or one open reading frame, since sequence information is
XX available. This sequence represents a genomic sequence tag (GST) used in
XX the method of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 475 BP; 132 A; 110 C; 144 G; 89 T; 0 other;
XX
XX Query Match 0.7%; Score 20; DB 24; Length 475;
XX Best Local Similarity 100.0%; Pred. No. 35;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1881 TGCAGAGACACAGGTCGAA 1900
XX |||||||||||||||||||
XX 378 TGCAGAGACACAGGTCGAA 397
XX
XX RESULT 50
XX ABK22734/c
XX ID ABK22734 standard; cDNA; 768 BP.
XX
XX AC ABK22734;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human cDNA encoding CLAN D.
XX
XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;
XX abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
XX autoimmune disease; inflammation; keratinocyte hyperplasia;

KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
KW Crohn's disease; graft-versus-host disease; stroke;
KW myocardial infarction; heart failure; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; HIV;
KW human immunodeficiency virus infection.
XX
XX Homo sapiens.
XX
XX WO200190156-A2.
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US17158.
XX
XX 24-MAY-2000; 2000US-0579240.
XX 10-OCT-2000; 2000US-0686347.
XX 14-MAR-2001; 2001US-275980P.
XX 23-MAY-2001; 2001US-0864921.
XX
XX (BURN-) BURNHAM INST.
XX
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
XX Oliveira VAM, Hayashi H, Pawlowski K;
XX
XX WPI; 2002-083086/11.
XX p-PSDB; AAU80864.
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
XX encoding nucleic acids, useful for treating abnormal cell proliferation
XX or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
XX arthritis or stroke -
XX
XX Claim 1; Page 178-179; 216pp; English.
XX
XX The invention relates to an isolated caspase recruitment domain (CARD)
XX -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
XX from it, and the polynucleotides encoding them. Also included are a
XX recombinant vector comprising the polynucleotide, recombinant cells
XX containing the vector (e.g. bacteria, yeast, plant, animal, mammalian
XX and insect cells) and an anti-CARD antibody. The CARD-containing
XX polypeptide and CARD-encoding nucleic acid are useful for treating a
XX pathology characterised by abnormal cell proliferation (e.g. cancer),
XX abnormal cell death (apoptosis), autoimmune diseases or inflammation. In
XX particular, the polypeptide and nucleic acid are useful for treating
XX keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth
XX muscle cell proliferation in arteries following balloon angioplasty
XX (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,
XX allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,
XX graft-versus-host disease, stroke, myocardial infarction, heart failure,
XX neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's
XX disease) or immunodeficiency associated disease (e.g. human
XX immunodeficiency virus (HIV) infection). The nucleic acids are useful
XX in a variety of diagnostic applications. The present sequence is a
XX cDNA encoding a CARD domain containing protein.
XX
XX Sequence 768 BP; 218 A; 157 C; 180 G; 213 T; 0 other;
XX

Query Match 0.7%; Score 20; DB 24; Length 768;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2331 AGAAGATGCTATAAACTAG 2350

Db 755 AGAAGATGCTATAAACTAG 736

Search completed: January 30, 2003, 23:02:21
Job time : 680 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 22:45:05 ; Search time 4070 Seconds
(without alignments)
12224.210 Million cell updates/sec

Title: US-09-697-089-3
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 12

Total number of hits satisfying chosen parameters: 4061249

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

Database :

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- 1: em_estba:*
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- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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c 2	446	14	5	480	10 AV719179
c 3	342	11	1	364	9 A1263294
c 4	315	10	3	748	13 B1908869
5	291	9	5	371	10 AV656315
6	289	9	4	741	13 B1824482

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5	291	9	5	371	10 AV656315
6	289	9	4	741	13 B1824482

c 7	223	7	3	261	10 AW337918
c 8	170	5	5	553	17 AQ320928
c 9	168	5	5	476	12 BG210375
c 10	146	4	8	630	17 AQ112439
c 11	136	4	5	509	10 AW418826
c 12	106	3	5	470	17 AQ624020
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c 68	20	0	7	521	17 F80031506
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c 79	20	0	7	577	12 BG385206

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BG210375 RST29913
AQ112439 CIT-HSP-2
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H25984 Y15607.r1
AI023795 ox08003.x
AQ283886 RPT11-78
B58691 CIT-HSP-201
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BH293386 CH230-44G
BF903662 IL2-MT018
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BF829853 MR3-HN005
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BQ204082 UI-R-DN1-
BQ894786 AGENCOURT
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AZ740007 RPT1-24-1
BH861125 SALK_0343
AZ086396 RPT1-23-2
AA784099 d1g08a1.f
AA821339 VS68a01.r
A1645009 VS68a01.y
AZ223093 RPT1-23-9
AQ555443 HS-5224_A
AI08892 Arab1dops
AZ360053 IM0103H11
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BT854236 603381263
BQ278245 AGENCOURT
BG571228 602592168
B1142462 SMOV3MCA8
BE638399 SMOVL2CAS
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BT315256 dal96e06.
AA493806 nh02f04.s
AI366637 SMOV3MCA8
AI603832 SMOV3MCA8
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AQ357412 40862 MAR
AQ952434 Sheared D
AA670222 ad19h11.s
AZ991565 2M0275B24
AA294641 SMOV3MCA8
AW838955 CM2-LT006
AA294540 SMOV3MCA7
T81898 YQ29a11.s1
AA294143 SMOV3MCA1
B1714609 B1714609
AQ209355 HS-3240_A
AQ209355 HS-3240_A
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AI643174 v946909.y
BF602580 267845 MA
BG382487 298398 MA
AI670486 SMOV3MCA8
AL027875 Fuqu rubr
B1394563 p9pln.pk0
BG351255 088b06 Ma
AZ221490 Gm_UMB001
BQ117309 EST602885
AZ298434 RPT1-23-1
BH386778 AG-ND-146
AQ270247 HS-2045_A
B1059717 BJ059717
B1070137 BJ070137
BF258009 HVSMEF001
BG385206 306845 MA

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c 83	20	0.7	605	12	BG098273	EST462792	156	19	0.6	435	10	AW002562	AW002562
84	20	0.7	605	13	BI537740	427953_MA	157	19	0.6	440	9	AI354218	AI354218
85	20	0.7	606	9	AL675250	AL675250	158	19	0.6	443	17	AQ646808	AQ646808
86	20	0.7	620	17	AZ802117	2M0061H04	c 159	19	0.6	444	17	AQ627994	AQ627994
87	20	0.7	627	9	AI511575	SWOV13CAN	c 160	19	0.6	447	10	BE504198	BE504198
88	20	0.7	633	17	AZ510047	IM0354H14	c 161	19	0.6	448	10	BE348517	BE348517
89	20	0.7	633	17	BH769908	BMBAC368E	c 162	19	0.6	450	10	BE671155	BE671155
90	20	0.7	642	9	AL678336	AL678336	c 163	19	0.6	457	17	AZ862909	AZ862909
91	20	0.7	644	10	AW874886	SWOVmFCAR	c 164	19	0.6	459	17	AQ469016	AQ469016
92	20	0.7	651	13	BI627371	RH86662.5	c 165	19	0.6	461	17	AZ293884	AZ293884
93	20	0.7	652	10	BE346038	SWOVL2CAS	c 166	19	0.6	462	10	AW176753	AW176753
94	20	0.7	653	9	AI317901	SWOV3MCMAM	c 167	19	0.6	463	10	BB698639	BB698639
95	20	0.7	656	10	BE636495	SWOVL2CAS	c 168	19	0.6	479	14	HI8652	HI8652
96	20	0.7	660	12	BG310513	SWOV3MCMAM	c 169	19	0.6	483	9	AI988626	AI988626
97	20	0.7	677	17	BH794115	ME_MBA000	c 170	19	0.6	487	13	BJ431712	BJ431712
98	20	0.7	701	13	BJ004970	BJ004970	c 171	19	0.6	490	17	AZ799198	AZ799198
c 99	20	0.7	726	17	AL186746	Tetraodon	c 172	19	0.6	493	17	FR0022665	FR0022665
c 100	20	0.7	729	17	B65395	CIT-HSP-202	c 173	19	0.6	494	10	AW174122	AW174122
c 101	20	0.7	731	12	BG250425	602362580	c 174	19	0.6	495	17	AZ857381	AZ857381
c 102	20	0.7	738	14	BM970986	UI-CP-EC1	c 175	19	0.6	500	9	AI319748	AI319748
c 103	20	0.7	742	17	AQ083585	Fan trogl	c 176	19	0.6	504	17	AZ650454	AZ650454
c 104	20	0.7	754	17	AQ329189	AQ329189 nbxb0044F	c 177	19	0.6	504	17	BH308171	BH308171
c 105	20	0.7	760	9	AI591096	tw91b09.x	c 178	19	0.6	505	9	AA956941	AA956941
c 106	20	0.7	760	13	BI918884	603180941	c 179	19	0.6	509	12	BF053859	BF053859
c 107	20	0.7	770	17	BH425589	BH425589 BOHJG60TF	c 180	19	0.6	510	17	AZ159794	AZ159794
c 108	20	0.7	772	12	BG310534	SWOV3MCMAM	c 181	19	0.6	513	10	AW385224	AW385224
c 109	20	0.7	779	12	BG350988	099C11_Ma	c 182	19	0.6	514	9	AI325989	AI325989
c 110	20	0.7	783	13	BI184833	SNL-P-FN-	c 183	19	0.6	520	17	B27212	B27212
c 111	20	0.7	784	12	BF824698	SWOV3MCMAM	c 184	19	0.6	520	9	AI716507	AI716507
c 112	20	0.7	838	17	BH665093	BOMDY48TF	c 185	19	0.6	520	17	AQ658864	AQ658864
c 113	20	0.7	871	14	BO736366	AGENCOURT	c 186	19	0.6	524	17	TA156807Q	TA156807Q
c 114	20	0.7	891	12	BG248945	602361385	c 187	19	0.6	525	10	AV836178	AV836178
c 115	20	0.7	937	17	CNS02507	Tetraodon	c 188	19	0.6	526	17	AZ219239	AZ219239
c 116	20	0.7	939	17	CNS02105	Tetraodon	c 189	19	0.6	529	17	AZ376550	AZ376550
c 117	20	0.7	1036	12	BM176063	602335289	c 190	19	0.6	531	10	BB175339	BB175339
c 118	20	0.7	1122	13	BM547558	AGENCOURT	c 191	19	0.6	532	9	AL730404	AL730404
c 119	20	0.7	1396	12	BG254706	602368693	c 192	19	0.6	535	17	FR0022682	FR0022682
c 120	19	0.6	207	10	AV365606	AV365606	c 193	19	0.6	538	10	AW659621	AW659621
c 121	19	0.6	209	9	AV144358	AV144358	c 194	19	0.6	539	14	BQ143315	BQ143315
c 122	19	0.6	238	10	AV371617	AV371617	c 195	19	0.6	543	10	AV605051	AV605051
c 123	19	0.6	254	14	BQ332700	RC6-ET006	c 196	19	0.6	544	12	BE666200	BE666200
c 124	19	0.6	256	9	AI340263	qx86g01.x	c 197	19	0.6	547	10	BE899936	BE899936
c 125	19	0.6	272	12	BG381720	UI-R-CTO-	c 198	19	0.6	548	9	AI399038	AI399038
c 126	19	0.6	283	9	AV048726	AV048726	c 199	19	0.6	548	10	BB644885	BB644885
c 127	19	0.6	296	13	BJ428394	BJ428394	c 200	19	0.6	548	12	BF286023	BF286023
c 128	19	0.6	299	14	BQ509473	BQ509473	c 201	19	0.6	549	9	AI0152272	AI0152272
c 129	19	0.6	304	17	AQ094693	AQ094693	c 202	19	0.6	557	17	AQ962795	AQ962795
c 130	19	0.6	314	17	B62990	CIT-HSP-714	c 203	19	0.6	562	14	BQ561096	BQ561096
c 131	19	0.6	322	10	BB318669	BB318669	c 204	19	0.6	570	14	BQ836529	BQ836529
c 132	19	0.6	334	17	AQ285454	RPC111-90	c 205	19	0.6	571	14	BQ557338	BQ557338
c 133	19	0.6	350	14	BQ023747	UI-1-BB1p	c 206	19	0.6	572	10	BE686715	BE686715
c 134	19	0.6	351	17	AZ748488	RPC1-24-1	c 207	19	0.6	573	13	BI706154	BI706154
c 135	19	0.6	353	10	AW356070	38057_MAR	c 208	19	0.6	576	13	BI807257	BI807257
c 136	19	0.6	355	14	H88536	YW29g02.sl	c 209	19	0.6	579	17	BH311536	BH311536
c 137	19	0.6	360	17	AQ039398	CIT-HSP-2	c 210	19	0.6	580	17	AZ375867	AZ375867
c 138	19	0.6	362	10	AW435221	UI-R-BJOp	c 211	19	0.6	582	13	BJ341772	BJ341772
c 139	19	0.6	368	17	AQ663225	HS_5463_B	c 212	19	0.6	588	13	BJ340962	BJ340962
c 140	19	0.6	369	9	AI082708	ox59f01.s	c 213	19	0.6	591	13	BJ341826	BJ341826
c 141	19	0.6	380	14	BQ909451	BQ909451	c 214	19	0.6	592	12	BG512024	BG512024
c 142	19	0.6	382	10	AW233739	f41c01.x	c 215	19	0.6	593	10	BE515396	BE515396
c 143	19	0.6	383	14	N59369	yz87e09.sl	c 216	19	0.6	598	13	BJ527326	BJ527326
c 144	19	0.6	394	9	AO581174	AO581174	c 217	19	0.6	602	17	AQ435526	AQ435526
c 145	19	0.6	395	14	H83224	mf23q01.r1	c 218	19	0.6	604	9	AA990951	AA990951
c 146	19	0.6	397	14	H05527	yl70f08.sl	c 219	19	0.6	605	17	FR0030367	FR0030367
c 147	19	0.6	403	9	AI239575	qf37a01.x	c 220	19	0.6	606	13	BJ436302	BJ436302
c 148	19	0.6	405	17	AO645771	RPC193-EC	c 221	19	0.6	609	17	BF519289	BF519289
c 149	19	0.6	420	9	AI214067	ap29e06.x	c 222	19	0.6	612	12	BE882860	BE882860
c 150	19	0.6	422	14	R44768	Yg23a04.sl	c 223	19	0.6	604	12	BE882860	BE882860
c 151	19	0.6	423	10	AW104704	xd44f06.x	c 224	19	0.6	605	17	FR0030366	FR0030366
c 152	19	0.6	423	14	H03699	yJ42e12.sl	c 225	19	0.6	606	13	BJ436302	BJ436302

c 226	19	0.6	614	14	BM890031	BM890031 fy64b04.y	299	19	0.6	896	17	BM135630	BM135630
c 227	19	0.6	615	13	BQ372342	BQ372342	c 300	19	0.6	898	17	AN935650	AN935650 ODG148 O1
c 228	19	0.6	616	17	AQ473825	AQ473825 CITBI-E1-	c 301	19	0.6	906	17	AL301591	AL301591 Tetraodon
c 229	19	0.6	619	17	BH267158	BH267158 CH230-19B	c 302	19	0.6	909	14	BQ922514	BQ922514 AGENCOURT
c 230	19	0.6	621	17	AZ216149	AZ216149 Sheared D	c 303	19	0.6	929	17	CNS03RWG	AL257785 Tetraodon
c 231	19	0.6	625	10	BB626089	BB626089	c 304	19	0.6	937	17	BH151493	BH151493 ENTQD75TF
c 232	19	0.6	628	17	AZ213893	AZ213893 Sheared D	c 305	19	0.6	956	12	BF233114	BF233114 602023855
c 233	19	0.6	628	14	BQ625451	BQ625451 rdl5b11.y	c 306	19	0.6	962	14	BQ876117	BQ876117 AGENCOURT
c 234	19	0.6	629	13	BM120821	BM120821 L0944E07-	c 307	19	0.6	967	14	BQ226680	BQ226680 AGENCOURT
c 235	19	0.6	631	17	AZ941662	AZ941662 2M0201E02	c 308	19	0.6	982	14	BQ434528	BQ434528 AGENCOURT
c 236	19	0.6	641	10	BB604577	BB604577	c 309	19	0.6	1032	17	CNS03313	AL226164 Tetraodon
c 237	19	0.6	641	17	BE41128	BE41128 CIT-HSP-202	c 310	19	0.6	1051	12	BE274184	BE274184 GA_EB002
c 238	19	0.6	646	17	AZ403793	AZ403793 LM0181C09	c 311	19	0.6	1066	12	BE887837	BE887837 601511220
c 239	19	0.6	646	17	BH532779	BH532779 BOHNJ47TR	c 312	19	0.6	1079	17	CNS02J25	AL119670 Tetraodon
c 240	19	0.6	649	12	BG263181	BG263181 WHE2339.A	c 313	19	0.6	1080	17	CNS03DMX	AL1332610 Tetraodon
c 241	19	0.6	651	12	BF917483	BF917483 IL3-UT011	c 314	19	0.6	1110	14	BM925342	BM925342 AGENCOURT
c 242	19	0.6	658	12	BG906258	BG906258 TAlr1147H	c 315	19	0.6	1111	14	BQ720307	BQ720307 AGENCOURT
c 243	19	0.6	664	13	BI271403	BI271403 NF050G10F	c 316	19	0.6	1152	14	BQ952091	BQ952091 AGENCOURT
c 244	19	0.6	665	14	BQ115180	BQ115180	c 317	19	0.6	1162	17	CNS0450K	AL274781 Tetraodon
c 245	19	0.6	667	10	BE387377	BE387377 601274417	c 318	19	0.6	1208	11	AK013250	AK013250 Mus muscu
c 246	19	0.6	668	17	AZ273926	AZ273926 RPCI-23-1	c 319	19	0.6	1259	13	BI857106	BI857106 603383691
c 247	19	0.6	669	17	AQ377545	AQ377545 RPCI11-14	c 320	19	0.6	1426	12	BG388238	BG388238 602413232
c 248	19	0.6	671	17	AZ590971	AZ590971 LM0400P15	c 321	19	0.6	1658	12	BF346046	BF346046 602018778
c 249	19	0.6	672	10	BB644884	BB644884	c 322	19	0.6	1117	12	BF885931	BF885931 PM3-TN010
c 250	19	0.6	674	14	BQ295048	BQ295048 WHE2857_F	c 323	18	0.6	117	17	BH407881	BH407881 100705160
c 251	19	0.6	681	9	AI425341	AI425341 mf23q01.y	c 324	18	0.6	121	13	BM661260	BM661260 952046C05
c 252	19	0.6	683	12	BG170358	BG170358 60233261	c 325	18	0.6	126	13	BI924452	BI924452 EST544341
c 253	19	0.6	692	13	BJ017593	BJ017593 RBJ017593	c 326	18	0.6	133	12	BF153251	BF153251 002D05 Ma
c 254	19	0.6	695	17	BH090963	BH090963 RPCI-24-2	c 327	18	0.6	148	10	AV388298	AV388298 AV388298
c 255	19	0.6	697	17	AG168094	AG168094 Pan trogl	c 328	18	0.6	152	14	H40912	H40912 YO050D04.s1
c 256	19	0.6	699	17	BH652451	BH652451 BOMBW90TF	c 329	18	0.6	162	10	AW096296	AW096296 EST289476
c 257	19	0.6	701	17	BH032664	BH032664 RPCI-24-2	c 330	18	0.6	168	14	BQ286227	BQ286227 lk27e04.y
c 258	19	0.6	706	13	BJ023107	BJ023107	c 331	18	0.6	175	12	BG041172	BG041172 sv30e09.y
c 259	19	0.6	707	14	BQ864276	BQ864276 QG226E07.	c 332	18	0.6	180	17	AQ318179	AQ318179 RPCI111-97
c 260	19	0.6	708	13	BJ342238	BJ342238	c 333	18	0.6	181	12	BF062689	BF062689 7h64a04.x
c 261	19	0.6	709	9	AU075934	AU075934 AU075934	c 334	18	0.6	182	12	BF070338	BF070338 stl7f10.y
c 262	19	0.6	709	17	BH538954	BH538954 BOGIC42TF	c 335	18	0.6	184	14	W09743	W09743 ma56b06.r1
c 263	19	0.6	711	17	AG179888	AG179888 Pan trogl	c 336	18	0.6	185	17	BH314482	BH314482 CH230-52F
c 264	19	0.6	717	14	BQ865213	BQ865213 QG22b11.y	c 337	18	0.6	186	17	TA92H01P	TA92H01P T. brucei
c 265	19	0.6	719	12	BG701546	BG701546 602682794	c 338	18	0.6	187	17	AZ066340	AZ066340 RPCI-23-3
c 266	19	0.6	722	13	CNS02934	AL186745 Tetraodon	c 339	18	0.6	188	9	AV282016	AV282016 AV282016
c 267	19	0.6	723	13	BQ021505	BQ021505	c 340	18	0.6	189	13	BI230117	BI230117 GM15358.5
c 268	19	0.6	728	17	AZ720059	AZ720059 RPCI-24-8	c 341	18	0.6	191	17	AZ135773	AZ135773 BBS343Sp6
c 269	19	0.6	736	14	BQ990517	BQ990517 QGF20G06.	c 342	18	0.6	194	9	AV272497	AV272497 AV272497
c 270	19	0.6	743	10	AV700456	AV700456	c 343	18	0.6	194	13	BI212163	BI212163 RE17188.5
c 271	19	0.6	744	17	AQ268111	AQ268111 RPCI111-75	c 344	18	0.6	194	14	BQ102780	BQ102780 UUGC0187
c 272	19	0.6	745	14	BQ858470	BQ858470 QGC10F08.	c 345	18	0.6	196	14	BQ517490	BQ517490 EST624905
c 273	19	0.6	748	17	AQ688715	AQ688715 nbxb0078M	c 346	18	0.6	201	9	AA802323	AA802323 GM04203.5
c 274	19	0.6	750	13	BI177675	BI177675 EST518620	c 347	18	0.6	201	9	AI489897	AI489897 EST248236
c 275	19	0.6	751	17	BH378950	BH378950 AG-ND-166	c 348	18	0.6	201	12	BE832522	BE832522 CM3-MT011
c 276	19	0.6	756	17	AQ629359	AQ629359 RPCI-11-4	c 349	18	0.6	202	9	AA596746	AA596746 GM08323.5
c 277	19	0.6	759	17	AQ157206	AQ157206 nbxb0009I	c 350	18	0.6	205	9	AV284408	AV284408 AV284408
c 278	19	0.6	762	17	BH291495	BH291495 CH230-43P	c 351	18	0.6	206	12	BG636401	BG636401 SD4107.5
c 279	19	0.6	763	17	AQ326033	AQ326033 nbxb0024B	c 352	18	0.6	207	9	AV044609	AV044609 AV044609
c 280	19	0.6	767	13	BJ533906	BJ533906	c 353	18	0.6	207	13	BI610920	BI610920 RH16938.5
c 281	19	0.6	775	14	BQ441308	BQ441308 AGENCOURT	c 354	18	0.6	208	12	BG099514	BG099514 naq53b03.
c 282	19	0.6	786	17	AQ896016	AQ896016 HS_3072_B	c 355	18	0.6	208	13	BG099514	BG099514 naq53b03.
c 283	19	0.6	792	17	BH525620	BH525620 BOGWX15TF	c 356	18	0.6	209	13	BI618208	BI618208 RH48803.5
c 284	19	0.6	797	12	BG645081	BG645081	c 357	18	0.6	212	12	BG642336	BG642336 SD4 Dros
c 285	19	0.6	804	12	BG749315	BG749315 602707966	c 358	18	0.6	213	9	AA419572	AA419572 zv03f07.r
c 286	19	0.6	809	17	AQ579476	AQ579476 nbxb0084B	c 359	18	0.6	215	13	BI588207	BI588207 RH29333.5
c 287	19	0.6	811	17	BH453059	BH453059 BOGV054TF	c 360	18	0.6	216	9	AI252945	AI252945 qv44h11.x
c 288	19	0.6	817	17	BH358172	BH358172 CH230-18E	c 361	18	0.6	216	10	AW086259	AW086259 KC70h02.x
c 289	19	0.6	822	17	AQ780828	AQ780828 HS_3104_B	c 362	18	0.6	216	10	BB545041	BB545041 BB545041
c 290	19	0.6	834	12	BG368974	BG368974 HVSM1002	c 363	18	0.6	218	10	BE043197	BE043197 hk36e02.y
c 291	19	0.6	852	17	AZ754120	AZ754120 RPCI-24-1	c 364	18	0.6	219	13	BI573417	BI573417 RH09057.5
c 292	19	0.6	854	17	AZ907362	AZ907362 RPCI-24-1	c 365	18	0.6	227	13	BI165019	BI165019 RH04818.5
c 293	19	0.6	857	17	CNS02U0C	AL214796 Tetraodon	c 366	18	0.6	228	10	BB019888	BB019888 BB019888
c 294	19	0.6	862	17	CNS01ZLU	AL174459 Tetraodon	c 367	18	0.6	232	9	AL826520	AL826520 AL826520
c 295	19	0.6	872	17	AZ545701	AZ545701 ENTQ07TR	c 368	18	0.6	232	13	BI167680	BI167680 RE08115.5
c 296	19	0.6	875	17	BH149586	BH149586 ENTQ023TF	c 369	18	0.6	233	9	AI345461	AI345461 tb82e11.x
c 297	19	0.6	881	14	BQ930451	BQ930451 AGENCOURT	c 370	18	0.6	234	10	AV351508	AV351508 AV351508
c 298	19	0.6	887	17	AZ532663	AZ532663 ENTBR74TR	c 371	18	0.6	235	9	AI345162	AI345162 tb80f10.x

372	18	0.6	235	10	BB068074	BB068074	BB068074	445	18	0.6	294	14	BQ102718	BQ102718	UDG0C102
373	18	0.6	237	10	AV347121	AV347121	AV347121	c 446	18	0.6	295	9	AA264935	AA264935	LD08560.5
374	18	0.6	237	17	AZ908204	RCPI-24-1	AZ908204	447	18	0.6	295	10	AV389602	AV389602	AV389602
375	18	0.6	241	10	BB563250	BB563250	BB563250	448	18	0.6	295	10	BB344311	BB344311	BB344311
376	18	0.6	242	9	AA032254	zk19h02.s	AA032254	c 449	18	0.6	295	13	BI573799	BI573799	BI573799
377	18	0.6	242	9	AI088395	qbl1c07.x	AI088395	c 450	18	0.6	296	10	AV910298	AV910298	RH09310.5
378	18	0.6	242	10	BB147654	BB147654	BB147654	c 451	18	0.6	298	9	AI032198	AI032198	AV910298
379	18	0.6	242	13	BI591860	BI591860	BI591860	c 452	18	0.6	298	13	BI358623	BI358623	GR96e05.s
380	18	0.6	243	9	AV281427	AV281427	AV281427	c 453	18	0.6	299	10	BB190128	BB190128	BI358623
381	18	0.6	243	9	AA385910	AA385910	AA385910	c 454	18	0.6	301	14	BB190128	BB190128	GR96e05.s
382	18	0.6	243	13	BI929718	BI929718	BI929718	c 455	18	0.6	302	13	BI634070	BI634070	BI358623
383	18	0.6	245	17	BH141519	BH141519	BH141519	c 456	18	0.6	303	9	AI461872	AI461872	GM27656.5
384	18	0.6	245	17	BH141801	BH141801	BH141801	c 457	18	0.6	303	9	AI164652	AI164652	GM27656.5
385	18	0.6	246	10	BE139683	BE139683	BE139683	c 458	18	0.6	305	9	AI378775	AI378775	GM27656.5
386	18	0.6	247	10	AV377125	AV377125	AV377125	c 459	18	0.6	305	12	BE935084	BE935084	GM27656.5
387	18	0.6	249	10	BB170120	BB170120	BB170120	c 460	18	0.6	306	9	AA573480	AA573480	GM27656.5
388	18	0.6	250	9	AI337698	AI337698	AI337698	c 461	18	0.6	307	12	BF773497	BF773497	GM27656.5
389	18	0.6	250	9	AV275662	AV275662	AV275662	c 462	18	0.6	308	9	AA264799	AA264799	GM27656.5
390	18	0.6	250	12	BG635500	BG635500	BG635500	c 463	18	0.6	309	10	AW836698	AW836698	GM27656.5
391	18	0.6	251	9	AI345606	AI345606	AI345606	c 464	18	0.6	309	17	AZ289805	AZ289805	GM27656.5
392	18	0.6	253	9	AI112984	AI112984	AI112984	c 465	18	0.6	310	13	BI584889	BI584889	GM27656.5
393	18	0.6	253	12	BF094446	BF094446	BF094446	c 466	18	0.6	312	13	BI641998	BI641998	GM27656.5
394	18	0.6	254	9	AL829350	AL829350	AL829350	c 467	18	0.6	312	17	AQ653919	AQ653919	GM27656.5
395	18	0.6	255	9	AA033624	AA033624	AA033624	c 468	18	0.6	313	13	BI584801	BI584801	GM27656.5
396	18	0.6	255	10	AW268081	AW268081	AW268081	c 469	18	0.6	313	9	AA802281	AA802281	GM27656.5
397	18	0.6	255	12	BG635835	BG635835	BG635835	c 470	18	0.6	315	13	BI573058	BI573058	GM27656.5
398	18	0.6	255	13	BI611990	BI611990	BI611990	c 471	18	0.6	318	9	AL801032	AL801032	GM27656.5
399	18	0.6	257	12	BG096433	BG096433	BG096433	c 472	18	0.6	318	10	BE580906	BE580906	GM27656.5
400	18	0.6	258	12	BG095203	BG095203	BG095203	c 473	18	0.6	318	13	RJ334416	RJ334416	GM27656.5
401	18	0.6	259	9	AV039539	AV039539	AV039539	c 474	18	0.6	318	14	R34823	R34823	GM27656.5
402	18	0.6	260	17	AQ007535	AQ007535	AQ007535	c 475	18	0.6	321	17	AZ637772	AZ637772	GM27656.5
403	18	0.6	261	12	BG201929	BG201929	BG201929	c 476	18	0.6	322	13	BM136658	BM136658	GM27656.5
404	18	0.6	262	17	AG188504	AG188504	AG188504	c 477	18	0.6	324	17	AZ876003	AZ876003	GM27656.5
405	18	0.6	262	12	BG186550	BG186550	BG186550	c 478	18	0.6	327	13	BI072613	BI072613	GM27656.5
406	18	0.6	262	13	BI634061	BI634061	BI634061	c 479	18	0.6	328	10	AW135716	AW135716	GM27656.5
407	18	0.6	264	9	AV237033	AV237033	AV237033	c 480	18	0.6	328	10	BE463993	BE463993	GM27656.5
408	18	0.6	265	9	AL820512	AL820512	AL820512	c 481	18	0.6	329	9	AI916821	AI916821	GM27656.5
409	18	0.6	267	12	BF883299	BF883299	BF883299	c 482	18	0.6	329	12	BG095557	BG095557	GM27656.5
410	18	0.6	268	10	BB055603	BB055603	BB055603	c 483	18	0.6	330	12	BE923694	BE923694	GM27656.5
411	18	0.6	268	13	BI612025	BI612025	BI612025	c 484	18	0.6	330	13	BI358650	BI358650	GM27656.5
412	18	0.6	269	9	AI387652	AI387652	AI387652	c 485	18	0.6	330	17	AZ135757	AZ135757	GM27656.5
413	18	0.6	269	9	AA614253	AA614253	AA614253	c 486	18	0.6	331	13	BI584107	BI584107	GM27656.5
414	18	0.6	269	14	F06306	F06306	F06306	c 487	18	0.6	332	9	AA169658	AA169658	GM27656.5
415	18	0.6	270	10	BB258936	BB258936	BB258936	c 488	18	0.6	332	12	BG636923	BG636923	GM27656.5
416	18	0.6	271	13	BJ367810	BJ367810	BJ367810	c 489	18	0.6	333	9	AA699714	AA699714	GM27656.5
417	18	0.6	272	9	AV085453	AV085453	AV085453	c 490	18	0.6	333	13	BG941635	BG941635	GM27656.5
418	18	0.6	272	17	AL761323	AL761323	AL761323	c 491	18	0.6	334	10	AW094553	AW094553	GM27656.5
419	18	0.6	272	17	AL761323	AL761323	AL761323	c 492	18	0.6	334	10	AW094553	AW094553	GM27656.5
420	18	0.6	273	17	AZ189861	AZ189861	AZ189861	c 493	18	0.6	334	12	BF515902	BF515902	GM27656.5
421	18	0.6	274	12	BG208844	BG208844	BG208844	c 494	18	0.6	336	9	AI895652	AI895652	GM27656.5
422	18	0.6	275	9	AV043383	AV043383	AV043383	c 495	18	0.6	336	9	AA391169	AA391169	GM27656.5
423	18	0.6	276	10	AW844415	AW844415	AW844415	c 496	18	0.6	336	13	BI434682	BI434682	GM27656.5
424	18	0.6	276	13	BJ368140	BJ368140	BJ368140	c 497	18	0.6	338	9	AI432219	AI432219	GM27656.5
425	18	0.6	277	9	AV135656	AV135656	AV135656	c 498	18	0.6	339	17	AZ015723	AZ015723	GM27656.5
426	18	0.6	277	12	BG217734	BG217734	BG217734	c 499	18	0.6	340	10	AV389501	AV389501	GM27656.5
427	18	0.6	277	12	BF228702	BF228702	BF228702	c 500	18	0.6	340	12	BE816931	BE816931	GM27656.5
428	18	0.6	278	9	AI341610	AI341610	AI341610	c 501	18	0.6	341	9	AA833676	AA833676	GM27656.5
429	18	0.6	278	9	AI638801	AI638801	AI638801	c 502	18	0.6	342	14	H72175	H72175	GM27656.5
430	18	0.6	284	10	AV410655	AV410655	AV410655	c 503	18	0.6	344	12	BF719135	BF719135	GM27656.5
431	18	0.6	284	10	AV633039	AV633039	AV633039	c 504	18	0.6	344	13	BI476125	BI476125	GM27656.5
432	18	0.6	284	10	AW072172	AW072172	AW072172	c 505	18	0.6	345	14	U46399	U46399	GM27656.5
433	18	0.6	284	10	BB370838	BB370838	BB370838	c 506	18	0.6	349	17	AQ114415	AQ114415	GM27656.5
434	18	0.6	285	9	AV137197	AV137197	AV137197	c 507	18	0.6	350	12	BG630568	BG630568	GM27656.5
435	18	0.6	288	9	AV296049	AV296049	AV296049	c 508	18	0.6	351	9	AA539612	AA539612	GM27656.5
436	18	0.6	288	10	BB010023	BB010023	BB010023	c 509	18	0.6	354	10	AV655290	AV655290	GM27656.5
437	18	0.6	289	10	AV390026	AV390026	AV390026	c 510	18	0.6	356	17	AZ906192	AZ906192	GM27656.5
438	18	0.6	289	10	BB087545	BB087545	BB087545	c 511	18	0.6	357	9	AA335101	AA335101	GM27656.5
439	18	0.6	289	10	BE678221	BE678221	BE678221	c 512	18	0.6	359	9	AI198996	AI198996	GM27656.5
440	18	0.6	290	10	BB212030	BB212030	BB212030	c 513	18	0.6	360	9	AI869500	AI869500	GM27656.5
441	18	0.6	291	9	AA804075	AA804075	AA804075	c 514	18	0.6	360	10	AW758445	AW758445	GM27656.5
442	18	0.6	293	9	AV092786	AV092786	AV092786	c 515	18	0.6	360	17	AZ643550	AZ643550	GM27656.5
443	18	0.6	293	10	AV389491	AV389491	AV389491	c 516	18	0.6	361	14	R87705	R87705	GM27656.5
444	18	0.6	293	10	AW929299	AW929299	AW929299	c 517	18	0.6	362	12	BF094402	BF094402	GM27656.5

664	18	0.6	413	10	AW837628	QV2-LT003	C 737	18	0.6	431	10	BB811876	BB811876
665	18	0.6	413	10	BB790231	BB790231	C 738	18	0.6	431	14	H21827	H21827 yn78a09.s1
666	18	0.6	413	13	BI614289	BI614289	C 739	18	0.6	432	9	AI010212	AI010212 EST204663
667	18	0.6	414	9	AA926759	OM2509.s	C 740	18	0.6	432	10	AW661736	AW661736 h180b05.x
668	18	0.6	414	9	AI469498	tm18g01.x	C 741	18	0.6	432	13	BI164246	BI164246 RE03882.5
669	18	0.6	414	10	AV638557	AV638557	C 742	18	0.6	433	9	AA821014	AA821014 GM05408.5
670	18	0.6	414	10	AV934315	AV934315	C 743	18	0.6	433	9	AA573027	AA573027 nm42c03.s
671	18	0.6	414	10	BE680728	BE680728	C 744	18	0.6	433	10	AW520179	AW520179 2822547.3
672	18	0.6	415	9	AI486464	EST244785	C 745	18	0.6	433	10	AW368131	AW368131 CM1-HT017
673	18	0.6	415	9	AA508379	nm65a11.s	C 746	18	0.6	433	13	BI593626	BI593626 RH04434.5
674	18	0.6	415	12	BF662236	maa80c05.	C 747	18	0.6	433	14	H08408	H08408 Y192d09.s1
675	18	0.6	415	13	BI576125	RH32628.5	C 748	18	0.6	434	10	AW368113	AW368113 CM0-HT018
676	18	0.6	416	12	BG363554	sac15b12.	C 749	18	0.6	434	12	BF286178	BF286178 EST450769
677	18	0.6	416	14	H52790	Yo22a06.s1	C 750	18	0.6	434	17	BH675588	BH675588 BOMLV75TF
678	18	0.6	416	17	AZ740668	RPCI-24-1	C 751	18	0.6	435	9	AI242421	AI242421 q136e05.x
679	18	0.6	417	14	BQ464646	HF02N19r	C 752	18	0.6	435	10	AV630299	AV630299 AV630299
680	18	0.6	418	9	AA803104	GM07004.5	C 753	18	0.6	435	10	AW368135	AW368135 CM1-HT017
681	18	0.6	418	9	AI060796	ub44a04.x	C 754	18	0.6	435	10	BE556236	BE556236 sp99c01.y
682	18	0.6	418	9	AI468411	tg81a10.x	C 755	18	0.6	435	14	W45427	W45427 zc83a05.s1
683	18	0.6	418	10	AW217349	EST296172	C 756	18	0.6	435	17	AZ159174	AZ159174 SP_0062.A
684	18	0.6	418	10	AW683596	AW683596	C 757	18	0.6	436	10	AW197616	AW197616 xm40a11.x
685	18	0.6	419	9	AA808249	oc40h11.s	C 758	18	0.6	436	10	BE552218	BE552218 hy04f01.x
686	18	0.6	419	10	BE691792	uv66g02.x	C 759	18	0.6	436	10	BE634358	BE634358 uv66g02.y
687	18	0.6	419	14	W60356	zc97e07.s1	C 760	18	0.6	437	13	BI778889	BI778889 EBR001-SQ
688	18	0.6	420	9	AI743438	wf63b12.x	C 761	18	0.6	437	17	AQ386609	AQ386609 RPCI11-14
689	18	0.6	420	10	BB784900	BB784900	C 762	18	0.6	438	17	AQ464184	AQ464184 HS_5098.A
690	18	0.6	420	12	BF877469	RC0-ET012	C 763	18	0.6	439	9	AA696495	AA696495 GM07782.5
691	18	0.6	420	17	B79236	CIT978SK-96	C 764	18	0.6	439	9	AI093465	AI093465 qb08d09.x
692	18	0.6	420	17	B79357	CIT978SK-96	C 765	18	0.6	439	9	AI363029	AI363029 q1788a09.x
693	18	0.6	421	9	AA430154	ab05306.s	C 766	18	0.6	439	9	AA200043	AA200043 m04b07.r
694	18	0.6	422	9	AA995769	os25f08.s	C 767	18	0.6	439	10	AW836700	AW836700 QV1-LT003
695	18	0.6	422	10	BE674319	7d78b09.x	C 768	18	0.6	439	17	BH404808	BH404808 AG-ND-137
696	18	0.6	422	13	BI634074	BI634074	C 769	18	0.6	440	10	AV636338	AV636338 AV636338
697	18	0.6	423	9	AA281900	zd28130.5	C 770	18	0.6	440	12	BF460530	BF460530 UT-M-CGOp
698	18	0.6	423	13	BI587726	RH28581.5	C 771	18	0.6	440	14	R46388	R46388 y950e01.s1
699	18	0.6	424	9	AA330625	LD09690.5	C 772	18	0.6	440	17	AZ440211	AZ440211 1M0231K10
700	18	0.6	424	10	AW917490	EST348794	C 773	18	0.6	441	9	AI543356	AI543356 SDOI084.5
701	18	0.6	424	10	BE686303	uv74c10.x	C 774	18	0.6	441	10	AW426292	AW426292 60049 MAR
702	18	0.6	424	13	BI628067	BI628067	C 775	18	0.6	441	10	AW899316	AW899316 MR0-NN008
703	18	0.6	425	9	AI533295	SD05056.5	C 776	18	0.6	441	14	H49294	H49294 yq19h12.r1
704	18	0.6	425	10	AV634314	AV634314	C 777	18	0.6	442	9	AI802123	AI802123 t330a07.x
705	18	0.6	425	10	BB778059	BB778059	C 778	18	0.6	442	10	AV389093	AV389093 AV389093
706	18	0.6	425	13	BI568783	RH37925.5	C 779	18	0.6	442	12	BF643782	BF643782 NP057F08E
707	18	0.6	426	9	AI531032	SD01888.5	C 780	18	0.6	442	13	BI363006	BI363006 RE47712.5
708	18	0.6	426	10	AW352773	UI-R-BU0-	C 781	18	0.6	442	13	BI620066	BI620066 RH46181.5
709	18	0.6	426	10	BB773651	BB773651	C 782	18	0.6	442	13	BI624053	BI624053 RH51227.5
710	18	0.6	426	13	BI239267	RE35714.5	C 783	18	0.6	442	13	BI624126	BI624126 RH54706.5
711	18	0.6	426	13	BI612019	RE16005.5	C 784	18	0.6	443	10	AV636493	AV636493 AV636493
712	18	0.6	426	14	H06210	y178b09.r1	C 785	18	0.6	443	13	BI163353	BI163353 RD02732.5
713	18	0.6	426	17	AQ202987	RPCI11-45	C 786	18	0.6	443	13	BI620063	BI620063 RH46078.5
714	18	0.6	427	9	AI391610	t193g03.x	C 787	18	0.6	443	17	AZ509114	AZ509114 1M0351119
715	18	0.6	427	10	AV624052	AV624052	C 788	18	0.6	443	17	BH728836	BH728836 BOMJW09TF
716	18	0.6	427	10	AV636734	AV636734	C 789	18	0.6	444	9	AA824443	AA824443 oc78d02.s
717	18	0.6	427	12	BE995481	UI-M-CGOp	C 790	18	0.6	444	10	AW598655	AW598655 s194b05.y
718	18	0.6	428	9	AA698514	HI04843.5	C 791	18	0.6	444	10	AW54893	AW54893 PC06H02.P
719	18	0.6	428	9	AI569711	tn04h08.x	C 792	18	0.6	444	12	BF322665	BF322665 maa31b06.
720	18	0.6	428	14	BQ352995	hd56c05.g	C 793	18	0.6	444	13	BI364882	BI364882 BJ364882
721	18	0.6	428	17	AQ318106	RPCI11-98	C 794	18	0.6	444	14	BM877679	BM877679 f188b03.y
722	18	0.6	429	9	AI298901	qm94e11.x	C 795	18	0.6	445	10	AV388493	AV388493 AV388493
723	18	0.6	429	10	AV397454	AV397454	C 796	18	0.6	445	10	AW836738	AW836738 QV1-LT003
724	18	0.6	429	10	AW203797	sf138d01.y	C 797	18	0.6	445	13	BI575056	BI575056 RH27919.5
725	18	0.6	429	10	BB788098	BB788098	C 798	18	0.6	446	9	AA482550	AA482550 zt33b05.s1
726	18	0.6	429	14	BQ612978	sap79e02.	C 799	18	0.6	446	14	H20299	H20299 yn62a05.s1
727	18	0.6	430	9	AI107390	GH04521.5	C 800	18	0.6	447	9	AI736607	AI736607 sb31b07.y
728	18	0.6	430	10	AW082723	xb61g05.x	C 801	18	0.6	447	13	BI166030	BI166030 RE06049.5
729	18	0.6	430	10	AW591169	xol1e12.x	C 802	18	0.6	447	13	BI1668754	BI1668754 RE09618.5
730	18	0.6	430	10	BB824340	BB824340	C 803	18	0.6	447	13	BI568779	BI568779 RH37475.5
731	18	0.6	430	13	BM202029	CO233G08-	C 804	18	0.6	447	13	BI576246	BI576246 RH32771.5
732	18	0.6	430	17	AQ685517	HS_5528.B	C 805	18	0.6	448	9	AA749075	AA749075 nyl1a01.s
733	18	0.6	430	17	AZ247836	RPCI-23-4	C 806	18	0.6	448	9	AI897008	AI897008 EST266451
734	18	0.6	431	9	AI579615	UI-R-AD0-	C 807	18	0.6	448	9	AA533769	AA533769 nj93c01.s
735	18	0.6	431	10	AV712526	AV712526	C 808	18	0.6	448	10	AW598462	AW598462 s19g01.y
736	18	0.6	431	10	BB779121	BB779121	C 809	18	0.6	448	10	BB775622	BB775622

c 810	18	0.6	448	13	BI624060	BI624060 RH516222.5	883	18	0.6	464	12	BF918005	BF918005 IL3-UT011
c 811	18	0.6	448	17	AQ199131	RPC111-45	884	18	0.6	465	9	AI827644	wf32d08.x
c 812	18	0.6	449	9	AI276053	ql69c11.x	885	18	0.6	465	12	BF286331	EST450922
c 813	18	0.6	449	9	AA117630	mp69g02.r	c 886	18	0.6	465	13	BJ532779	BJ532779
c 814	18	0.6	449	10	AV389665	AV389665	887	18	0.6	466	9	AI005339	AI005339 ou60f03.x
c 815	18	0.6	449	10	AW164461	se72h08.y	888	18	0.6	466	9	AI847379	AI847379 UI-N-ANI-
c 816	18	0.6	449	13	BI169563	RE10775.5	c 889	18	0.6	466	10	BE354547	BE354547
c 817	18	0.6	449	17	AQ559738	AQ559738 HS_5241_A	c 890	18	0.6	466	13	BI584519	BI584519 RH23745.5
c 818	18	0.6	450	9	AI533587	AI533587 SD05473.5	c 891	18	0.6	467	9	AA987505	AA987505 os03g09.s
c 819	18	0.6	450	10	AV636072	AV636072	c 892	18	0.6	467	9	AI777537	AI777537 EST258511
c 820	18	0.6	450	13	BI161486	BI161486 RE01001.5	c 893	18	0.6	467	9	AL373674	MCB802B08
c 821	18	0.6	450	13	BI616091	BI616091 RH45027.5	894	18	0.6	467	10	AV623232	AV623232
c 822	18	0.6	450	13	BI620080	RH47162.5	c 895	18	0.6	467	10	AW519283	xt80a06.x
c 823	18	0.6	451	9	AI634192	AI634192 ts55b05.x	c 896	18	0.6	467	12	BF438301	BF438301 7q07f03.x
c 824	18	0.6	451	10	AW342988	f171g03.y	c 897	18	0.6	467	13	BI576937	BI576937 RH33626.5
c 825	18	0.6	451	10	BI368219	BI368219 CM0-HR018	898	18	0.6	467	13	BI950756	BI950756 HVSMEL002
c 826	18	0.6	451	13	BI924366	BI924366 EST544255	899	18	0.6	467	17	AQ537489	AQ537489 RPC1-11-3
c 827	18	0.6	451	17	AZ046725	AZ046725 nbe0085B	900	18	0.6	468	9	AA854342	AA854342 aj73e08.s
c 828	18	0.6	452	10	AV624007	AV624007	901	18	0.6	468	9	AA935605	AA935605 op26g03.s
c 829	18	0.6	452	10	BE144847	BE144847 CM0-HT018	902	18	0.6	468	10	AV386690	AV386690
c 830	18	0.6	453	12	BF883393	OV3-ET020	c 903	18	0.6	468	10	BE354518	BE354518 EST355861
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c 832	18	0.6	454	10	AV632062	AV632062	905	18	0.6	469	10	AV634942	AV634942
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c 842	18	0.6	455	17	B82358	B82358 RPC111-14N2	c 915	18	0.6	471	13	BI161790	BI161790 RE01191.5
c 843	18	0.6	455	17	AQ638483	AQ638483 927P1-3E4	c 916	18	0.6	472	9	AA695581	AA695581 GM03064.5
c 844	18	0.6	456	9	AI705666	AI705666 UI-P-AD1-	c 917	18	0.6	472	12	BF057448	BF057448 7k44a09.x
c 845	18	0.6	456	10	AW246747	AW246747 2822210.3	c 918	18	0.6	473	13	BI616069	BI616069 RH43988.5
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c 851	18	0.6	457	10	AW337696	AW337696 wu99a04.x	c 924	18	0.6	475	9	AI488644	EST246983
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c 872	18	0.6	461	17	AQ421831	AQ421831 RPC1-11-1	c 945	18	0.6	480	9	AJ469224	AJ469224
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ALIGNMENTS

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DEFINITION DNA sequence.
ACCESSION AQ309404
VERSION AQ309404.1 GI:4041438
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 552)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other GSSs: CITBI-EI-2528J13.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
```

```
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeatigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
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Caltech Human BAC Library D"
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Best Local Similarity 100.0%; Pred. No. 2.7e-267;
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QY 1547 GTCGCTTCTCGGAGCTTTCCATGCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAA 1606
DB 432 GTCGCTTCTCGGAGCTTTCCATGCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAA 373
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DB 312 AGTGTGCACTCCATTTATATCAAGAGAGTATCATCAATCAGCCCTGAGCCAAAGAAATTG 253
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DB 252 AAGCTTCTTCAAGGTAAGGCTTATATCAACTCAGGGAACATCCCGATTACTTAT 193
QY 1787 TTGACTTCTTTGAACATTTGCCCAATTTGCAAGTGTCTGGACTTCATTAAACTGGACT 1846
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QY 1847 TTTATGGGGAGCTATGGCTTCATGGGAAAGGCTGCAGAGACACAGGTGGGAATCCACA 1906
DB 132 TTTATGGGGAGCTATGGCTTCATGGGAAAGGCTGCAGAGACACAGGTGGGAATCCACA 73
QY 1907 TGAAGAGGCCCCCAAGAACCTACATTCACAGCAGGCTGTATCTTTTCTTCAACTGGA 1966
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QY 1967 AGCAGGAATTC 1977
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AV719179/c
LOCUS AV719179
DEFINITION AV719179 GLC Homo sapiens cDNA clone G1CEQA10 5', mRNA sequence.
ACCESSION AV719179
VERSION AV719179.1 GI:10816331
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KEYWORDS SOURCE ORGANISM
EST. human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Qian,B., Wu,T., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L.,
AUTHORS Xu,X., Li,N., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H.,
Y., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GLC clones
Unpublished (2000)
CONTACT: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzge@hgc.sh.cn
This clone is available at CHGC in Shanghai.
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Location/Qualifiers
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XhoI"
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QY 2665 GCGTGTGACGTGAAGCGCCTGAGCAGCCTGTTGAACATTTGAGAGAGGTCCACAA 2724
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QY 2725 CTCGTCAAGCTTGGTGTGAAGAACTGGAGACTCACAGATACAGATTAGATTAGT 2784
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QY 2785 GCATTTTTTGGAAAGAACCCCTCTGAAAACTTCCAGCAGTTGAATTTGGCGGGAATCGT 2844
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QY 2965 CAAGTGTATCAAGTTAACTTTCTGCAAGAGCTAGGCTTGTGGGTGGCAATTTGAT 3024
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DEFINITION qx57b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3',
mRNA sequence.
ACCESSION AI263294
VERSION AI263294.1 GI:3871497
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 364)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbbrp/image/image.html
Insert Length: 2146 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 364.
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Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2971 TTATCCAAGTTAACTTTCTGCAAGAGCTAGGCTTGTGGGTGGCAATTTGATGATGAT 3030
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BI908869
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DEFINITION 603066455F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215669 5',

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mRNA sequence.
ACCESSION B1908869
VERSION B1908869.1 GI:16171950
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KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC http://mhc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
http://image.llnl.gov
Plate: L14M11541 row: m column: 14
High quality sequence start: 7
High quality sequence stop: 744.
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and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 Kb, insert size range
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full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
BASE COUNT 236 a 148 c 166 g 198 t
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Best Local Similarity 100.0%; Pred. NO. 1.1e-147;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 TTTGAGACTTGAATGACAAAGTCTTTTTCATCAGACATCAGAGGAGCTTCGAGCAT 300
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RESULT 5
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LOCUS AV656315 GLC Homo sapiens cDNA clone GLCEQA10 3', mRNA sequence.
DEFINITION AV656315 GLC Homo sapiens cDNA clone GLCEQA10 3', mRNA sequence.
ACCESSION AV656315
VERSION AV656315.1 GI:9877329
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 371)
Xiao, H., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z., and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
JOURNAL 21625106
MEDLINE
COMMENT Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzq@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
Location/Qualifiers
1..371
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCEQA10"
/clone_lib="GLC"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 112 a 85 c 91 g 82 t 1 others
ORIGIN
Query Match 9.5%; Score 291; DB 10; Length 371;
Best Local Similarity 99.7%; Pred. NO. 1.2e-135;
Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1873 GAAAGGCTCGAGAGACACAGGTGGATCCACATGGAGAGGCCCCAGAAACCTACATT 1932
DB 1 GAAAGGCTCGAGAGACACAGGTGGATCCACATGGAGAGGCCCCAGAAACCTACATT 60
QY 1933 CCCAGCAGGCTGTATCTTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGAGGTC 1992
DB 61 CCCAGCAGGCTGTATCTTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGAGGTC 120
QY 1993 ACATCCGGGGATTTTCAGCAAGTTCGAATTAAGCAAGATATCATATCTGGGAAAATATTC 2052
DB 121 ACATCCGGGGATTTTCAGCAAGTTCGAATTAAGCAAGATATCATATCTGGGAAAATATTC 180
QY 2053 AGCTCTGCCACAAAGCCCTCAGGCTGCAATTAAGAGATGTGCTGTGTGGCTGGAAGCCTC 2112
DB 181 AGCTCTGCCACAAAGCCCTCAGGCTGCAATTAAGAGATGTGCTGTGTGGCTGGAAGCCTC 240
QY 2113 AGTTTGTCTCTCAGCAAGTTCGAATTAAGCAAGATATCATATCTGGGAAAATATTC 2172
DB 241 AGTTTGTCTCTCAGCAAGTTCGAATTAAGCAAGATATCATATCTGGGAAAATATTC 300
QY 2173 ACCATAGAAGATGAGAGGCACATCATCATCTCTGTAACAAACCTG 2214
DB 301 ACCATAGAAGATGAGAGGCACATCATCATCTCTGTAACAAACCTG 342

```

RESULT 6

```
BI824482
LOCUS      BI824482              741 bp    mRNA    linear    EST 04-OCT-2001
DEFINITION 603038854F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5179909 5',
            mRNA sequence.
ACCESSION  BI824482
VERSION     BI824482.1  GI:15936032
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 741)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1448 row: k column: 14
            High quality sequence start: 3
            High quality sequence stop: 705.
            Location/Qualifiers
                1..741
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:5179909"
                /clone.lib="NIH_MGC_115"
                /lab_host="DH10B"
                /note="Organ: pooled brain, lung, testis; Vector:
                pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA
                source anonymous pool of 6 male brains, age range 23-27; 1
                male lung, age 27; and 1 male testis, age 69. Library is
                oligo-dT primed and directionally cloned (EcoRV site is
                destroyed upon cloning). Average insert size 1.8 kb,
                insert size range 1-3 kb. Library is normalized and
                enriched for full-length clones and was constructed by C.
                Gruber (Invitrogen). Research Genetics tracking code
                021. Note: this is a NIH_MGC Library."
                233 a 147 c 164 g 197 t

BASE COUNT  233 a 147 c 164 g 197 t
ORIGIN
Query Match 9.4%; Score 289; DB 13; Length 741;
Best Local Similarity 100.0%; Pred. No. 1.6e-134;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 AGCCCTTATCAAGAAATCGGAATGACTGTTTATAAGCAAAATCACAGATGACCTATTGCT 86
Db 256 AGCCCTTATCAAGAAATCGGAATGACTGTTTATAAGCAAAATCACAGATGACCTATTGCT 315
QY 87 ATGGAAATGTTCTGAATCGCGAAGAGTAACATCATTTCTCGGAGAAGGTGGAGCAGGA 146
Db 316 ATGGAAATGTTCTGAATCGCGAAGAGTAACATCATTTCTCGGAGAAGGTGGAGCAGGA 375
QY 147 TGCTGCTAGAGGATCATTCACATGATTTTGAAGAAGGGTTTCAGAGTCCCTGTAACCTCTT 206
Db 376 TGCTGCTAGAGGATCATTCACATGATTTTGAAGAAGGGTTTCAGAGTCCCTGTAACCTCTT 435
QY 207 TCTTAAATCCCTTAGGAGTGAACATATCCTCTATTTTCAGGACTTGAATGGACAAGTCT 266
Db 436 TCTTAAATCCCTTAGGAGTGAACATATCCTCTATTTTCAGGACTTGAATGGACAAGTCT 495
QY 267 TTTTTCATCAGACATCAGAGGAGAGCTTGGACGATTTGGCTCAGGATTTTA 315
Db 496 TTTTTCATCAGACATCAGAGGAGAGCTTGGACGATTTGGCTCAGGATTTTA 544

RESULT 7

AW337918/c
LOCUS      AW337918              261 bp    mRNA    linear    EST 31-JAN-2000
DEFINITION he12h11.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918853 3',
            mRNA sequence.
ACCESSION  AW337918
VERSION     AW337918.1  GI:6834544
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 261)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            Tissue Procurement: Elisabeth Paletta, Jonathan D. Licht, M.D.,
            Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
            Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/dbrrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 201.
            Location/Qualifiers
                1..261
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:2918853"
                /clone.lib="NCI_CGAP_CML1"
                /tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL
                rearrangement positive, includes both chronic phase and
                myeloid blast crisis"
                /lab_host="DH10B"
                /note="Organ: whole blood; Vector: pCMV-SPORT6; Site.1:
                SalI; Site.2: NotI; Cloned unidirectionally. Primer:
                Oligo dT. Library constructed by Life Technologies."
                86 a 54 c 38 g 83 t

BASE COUNT  86 a 54 c 38 g 83 t
ORIGIN
Query Match 7.3%; Score 223; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.1e-101;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2850 CAGTGATGGATGGCTTGCCTTCATGGTGTATTTGAGAAATCTTAAGCAATTAGTGTGTTT 2909
Db 261 CAGTGATGGATGGCTTGCCTTCATGGTGTATTTGAGAAATCTTAAGCAATTAGTGTGTTT 202
QY 2910 TGACTTTAGTACTAAGAATTTCTACCTGATCCAGCATTTAGTCAGAAAACTTAGCCAACT 2969
Db 201 TGACTTTAGTACTAAGAATTTCTACCTGATCCAGCATTTAGTCAGAAAACTTAGCCAACT 142
QY 2970 GTATCCAAAGTTAACTTTTCTCGCAAGAACTAGGCTTTGGTGGCAATTTGATCATCA 3029
Db 141 GTATCCAAAGTTAACTTTTCTCGCAAGAACTAGGCTTTGGTGGCAATTTGATCATCA 82
QY 3030 TGATCTCAGTGTATTACAGGTGCTTTTAAACTAGTAACCTGCT 3072
Db 81 TGATCTCAGTGTATTACAGGTGCTTTTAAACTAGTAACCTGCT 39

RESULT 8
LOCUS      AQ320928/c
DEFINITION RPC111-93C9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-93C9, DNA
            sequence.
ACCESSION  AQ320928
VERSION     AQ320928.1  GI:4053662
KEYWORDS    GSS.
GSS.
```

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 553)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
 TITLE Use of human BAC End Sequences for Sequence-Ready Map Building
 JOURNAL Unpublished (1998)
 COMMENT Other.GSSs: RPC111-93C9.TJ
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPC11-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1..553
 /organism="Homo sapiens"
 /db_xref="GDB:7535384"
 /db_xref="taxon:9606"
 /clone="RPC11-11-93C9"
 /clone_lib="RPC11-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; RPC111 Human Male BAC Library"
 BASE COUNT 170 a 107 c 114 g 162 t
 ORIGIN
 Query Match 5.5%; Score 170; DB 17; Length 553;
 Best Local Similarity 100.0%; Pred. No. 2.7e-74;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2615 TCGACAGATGAAGTGTGACAGCTACCGCAGCTGCTGCCCTGGGGCTGTGAAGC 2674
 Db 258 TCGACAGATGAAGTGTGACAGCTACCGCAGCTGCTGCCCTGGGGCTGTGAAGC 199
 Qy 2675 TGCAGGAGCGCTGAGCAGCTGTGAACATTTGGAGGAGTCCCACTCGTCAAGC 2734
 Db 198 TGCAGGAGCGCTGAGCAGCTGTGAACATTTGGAGGAGTCCCACTCGTCAAGC 139
 Qy 2735 TTGGGTTGAAAACCTGGAGACTCACAGATACAGATAGATTTAGGT 2784
 Db 138 TTGGGTTGAAAACCTGGAGACTCACAGATACAGATAGATTTAGGT 89
 RESULT 9
 BG210375
 LOCUS BG210375 476 bp mRNA linear EST 21-APR-2001
 DEFINITION RST29913 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION BG210375
 VERSION BG210375.1 GI:13732062
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 476)
 AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
 MEDLINE 21227151
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scain@atersys.com
 High quality sequence stop: 360.
 FEATURES
 source
 Location/Qualifiers
 1..476
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
 BASE COUNT 120 a 99 c 107 g 149 t
 ORIGIN
 Query Match 5.5%; Score 168; DB 12; Length 476;
 Best Local Similarity 100.0%; Pred. No. 2.7e-73;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2873 TGGGTGATTGAGAATCTTAAGCAATTAGTGTGTTTGTGACTTTAGTACTAAAGAATTC 2932
 Db 242 TGGGTGATTGAGAATCTTAAGCAATTAGTGTGTTTGTGACTTTAGTACTAAAGAATTC 301
 Qy 2933 TACCTGATCCAGCATTAGTCAGAAACTTAGCCAAAGTGTATCCAACTTACTTTCTGC 2992
 Db 302 TACCTGATCCAGCATTAGTCAGAAACTTAGCCAAAGTGTATCCAACTTACTTTCTGC 361
 Qy 2993 AAGAAGCTAGGCTTGTGGTGCAATTTGATGATGATGATCTCAGTG 3040
 Db 362 AAGAAGCTAGGCTTGTGGTGCAATTTGATGATGATGATCTCAGTG 409
 RESULT 10
 AQ112439
 LOCUS AQ112439 630 bp DNA linear GSS 29-AUG-1998
 DEFINITION CIT-HSP-2372C1.TR CIT-HSP Homo sapiens genomic clone 2372C1, DNA sequence.
 ACCESSION AQ112439
 VERSION AQ112439.1 GI:3484599
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 630)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
 TITLE Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
 JOURNAL Unpublished (1998)
 COMMENT Other.GSSs: CIT-HSP-2372C1.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites" 3 others

BASE COUNT 142 a 101 c 107 g 117 t Mismatches 0; Indels 0; Gaps 0;

Query Match 3.5%; Score 106; DB 17; Length 470;
Best Local Similarity 100.0%; Pred. No. 6.8e-42;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2034 ATATCTGGGAAAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCACAAATAAAGAGATGTC 2093
|||||
Db 64 ATATCTGGGAAAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCACAAATAAAGAGATGTC 123
|||||

QY 2094 TGGTGTGGCTGGAAGCCTCAGTTGGTCTCAGCACCCTGTAAGAAC 2139
|||||
Db 124 TGGTGTGGCTGGAAGCCTCAGTTGGTCTCAGCACCCTGTAAGAAC 169
|||||

RESULT 13
H25984/c
LOCUS 412 bp mRNA linear EST 10-JUL-1995
DEFINITION y156g07.r1 Soares breast 3NHBst Homo sapiens cDNA clone
IMAGE:162300 5', mRNA sequence.

ACCESSION H25984
VERSION H25984.1 GI:895107
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 412)

REFERENCE Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 942
High quality sequence stops: 347

Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 942 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 347.
Location/Qualifiers
1. .412
/organism="Homo sapiens"
/db_xref="GDB:576544"
/db_xref="taxon:9606"
/clone="IMAGE:162300"
/clone_lib="Soares breast 3NHBst"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: breast; Vector: pT73D (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCATCTCAAGTGGGAGCGCGCCCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of a modified pT73 vector (Pharmacia).
Library went through one round of normalization to a Cot =
20. Library constructed by Bento Soares and M.Fatima
Bonaldo."

BASE COUNT 129 a 84 c 73 g 124 t 2 others
ORIGIN

Query Match 3.2%; Score 98; DB 14; Length 412;
Best Local Similarity 100.0%; Pred. No. 7.4e-38;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2975 CCAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATTTGATGATGATGC 3034
|||||
Db 340 CCAAGTTAACTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATTTGATGATGATGC 281
|||||

QY 3035 TCAGTGTATTACAGGTCGCTTTTAAACTAGTAAGTCT 3072
|||||
Db 280 TCAGTGTATTACAGGTCGCTTTTAAACTAGTAAGTCT 243
|||||

RESULT 14
AI023795
LOCUS 499 bp mRNA linear EST 28-AUG-1998
DEFINITION ox08403.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA
clone IMAGE:1655717 3', mRNA sequence.

ACCESSION AI023795
VERSION AI023795.1 GI:3238839
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 499)

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov

COMMENT This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1179 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 439.
Location/Qualifiers
1. .499
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1655717"
/clone_lib="Soares_fetal_liver_spleen_INFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site.1: Pac I; Site.2: Eco RI;
This is a subtracted version of the Original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5'
AAGTGAAGAATTAATTAAGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 144 a 109 c 98 g 148 t
ORIGIN

Query Match 3.0%; Score 93; DB 9; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.7e-35;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GTCTTTTTCATCAGACATCAGAGGAGCTTGGACGATTTGGCTCAGGATTTAAAGGACT 322
|||||
Db 407 GTCTTTTTCATCAGACATCAGAGGAGCTTGGACGATTTGGCTCAGGATTTAAAGGACT 466
|||||

QY 323 TGTTACCATCCCATCTTTCTGAACCTTTATC 355
|||||
Db 467 TGTTACCATCCCATCTTTCTGAACCTTTATC 499
|||||

Site_1: SfiI (ggcgcctggcc); Site_2: SfiI (ggcattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCATTTGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGAGCGCGGACATG-GT(30)BN-3', (where B = A, C, G or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 276 a 143 c 165 g 256 t
ORIGIN

Query Match 1.0%; Score 55; DB 12; Length 840;
Best Local Similarity 100.0%; Pred. No. 5.6e-16;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3018 ATTTGATGATGATCTCAGTGTATTACAGGTGCTTTTAACTAGTAAGTCT 3072
|||||

Db 518 ATTTGATGATGATCTCAGTGTATTACAGGTGCTTTTAACTAGTAAGTCT 464
|||||

RESULT 18
AI222422 446 bp mRNA linear EST 30-NOV-1998
LOCUS
DEFINITION qn04f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1843715 3', mRNA sequence.
ACCESSION AI222422
VERSION AI222422.1 GI:3804625
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 446)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapb@rmail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 546 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 437.

FEATURES
source
1..446
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1843715"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
/notes="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI-CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 128 a 95 c 86 g 137 t
ORIGIN

Query Match 1.0%; Score 32; DB 9; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 263 GTCCTTTTCACATCAGAGGAGACTTG 294

Db 415 GTCCTTTTCACATCAGAGGAGACTTG 446
|||||

RESULT 19
BH348412 518 bp DNA linear GSS 03-DEC-2001
LOCUS
DEFINITION CH230-42F7.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-42F7, DNA sequence.
ACCESSION BH348412
VERSION BH348412.1 GI:17279146
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 518)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsagaye,G., Geer,K., Shvartsbeyn ,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: CH230-42F7.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering-information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 42 row: F column: 7
Seq primer: T7
Class: BAC ends.

FEATURES
source
1..518
/organism="Rattus norvegicus"
/strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-42F7"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by Pieter de Jong"

BASE COUNT 133 a 124 c 146 g 115 t
ORIGIN

Query Match 1.0%; Score 32; DB 17; Length 518;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1198 GGTGTGTTCTCCACAGTTTGATTTTCAACT 1229
|||||

Db 420 GGTGTGTTCTCCACAGTTTGATTTTCAACT 451
|||||

RESULT 20
BH293386 697 bp DNA linear GSS 30-NOV-2001
LOCUS
DEFINITION CH230-44G15.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-44G15, DNA sequence.
ACCESSION BH293386
VERSION BH293386.1 GI:17205794
KEYWORDS GSS.
SOURCE Norway rat.

ORGANISM	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 697)
AUTHORS	Zhao,S., Shetty,J., Shatsman,S., Tsegave,G., Geer,K., Shvartsbeyn J., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
TITLE	Rat BAC End Sequences from Library CHORI-230 EcoRI segment
JOURNAL	Unpublished (1999)
COMMENT	Other_GSSs: CH230-44G15.TJ Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat30.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 44 row: G column: 15 Seq primer: T7 Class: BAC ends.
FEATURES	Location/Qualifiers
source	1..697 /organism="Rattus norvegicus" /strain="BN/SSNHsd/MCW" /db_xref="taxon:10116" /clone="CH230-44G15" /clone_lib="CHORI-230 Segment 1" /sex="Female" /cell_type="Brain" /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by Pieter de Jong"
BASE COUNT	182 a 165 c 190 g 160 t
ORIGIN	
Query Match	1.0%; Score 32; DB 17; Length 697;
Best Local Similarity	100.0%; Pred. No. 0.00024;
Matches	32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1198 GGTGTTCTCCACAAAGTTTGATTTCGAAC 1229
Db	412 GGTGTTCTCCACAAAGTTTGATTTCGAAC 443
RESULT	21
LOCUS	BF903662
DEFINITION	IL2-MT0180-181200-276-F03 MT0180 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BF903662
VERSION	BF903662.1 GI:12295121
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 251)
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663

COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-MT0180-181200-276-F03&t3=2000-12-18&t4=1) Seq primer: puc 18 forward High quality sequence start: 45 High quality sequence stop: 96.
FEATURES	Location/Qualifiers
source	1..251 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MT0180" /dev_stage="Adult" /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT	72 a 62 c 56 g 61 t
ORIGIN	
Query Match	1.0%; Score 30; DB 12; Length 251;
Best Local Similarity	100.0%; Pred. No. 0.0018;
Matches	30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1057 GAGTTCACCTCTCACACAAACGCTG 1086
Db	52 GAGTTCACCTCTCACACAAACGCTG 81
RESULT	22
LOCUS	AQ889169/c
DEFINITION	HS_2161_B1_A01_P7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2161 Col=1 Row=B, DNA sequence.
ACCESSION	AQ889169
VERSION	AQ889169.1 GI:6345359
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 404)
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallaceu.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 2161 row: B column: 1 Seq primer: T7 Class: BAC ends High quality sequence stop: 404.

```

FEATURES
  source
    Location/Qualifiers
      1. .404
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="Plate=2161 Col=1 Row=B"
        /clone_lib="CIT Approved Human Genomic Sperm Library D"
        /sex="male"
        /note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in
          E-Coli DH10B"
BASE COUNT      119 a   93 c   70 g   122 t
ORIGIN
Query Match      0.9%; Score 28; DB 17; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 TAGAGGATCATTCACATGATTTTGAAA 180
|||||
Db 200 TAGAGGATCATTCACATGATTTTGAAA 173

RESULT 23
Bi964738/c
LOCUS      Bi964738              542 bp      mRNA      linear      EST 12-MAR-2002
DEFINITION 1c55h09.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:5671144 5' similar to TR:Q9VAF0 Q9VAF0 CG7816
PROTEIN.  ; , mRNA sequence.
ACCESSION  Bi964738
VERSION    Bi964738.1 GI:16339143
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 542)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Secorce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
JOURNAL   Endocrine Pancreas Consortium
COMMENT   Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
High quality sequence stop: 456.
Location/Qualifiers
  1. .542
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:5671144"
    /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
    /sex="Both"
    /tissue_type="Islets of Langerhans"
    /dev_stage="Adult"
    /lab_host="DH10B"
    /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
      Site_2: Sal 1; Starting library constructed using
      SuperScript Plasmid Library kit (Life Technologies). cDNA
      made by oligo-dt priming. Size-selected by column
      fractionation; average insert size 1.08 kb. Library was
      amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."
BASE COUNT      87 a   182 c   160 g   113 t
ORIGIN
Query Match      0.7%; Score 23; DB 13; Length 542;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1887 AGACACAGGTGGGAATCCACATGG 1909
|||||
Db 433 AGACACAGGTGGGAATCCACATGG 411

RESULT 24
Bi9629853
LOCUS      Bi9629853              606 bp      mRNA      linear      EST 13-JAN-2001
DEFINITION MR3-HN0052-261200-002-cl2 HN0052 Homo sapiens cDNA, mRNA sequence.
ACCESSION  Bi9629853
VERSION    Bi9629853.1 GI:12175855
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 606)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
JOURNAL   Shotgun sequencing of the human transcriptome with ORF expressed
COMMENT   sequence tags
PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-HN0052-
261200-002-cl2&t3=2000-12-26&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 538.
Location/Qualifiers
  1. .606
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_lib="HN0052"
    /dev_stage="Adult"
    /note="Organ: head_normal; Vector: puc18; Site_1: SmaI;
      Site_2: SmaI; A mini-library was made by cloning products
      derived from ORESTES PCR (U.S. Letters Patent application
      No.196,716 - Ludwig Institute for Cancer Research)
      profiles into the pUC 18 vector. Reverse transcription of
      tissue mRNA and cDNA amplification were performed under
      low stringency conditions."
BASE COUNT      119 a   177 c   195 g   113 t
ORIGIN

```


/db_xref="taxon:10116"
 /clone="UI-R-DNI-cmv-e-08-0-UI"
 /clone_lib="UI-R-DNI"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-DNI library is a normalized Rat Distal Colon library (nrDC) constructed in pT377 PAC vector according to the procedure described by Bonaldo, Lennon & Soares (Normalization and Subtraction: Two Approaches to Facilitate Gene Discovery. Genome Research 6: 791-806, 1996). The oligonucleotide used to prime first strand synthesis contained the sequence tag GAAGTGCTCC between the Not I cloning site and DRI8 stretch. The Rat Distal Colon tissue was provided by Tom Freeman of the Sanger Center.

TAG_LIB=UI-R-DNI
 TAG_TISSUE=distal colon
 TAG_SEQ=GAAGTGCTCC

BASE COUNT 184 a 185 c 146 g 203 t 1 others

Query Match 0.7% Score 23; DB 14; Length 719;
 Best Local Similarity 100.0%; Pred. No. 8.6;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2843 GTGTGACGAGTGATGGTGGCTT 2865
 BQ894786
 |||||||
 Db 516 GTGTGACGAGTGATGGTGGCTT 494

RESULT 27
 BQ894786/c

LOCUS
 DEFINITION AGENCOURT 8119214 Lupsaki_dorsal_root_ganglion Homo sapiens cDNA EST 16-AUG-2002
 clone IMAGE:6179738 5', mRNA sequence.

ACCESSION BQ894786
 VERSION BQ894786.1 GI:22286800
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 914)

TITLE NTH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabps@email.nih.gov

Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LHAM3561 row: g column: 03
 High quality sequence stop: 568.

FEATURES
 source

Location/Qualifiers
 1..914
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6179738"
 /clone_lib="Lupski_dorsal_root_ganglion"
 /sex="male"
 /tissue_type="dorsal root ganglia"
 /dev_stage="adult, 36 Yr"
 /lab_host="DH10B"

/note="Vector: pCMV-SPT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors:
 5'-TCGACCCACCGGCGCG-3' and
 5'-GACTAGTCTAGATCGGCGCGCGCCCT(15)-3'. Size selected >

1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

BASE COUNT 132 a 321 c 249 g 212 t

Query Match 0.7% Score 23; DB 14; Length 914;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1887 AGACACAGGTGGATCCACATGG 1909
 |||||||
 Db 476 AGACACAGGTGGATCCACATGG 454

RESULT 28
 AV268403

LOCUS
 DEFINITION AV268403 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930534P12 3', mRNA sequence.

ACCESSION AV268403
 VERSION AV268403.1 GI:6256440
 KEYWORDS EST.
 SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 256)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tatenomura, T., Tomimaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Konno, H., et al. 1999)
 Unpublished (1999)

TITLE
 JOURNAL
 COMMENT

Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y., Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh, M., Kitzunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
 Location/Qualifiers
 1..256
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="4930534P12"
 /clone_lib="RIKEN full-length enriched, adult male testis"

FEATURES
 source

Location/Qualifiers
 1..256
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="4930534P12"
 /clone_lib="RIKEN full-length enriched, adult male testis"


```

RESULT 31
A2086396
LOCUS
DEFINITION
  163 bp      DNA      linear      GSS 08-MAY-2000
  RPCI-23-26D1.TV RPCI-23 Mus musculus genomic clone RPCI-23-26D1,
  DNA sequence.
ACCESSION
A2086396
VERSION
A2086396.1 GI:7728130
KEYWORDS
GSS.
SOURCE
  house mouse.
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 163)
  Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
  ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
  and Fraser,C.M.
  Mouse BAC End Sequences from Library RPCI-23
  Unpublished (1999)
  Other_GSSs: RPCI-23-26D1.TJ
  Contact: Shaying Zhao
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: szhao@tigr.org
  Clones are derived from the mouse BAC library RPCI-23. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
  or from Resea ch Genetics (info@resgen.com). BAC end page:
  http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
  plate: 26 row: D column: 1
  Seq primer: T7
  Class: BAC ends.
FEATURES
  source
    Location/Qualifiers
      1..163
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="RPCI-23-26D1"
        /clone_lib="RPCI-23"
        /sex="Female"
        /lab_host="DH10B"
        /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
        EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
        brain genomic DNA was isolated and partially digested
        with a combination of EcoRI and EcoRI Methylase. Size
        selected DNA was cloned into the pBACe3.6 vector at the
        EcoRI sites. The ligation products were transformed into
        DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT
  57 a 32 c 21 g 53 t
ORIGIN
  Query Match 0.7%; Score 21; DB 17; Length 163;
  Best Local Similarity 100.0%; Pred. No. 57;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1117 AAAACAACAACAACATATAA 1137
      |||||||
Db 140 AAAACAACAACAACATATAA 160

RESULT 32
AA784099
LOCUS
DEFINITION
  343 bp      mRNA      linear      EST 29-JUL-1998
  dig08a1.f1 Aspergillus nidulans 24hr asexual developmental and
  vegetative cDNA lambda zap library Emericella nidulans cDNA clone
  dig08a1 3', mRNA sequence.
ACCESSION
AA784099
VERSION
AA784099.1 GI:2844267

```

```

KEYWORDS
SOURCE
  EST.
  Emericella nidulans.
  Emericella nidulans
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
  Eurotiales; Trichocomaceae; Emericella.
REFERENCE
  1 (bases 1 to 343)
  Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R.,
  Prade,R. and Roe,B.
  An Aspergillus nidulans EST Database
  Unpublished (1998)
  Other_ESTs: dlq08a1.r1
  Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
  Department of Chemistry and Biochemistry
  Advanced Center for Genome Technology, University of Oklahoma
  620 Parrington Oval, Norman, OK 73019, USA
  Tel: 405 325 4912
  Fax: 405 325 7762
  Email: broe@ou.edu
  We anticipate the future release of the cDNA clones to the Fungal
  Genetics Stock Center
  Seq primer: M13-20
  High quality sequence stop: 301.
  Location/Qualifiers
    1..343
      /organism="Emericella nidulans"
      /strain="FGSC A26"
      /db_xref="taxon:162425"
      /clone="dig08a1"
      /clone_lib="Aspergillus nidulans 24hr asexual
      developmental and vegetative cDNA lambda zap library"
      /tissue_type="vegetative mycelia, asexual structures"
      /note="vector: pBluescript SK-; site_1: EcoRI; Site_2:
      xhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
      3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT
  85 a 94 c 75 g 89 t
ORIGIN
  Query Match 0.7%; Score 21; DB 9; Length 343;
  Best Local Similarity 100.0%; Pred. No. 71;
  Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2880 ATTGAGAATCTTAAGCAATT 2900
      |||||||
Db 19 ATTGAGAATCTTAAGCAATT 39

RESULT 33
AA821339
LOCUS
DEFINITION
  vs68a01.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
  IMAGE:1151400 5', mRNA sequence.
ACCESSION
AA821339
VERSION
AA821339.1 GI:2891207
KEYWORDS
EST.
SOURCE
  house mouse.
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 343)
  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
  Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
  Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
  Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
  Waterston,R.
  The WashU-HMMI Mouse EST Project
  Unpublished (1996)
  Contact: Marra M/Mouse EST Project
  WashU-HMMI Mouse EST Project
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: mouseest@watson.wustl.edu

```

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28ml3 rev1 ET from Amersham

High quality sequence stop: 336.
Location/Qualifiers

FEATURES

1..343
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1151400"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI ; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

BASE COUNT 84 a 103 c 95 g 61 t

ORIGIN

Query Match 0.7% Score 21; DB 9; Length 343;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 ATGAATTCAGCCCGACGAACT 772

|||||

Db 319 ATGAATTCAGCCCGACGAACT 339

RESULT 34

A1645009

LOCUS

DEFINITION AI645009 371 bp mRNA linear EST 29-APR-1999
IMAGE:1151400 5', mRNA sequence.

ACCESSION AI645009

VERSION AI645009.1 GI:4723484

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 371)

REFERENCE
AUTHORS Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

CONTACT: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:624608

This read is a RESEQUENCE of a previously sequenced mouse clone correct orientation)

Seq primer: -40RP from Gibco

High quality sequence stop: 355.

Location/Qualifiers

1..371

/organism="Mus musculus"

/strain="C57BL/6"

/db_xref="taxon:10090"

FEATURES

source

/clone="IMAGE:1151400"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"

/tissue_type="whole skin"

/dev_stage="11 weeks old"

/lab_host="SOLR (kanamycin resistant)"

/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI ; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

BASE COUNT 92 a 109 c 101 g 69 t

ORIGIN

Query Match 0.7% Score 21; DB 9; Length 371;

Best Local Similarity 100.0%; Pred. No. 73;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 ATGAATTCAGCCCGACGAACT 772

|||||

Db 321 ATGAATTCAGCCCGACGAACT 341

RESULT 35

A2223093/c

LOCUS

DEFINITION A2223093 432 bp DNA linear GSS 14-JUN-2000
RPCI-23-94H20-TV RPCI-23 Mus musculus genomic clone RPCI-23-94H20, DNA sequence.

ACCESSION A2223093

VERSION A2223093.1 GI:8531142

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 432)

REFERENCE
AUTHORS Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other_GSSs: RPCI-23-94H20.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html

Plate: 94 row: H column: 20

Seq primer: 37

Class: BAC ends.

Location/Qualifiers

1..432

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-94H20"

/clone_lib="RPCI-23"

/sex="Female"

/lab_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:

EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or

brain genomic DNA was isolated and partially digested

with a combination of EcoRI and EcoRI Methylase. Size

selected DNA was cloned into the pBACe3.6 vector at the

EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). *

```

BASE COUNT      75 a   123 c   122 g   112 t
ORIGIN
Query Match      0.7%; Score 21; DB 17; Length 432;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 752 ATGAATTCACGCCAGAACT 772
      |||||||
Db 115 ATGAATTCACGCCAGAACT 95

RESULT 36
AQ555443/c
LOCUS
DEFINITION HS_5224_A2_B05_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=800 Col=10 Row=C, DNA sequence.
ACCESSION AQ555443
VERSION AQ555443.1 GI:4914996
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 437)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 800 row: C column: 10
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 437.
FEATURES
source
1..437
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=800 Col=10 Row=C"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"
BASE COUNT 168 a 60 c 81 g 128 t
ORIGIN

Query Match      0.7%; Score 21; DB 17; Length 437;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1670 GTGGCATCCATTATATCAAG 1690
      |||||||
Db 387 GTGGCATCCATTATATCAAG 367

RESULT 37
CNS00SV2
LOCUS
DEFINITION Arabidopsis thaliana genome survey sequence SP6 end of BAC T2N9 of
TAMU library from strain Columbia of Arabidopsis thaliana, genomic
survey sequence.
ACCESSION AL088892
VERSION AL088892.1 GI:5290032
KEYWORDS GSS.
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
SpERMATOPHYTES; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 462)
AUTHORS Salanoubat,M., Choisme,N., Artiguenave,F., Brottier,P., Wincker,P.,
Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 462)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- web : www.genoscope.cns.fr)
FEATURES
source
1..462
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="T2N9"
/clone_lib="TAMU"
/note="end : SP6"
BASE COUNT 129 a 87 c 70 g 176 t
ORIGIN

Query Match      0.7%; Score 21; DB 17; Length 462;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 591 CAAATTCGTCTCTCTCTCCG 611
      |||||||
Db 239 CAAATTCGTCTCTCTCTCCG 219

RESULT 38
AZ360053/c
LOCUS
DEFINITION 1M0103H11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0103H11 F, DNA sequence.
ACCESSION AZ360053
VERSION AZ360053.1 GI:10473753
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 602)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

```



```
RESULT 40
BI854236      775 bp      mRNA      linear      EST 10-OCT-2001
LOCUS        603381263F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5389239 5',
DEFINITION   mRNA sequence.
ACCESSION    BI854236
VERSION      BI854236.1 GI:15994983
KEYWORDS     EST.
SOURCE       house mouse.
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      1 (bases 1 to 775)
TITLE        NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1991 row: m column: 16
High quality sequence stop: 764.
FEATURES     source
             Location/Qualifiers
             1..775
             /organism="Mus musculus"
             /strain="NMRI"
             /db_xref="taxon:10090"
             /clone="IMAGE:5389239"
             /clone_lib="NCI_CGAP_Mam4"
             /tissue_type="tumor, gross tissue"
             /dev_stage="5 months"
             /lab_host="DH10B"
             /note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: SalI;
             Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
             Library constructed by Life Technologies. Investigators
             providing samples: Lothar Hennighausen/Priscilla Furth,
             NIH Reference for transgenic model: Li et al., Cell Growth
             and Differentiation 7, 3-11 (1996)."
```

```
BASE COUNT      226 a  162 c  196 g  191 t
ORIGIN
Query Match      0.7%; Score 21; DB 13; Length 775;
Best Local Similarity 100.0%; Pred. NO. 91;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2965 CAAGTGTATCCAAAGTTAACT 2985
|||||
DB 386 CAAGTGTATCCAAAGTTAACT 406

RESULT 41
BQ278245      950 bp      mRNA      linear      EST 07-MAY-2002
LOCUS        AGENCOURT_6838625 NIH_MGC_128 Homo sapiens cDNA clone IMAGE:5811028
DEFINITION   5', mRNA sequence.
ACCESSION    BQ278245
VERSION      BQ278245.1 GI:20488453
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      1 (bases 1 to 950)
TITLE        NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
```

```
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgabs-r@mail.nih.gov
             Tissue Procurement: NCI
             cDNA Library Preparation: Michael Brownstein Laboratory
             DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2059 row: d column: 05
             High quality sequence stop: 447.
FEATURES     source
             Location/Qualifiers
             1..950
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="IMAGE:5811028"
             /clone_lib="NIH_MGC_128"
             /tissue_type="mixed (pool of 40 RNAs)"
             /lab_host="DH10B (T1-phage-resistant)"
             /note="Vector: pDNR-LIB; Site.1: SfiI (ggccattatggcc);
             Site.2: SfiI (ggccgctcgcc); Double-stranded cDNA was
             prepared from a pool of 40 cell line polyA+ RNAs (bladder
             - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
             4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
             kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
             , ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
             gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
             used in cloning as follows:
             5'-AACGAGTGTATCAGCGACAGTGGCATTACGCCGGG-3' and
             5'-ATTCTAGAGCCGAGCGCCGACATG-qf(30)NN-3'. Full-length
             enriched library was constructed using the Clontech
             Creator SMART kit and size-selected to contain the >2 kb
             size fraction (other fractions present in NIH_MGC_126 and
             NIH_MGC_127). Library created in the laboratory of T.
             Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
             Library."
BASE COUNT      286 a  297 c  140 g  218 t  9 others
ORIGIN
Query Match      0.7%; Score 21; DB 14; Length 950;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1117 AAAACAAACACAAACATAAA 1137
|||||
DB 520 AAAACAAACACAAACATAAA 540

RESULT 42
BG571228      1147 bp      mRNA      linear      EST 10-APR-2001
LOCUS        602592168F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4719424 5',
DEFINITION   mRNA sequence.
ACCESSION    BG571228
VERSION      BG571228.1 GI:13578881
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      1 (bases 1 to 1147)
TITLE        NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgabs-r@mail.nih.gov
             Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
```


Plate: LLCM1572 row: h column: 17
High quality sequence stop: 240.

FEATURES

source

Location/Qualifiers

1. .1147

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="IMAGE:4719424"

/lab_host="NIH_MGC_79"

/note="Organ: placenta; Vector: pDNR-LIB (Clontech);"

Site_1: Sfil (ggcgctcgcc); Site_2: Sfil (ggccatagggc

); 5' and 3' adaptors were used in cloning as follows: 5'

adaptor sequence: 5'-CAGGCCATATGGCC-3' and 3' adaptor

sequence: 5'-ATTCTAGAGCGGCGGCGCATG-dT(30)BN-3'

(where B = A, C, or G and N = A, C, G, or T). Average

insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies

contained inserts by PCR. This library was enriched for

full-length clones and was constructed by Clontech

Laboratories (Palo Alto, CA). Note: this is a NIH_MGC

Library."

BASE COUNT 477 a 135 c 499 g 36 t

ORIGIN

Query Match 0.7%; Score 21; DB 12; Length 1147;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1113 ACAGAAAAACAACAACAACA 1133

Db 298 ACAGAAAAACAACAACAACA 318

RESULT 43

LOCUS B1142462

DEFINITION SWOV3MCAm62G10SK Onchocerca volvulus molting L3 larva cDNA

(SL96MLW-Ovml3) Onchocerca volvulus cDNA clone SWOV3MCAm62G10 5',

mRNA sequence.

ACCESSION B1142462

VERSION B1142462.1 GI:14624172

KEYWORDS EST.

SOURCE Onchocerca volvulus.

ORGANISM Onchocerca volvulus

REFERENCE Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.

Genes expressed in molting L3 larvae of Onchocerca volvulus

Unpublished (1997)

Contact: Steven A. Williams

Molecular Parasitology

Smith College Department of Biological Sciences

Department of Biological Sciences, Clark Science Center, Smith

College, Northampton, MA, 01063, USA

Tel: 4135853826

Fax: 4135853786

Email: genome@smith.edu

Seq primer: pBluescript SK.

Location/Qualifiers

1. .64

/organism="Onchocerca volvulus"

/strain="Kumba, Cameroon"

/db_xref="taxon:6282"

/clone_lib="SWOV3MCAm62G10"

(SL96MLW-Ovml3)

/dev_stage="molting L3"

/lab_host="xLi-Blue MRF"

/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:

Xho I; Filarial nematode parasite of humans. Third-stage

larvae, L3, were isolated from infected black flies in

Cameroon (forest strain). The L3 were cultured in 20% FCS

in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in

culture. L3 of O. volvulus molt to fourth-stage larvae by

day 5 in culture. mRNA was isolated from approximately

6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3

in culture, and converted to double-stranded cDNA using

reverse transcriptase and oligo(dT) followed by RNase H

and DNA pol I. The library was constructed in the lambda

Uni-zap XR vector and has 1 x 10E6 independent

recombinants and the average insert size is ~1200 bp. The

library was constructed by Sara Lustigman and Michelle

Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.

The library is available from Dr. Sara Lustigman (email:

slustig@nyc.org)."

BASE COUNT 22 a 11 c 19 g 21 t

ORIGIN

Query Match 0.7%; Score 20; DB 10; Length 73;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

QY 2329 GAAGAAGATGCTATAAACT 2348

Db 42 GAAGAAGATGCTATAAACT 61

RESULT 44

LOCUS BE638399

DEFINITION SWOVLCAS15B03SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OVL2)

Onchocerca volvulus cDNA clone SWOVLCAS15B03 5', mRNA sequence.

ACCESSION BE638399

VERSION BE638399.1 GI:9937018

KEYWORDS EST.

SOURCE Onchocerca volvulus.

ORGANISM Onchocerca volvulus

REFERENCE Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.

Genes expressed in molting L3 larvae of Onchocerca volvulus

Unpublished (1997)

Contact: Steven A. Williams

Molecular Parasitology

Smith College Department of Biological Sciences

Department of Biological Sciences, Clark Science Center, Smith

College, Northampton, MA, 01063, USA

Tel: 4135853826

Fax: 4135853786

Email: genome@smith.edu

Seq primer: pBluescript SK.

Location/Qualifiers

1. .73

/organism="Onchocerca volvulus"

/db_xref="taxon:6282"

/clone_lib="SWOVLCAS15B03"

(SAW98MLW-OVL2)

/dev_stage="L2"

/lab_host="xLi-Blue MRF"

/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:

Xho I; Filarial nematode parasite of humans. mRNA was

prepared from approximately 9,000 L2s isolated from

infected mosquitoes from Kumba, Cameroon and converted to

double-stranded cDNA using reverse transcriptase and

oligo(dT) followed by RNase H and DNA pol I. The library

has 7.3 x 10E4 independent recombinants and the average

insert size is approximately 1kb. The library was

constructed by Michelle Lizotte-Waniewski. The library is

available from Dr. S.A. Williams, email: genome@smith.edu."

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2329 GAAGAAGATGCTATAAAACT 2348
|||||
Db 27 GAAGAAGATGCTATAAAACT 46

RESULT 45
A0069062/c
LOCUS
DEFINITION HS_2255_B2_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=6 Row=P, DNA sequence.
ACCESSION A0069062
VERSION A0069062.1 GI:3384261
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 205)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2255 row: P column: 6
Class: BAC ends
High quality sequence stop: 205.
Location/Qualifiers
1..205
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 54 a 41 c 52 g 57 t 1 others
ORIGIN
Query Match 0.7%; Score 20; DB 17; Length 205;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1112 TACAGAAAACAAACACAAA 1131
|||||
Db 134 TACAGAAAACAAACACAAA 115

RESULT 46
B1315256
LOCUS
DEFINITION B1315256 dah96e06.y1 NICHID XGC Emb4 Xenopus laevis cdna clone IMAGE:4957906 5', mRNA sequence.
ACCESSION B1315256
VERSION B1315256.1 GI:14989583
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus.
1 (bases 1 to 215)

FEATURES
source
1..215
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:943135"

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 197.
Location/Qualifiers
1..215
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:4957906"
/clone_lib="NICHID XGC Emb4"
/dev_stage="embryo, stage 31-32"
/lab_host="DH10B (phage-resistant)"
/note="Organ: whole embryo; Vector: pCMV-SPORT6; Site_1: Noti; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."

BASE COUNT 72 a 32 c 37 g 74 t
ORIGIN
Query Match 0.7%; Score 20; DB 13; Length 215;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2790 TTTTGGAAAGAACCTCTGA 2809
|||||
Db 196 TTTTGGAAAGAACCTCTGA 215

RESULT 47
AA493806
LOCUS
DEFINITION AA493806 nh02f04.s1 NCI-CGAP_Thy1 Homo sapiens cdna clone IMAGE:943135, mRNA sequence.
ACCESSION AA493806
VERSION AA493806.1 GI:2223647
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 216)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 294 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
1..216
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:943135"

FEATURES
source
1..216
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:943135"

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/clone_lib="NCI_CGAP_Thy1"
/tissue_type="thyroid"
/lab_host="DH10B"
/notes="Vector: pAMP10; mRNA made from invasive thyroid
tumor, cDNA made by oligo-dT priming. Non-directionally
cloned. Size-selected on agarose gel, average insert size
600 bp. Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
BASE COUNT      57 a      65 c      37 g      57 t
ORIGIN

Query Match      0.7%; Score 20; DB 9; Length 216;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2190 GCACATCACATCTGTAACAA 2209
|||||
Db 92 GCACATCACATCTGTAACAA 111

RESULT 48
LOCUS      AI366637      225 bp      mRNA      linear      EST 08-JAN-1999
DEFINITION SWOV3MCAM11C04SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-Ovml3) Onchocerca volvulus cDNA clone SWOV3MCAM11C04 5',
mRNA sequence.
ACCESSION  AI366637
VERSION     AI366637.1 GI:4136382
KEYWORDS    EST.
SOURCE      Onchocerca volvulus.
ORGANISM    Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
REFERENCE   1 (bases 1 to 225)
AUTHORS    Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.
TITLE      Genes expressed in molting L3 larvae of Onchocerca volvulus
JOURNAL    Unpublished (1997)
COMMENT     Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pbluescript SK.
Location/Qualifiers
1..225
/organism="Onchocerca volvulus"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone_lib="SWOV3MCAM11C04"
/clone_lib="Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-Ovml3)"
/dev_stage="molting L3"
/lab_host="XLI-Blue MRF"
/notes="Vector: Lambda Uni-ZAP XR; Site.1: Eco RI; Site.2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black flies in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is ~1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
The library is available from Dr. Sara Lustigman (email:
slustigm@nyc.org)."

FEATURES
source
1..225
/organism="Onchocerca volvulus"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone_lib="SWOV3MCAM11C04"
/clone_lib="Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-Ovml3)"
/dev_stage="molting L3"
/lab_host="XLI-Blue MRF"
/notes="Vector: Lambda Uni-ZAP XR; Site.1: Eco RI; Site.2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black flies in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is ~1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
The library is available from Dr. Sara Lustigman (email:
slustigm@nyc.org)."

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```

BASE COUNT      65 a      39 c      57 g      64 t
ORIGIN

Query Match      0.7%; Score 20; DB 9; Length 225;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2329 GAAGAAGATGCTATAAAACT 2348
|||||
Db 30 GAAGAAGATGCTATAAAACT 49

RESULT 49
LOCUS      AI603832      248 bp      mRNA      linear      EST 21-APR-1999
DEFINITION SWOV3MCAM27A08SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-Ovml3) Onchocerca volvulus cDNA clone SWOV3MCAM27A08 5',
mRNA sequence.
ACCESSION  AI603832
VERSION     AI603832.1 GI:4612981
KEYWORDS    EST.
SOURCE      Onchocerca volvulus.
ORGANISM    Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
REFERENCE   1 (bases 1 to 248)
AUTHORS    Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.
TITLE      Genes expressed in molting L3 larvae of Onchocerca volvulus
JOURNAL    Unpublished (1997)
COMMENT     Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pbluescript SK.
Location/Qualifiers
1..248
/organism="Onchocerca volvulus"
/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone_lib="SWOV3MCAM27A08"
/clone_lib="Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-Ovml3)"
/dev_stage="molting L3"
/lab_host="XLI-Blue MRF"
/notes="Vector: Lambda Uni-ZAP XR; Site.1: Eco RI; Site.2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black flies in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is ~1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
The library is available from Dr. Sara Lustigman (email:
slustigm@nyc.org)."

BASE COUNT      71 a      47 c      58 g      69 t
ORIGIN

Query Match      0.7%; Score 20; DB 9; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2329 GAAGAAGATGCTATAAAACT 2348

```

```
|||||
Db 14 GAAGAAATGCTATAAACT 33

RESULT 50
AZ891870
LOCUS
DEFINITION A2891870 299 bp DNA linear GSS 05-MAR-2001
            RPCI-24-180D14.TJ RPCI-24 Mus musculus genomic clone RPCI-24-180D14
            , DNA sequence.
ACCESSION
A2891870
VERSION A2891870.1 GI:13210815
KEYWORDS
SOURCE GSS.
ORGANISM house mouse.
            Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 299)
            Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
            Mouse BAC End Sequences from Library RPCI-24
            Unpublished (1999)
            Other_GSSs: RPCI-24-180D14.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pjejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html
            Plate: 180 row: D column: 14
            Seq primer: SP6
            Class: BAC ends.
FEATURES
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        Location/Qualifiers
            1..299
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                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="RPCI-24-180D14"
                /clone_lib="RPCI-24"
                /sex="Male"
                /cell_type="Spleen/Brain"
                /note="Vector: pFARBAC1; Site_1: BamH1; Site_2: BamH1;
                RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                library was cloned in the pFARBAC1 cloning vector at the
                BamH1 sites using MboI partially digested male C57BL/6J
                DNA."
BASE COUNT 103 a 57 c 85 g 54 t
ORIGIN

Query Match 0.7%; Score 20; DB 17; Length 299;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 954 TGAAGGCTTGTGTGCTCCAAA 973
    |||||||||||||||
Db 202 TGAAGGCTTGTGTGCTCCAAA 221

Search completed: January 31, 2003, 00:11:01
Job time : 4188 secs
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GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 22:51:05 ; Search time 102 Seconds
(without alignments)
9236.382 Million cell updates/sec

Title: US-09-697-089-3
Perfect score: 3072
Sequence: 1 atgaattcataaagacaa.....cttttaactagtaactgct 3072

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 12

Total number of hits satisfying chosen parameters: 47916

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_NA:*1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	0.6	888	4	US-09-071-035-425
2	18	0.6	1094	2	US-08-870-518-34
3	18	0.6	1515	3	US-08-747-221B-16
4	18	0.6	1515	3	US-08-747-221B-17
5	18	0.6	1515	4	US-09-005-051-16
6	18	0.6	1515	4	US-09-005-051-17
7	18	0.6	1611	6	5213972-6
8	18	0.6	1550	3	US-08-747-221B-60
9	18	0.6	1650	3	US-08-747-221B-61
10	18	0.6	1650	4	US-09-005-051-60
11	18	0.6	1650	4	US-09-005-051-61
12	18	0.6	1721	3	US-08-857-213-2
13	18	0.6	1800	1	US-08-139-937-11
14	18	0.6	1800	5	PCT-US93-11310-11
15	18	0.6	1926	4	US-09-079-955-10
16	18	0.6	1982	3	US-08-747-221B-13
17	18	0.6	1982	3	US-08-747-221B-15
18	18	0.6	1982	4	US-09-005-051-13
19	18	0.6	1982	4	US-09-005-051-15
20	18	0.6	2144	3	US-08-747-221B-57
21	18	0.6	2144	3	US-08-747-221B-59
22	18	0.6	2144	4	US-09-005-051-57
23	18	0.6	2144	4	US-09-005-051-59
24	18	0.6	3000	4	US-09-192-104-1
25	18	0.6	3000	4	US-09-543-446-1
26	18	0.6	3969	4	US-09-518-386B-4
27	18	0.6	4982	3	US-08-699-103B-1
					Sequence 425, App
					Sequence 34, Appl
					Sequence 16, Appl
					Sequence 17, Appl
					Sequence 16, Appl
					Sequence 17, Appl
					Patent No. 5213972
					Sequence 60, Appl
					Sequence 61, Appl
					Sequence 60, Appl
					Sequence 61, Appl
					Sequence 2, Appl
					Sequence 11, Appl
					Sequence 10, Appl
					Sequence 11, Appl
					Sequence 10, Appl
					Sequence 13, Appl
					Sequence 15, Appl
					Sequence 13, Appl
					Sequence 15, Appl
					Sequence 57, Appl
					Sequence 59, Appl
					Sequence 1, Appl
					Sequence 4, Appl
					Sequence 1, Appl

101	16	0.5	733	1	US-08-461-360A-3	Sequence 3, Appli	c 174	16	0.5	1824	4	US-09-616-990-1	Sequence 1, Appli
102	16	0.5	733	1	US-08-461-359-3	Sequence 3, Appli	c 175	16	0.5	1828	4	US-09-280-116-103	Sequence 108, App
103	16	0.5	733	1	PCT-US94-12904-3	Sequence 3, Appli	c 176	16	0.5	1857	4	US-08-456-200B-18	Sequence 13, Appl
104	16	0.5	795	2	US-08-822-028-11	Sequence 11, Appl	c 177	16	0.5	1927	4	US-08-837-199A-9	Sequence 9, Appli
105	16	0.5	795	2	US-08-479-285-11	Sequence 11, Appl	c 178	16	0.5	1927	4	US-08-837-199A-40	Sequence 40, Appli
c 106	16	0.5	803	3	US-08-454-928-9	Sequence 9, Appli	c 179	16	0.5	1929	4	US-08-837-199A-11	Sequence 11, Appl
107	16	0.5	803	4	US-09-221-017B-684	Sequence 684, App	c 180	16	0.5	1929	4	US-08-837-199A-41	Sequence 41, Appli
c 108	16	0.5	843	4	US-09-296-284-24	Sequence 24, Appl	c 181	16	0.5	1964	4	US-09-117-853-1	Sequence 1, Appli
c 109	16	0.5	897	5	PCT-US96-05320A-303	Sequence 303, App	c 182	16	0.5	2157	4	US-08-837-199A-15	Sequence 15, Appl
c 110	16	0.5	921	4	US-09-296-284-3	Sequence 3, Appli	c 183	16	0.5	2158	4	US-08-837-199A-43	Sequence 43, Appl
111	16	0.5	1001	4	US-08-641-638-370	Sequence 370, App	c 184	16	0.5	2222	3	US-09-197-380-1	Sequence 1, Appli
112	16	0.5	1001	4	US-08-641-638-371	Sequence 371, App	c 185	16	0.5	2224	4	US-09-261-855-1	Sequence 1, Appli
113	16	0.5	1001	4	US-09-641-638-372	Sequence 372, App	c 186	16	0.5	2356	1	US-08-105-483-222	Sequence 222, App
114	16	0.5	1047	2	US-08-535-276-7	Sequence 7, Appli	c 187	16	0.5	2356	1	US-08-220-151-75	Sequence 75, Appl
115	16	0.5	1047	2	US-09-335-234-7	Sequence 7, Appli	c 188	16	0.5	2356	1	US-08-413-118-75	Sequence 75, Appl
116	16	0.5	1054	1	US-08-152-485-1	Sequence 1, Appli	c 189	16	0.5	2356	1	US-08-224-657-51	Sequence 51, Appl
117	16	0.5	1054	1	US-08-463-089-1	Sequence 1, Appli	c 190	16	0.5	2356	1	US-08-709-209-222	Sequence 222, App
118	16	0.5	1054	1	US-08-461-360A-1	Sequence 1, Appli	c 191	16	0.5	2356	1	US-08-458-101-222	Sequence 222, App
119	16	0.5	1054	1	US-08-461-359-1	Sequence 1, Appli	c 192	16	0.5	2356	1	US-08-184-009-78	Sequence 78, Appl
120	16	0.5	1054	5	PCT-US94-12904-1	Sequence 1, Appli	c 193	16	0.5	2356	2	US-08-417-210A-68	Sequence 68, Appl
c 121	16	0.5	1059	4	US-08-837-199A-23	Sequence 23, Appl	c 194	16	0.5	2356	2	US-08-458-356-78	Sequence 78, Appl
c 122	16	0.5	1059	4	US-08-837-199A-47	Sequence 47, Appl	c 195	16	0.5	2356	3	US-08-458-356-78	Sequence 75, Appl
c 123	16	0.5	1073	4	US-08-476-102A-1	Sequence 1, Appli	c 196	16	0.5	2356	4	US-08-473-446-75	Sequence 78, Appl
c 124	16	0.5	1075	4	US-08-837-199A-21	Sequence 21, Appl	c 197	16	0.5	2356	4	US-08-460-736-78	Sequence 51, Appl
c 125	16	0.5	1076	4	US-08-837-199A-46	Sequence 46, Appl	c 198	16	0.5	2413	4	US-09-367-206-2	Sequence 2, Appli
126	16	0.5	1081	2	US-08-832-883-57	Sequence 57, Appl	c 199	16	0.5	2429	4	US-09-360-545-68	Sequence 68, Appl
127	16	0.5	1081	2	US-08-832-877-57	Sequence 57, Appl	c 200	16	0.5	2453	5	PCT-US95-07180-1	Sequence 1, Appli
c 128	16	0.5	1103	3	US-08-899-786-13	Sequence 13, Appl	c 201	16	0.5	2465	1	US-08-421-661-5	Sequence 5, Appli
c 129	16	0.5	1104	4	US-08-423-399B-36	Sequence 36, Appl	c 202	16	0.5	2545	1	US-07-869-933-22	Sequence 22, Appl
c 130	16	0.5	1113	4	US-09-134-001C-566	Sequence 566, App	c 203	16	0.5	2545	4	US-09-103-663-22	Sequence 22, Appl
c 131	16	0.5	1134	4	US-08-432-999A-9	Sequence 9, Appli	c 204	16	0.5	2568	4	US-08-837-199A-1	Sequence 1, Appli
c 132	16	0.5	1162	1	US-08-423-399B-34	Sequence 34, Appl	c 205	16	0.5	2608	4	US-09-404-879A-386	Sequence 386, App
c 133	16	0.5	1166	5	PCT-US96-12129B-1	Sequence 1, Appli	c 206	16	0.5	2652	1	US-08-318-831-1	Sequence 1, Appli
c 134	16	0.5	1168	4	US-08-858-207A-182	Sequence 182, App	c 207	16	0.5	2675	1	US-08-232-079-1	Sequence 1, Appli
c 135	16	0.5	1173	3	US-08-740-644-1	Sequence 1, Appli	c 208	16	0.5	2700	4	US-09-236-284-8	Sequence 8, Appli
c 136	16	0.5	1178	2	US-08-933-750C-88	Sequence 88, Appl	c 209	16	0.5	2916	4	US-08-976-259-22	Sequence 22, Appl
c 137	16	0.5	1178	3	US-09-234-613-88	Sequence 88, Appl	c 210	16	0.5	2943	4	US-09-404-879A-385	Sequence 385, App
c 138	16	0.5	1196	4	US-09-149-476-225	Sequence 25, App	c 211	16	0.5	2980	4	US-08-456-200B-12	Sequence 12, Appl
c 139	16	0.5	1220	4	US-09-149-476-57	Sequence 57, Appl	c 212	16	0.5	2996	4	US-09-404-879A-311	Sequence 311, App
c 140	16	0.5	1244	2	US-08-204-288-3	Sequence 3, Appli	c 213	16	0.5	3014	2	US-08-808-982-1	Sequence 1, Appli
c 141	16	0.5	1284	1	US-07-882-790-3	Sequence 3, Appli	c 214	16	0.5	3014	4	US-08-306-902A-1	Sequence 1, Appli
c 142	16	0.5	1311	4	US-09-134-001C-386	Sequence 386, App	c 215	16	0.5	3018	3	US-08-942-572-1	Sequence 1, Appli
c 143	16	0.5	1330	2	US-08-868-288A-4	Sequence 4, Appli	c 216	16	0.5	3147	4	US-08-887-534A-84	Sequence 84, Appl
c 144	16	0.5	1330	3	US-09-235-373-4	Sequence 4, Appli	c 217	16	0.5	3209	4	US-08-837-199A-5	Sequence 5, Appli
c 145	16	0.5	1330	3	US-09-388-993-4	Sequence 4, Appli	c 218	16	0.5	3209	4	US-08-837-199A-37	Sequence 37, Appl
c 146	16	0.5	1343	4	US-09-455-921A-1	Sequence 1, Appli	c 219	16	0.5	3218	2	US-08-677-862-1	Sequence 1, Appli
c 147	16	0.5	1370	1	US-08-592-126-79	Sequence 79, Appl	c 220	16	0.5	3218	2	US-09-252-571-1	Sequence 1, Appli
c 148	16	0.5	1404	3	US-08-961-083-9	Sequence 9, Appli	c 221	16	0.5	3218	3	US-09-434-065-1	Sequence 1, Appli
c 149	16	0.5	1431	4	US-09-465-558-67	Sequence 67, Appl	c 222	16	0.5	3403	4	US-08-448-489-2	Sequence 2, Appli
c 150	16	0.5	1455	1	US-08-423-399B-32	Sequence 32, Appl	c 223	16	0.5	3437	3	US-08-704-711A-9	Sequence 9, Appli
c 151	16	0.5	1477	3	US-08-096-181A-7	Sequence 7, Appli	c 224	16	0.5	3437	4	US-09-521-220-9	Sequence 9, Appli
c 152	16	0.5	1477	5	PCT-US94-08326-7	Sequence 7, Appli	c 225	16	0.5	3456	3	US-08-704-711A-8	Sequence 8, Appli
c 153	16	0.5	1491	4	US-09-058-947A-3	Sequence 3, Appli	c 226	16	0.5	3456	4	US-09-521-220-8	Sequence 8, Appli
c 154	16	0.5	1502	4	US-08-868-373-11	Sequence 11, Appl	c 227	16	0.5	3636	4	US-09-090-535-5	Sequence 5, Appli
c 155	16	0.5	1509	1	US-08-113-052-1	Sequence 1, Appli	c 228	16	0.5	3636	4	US-09-090-535-6	Sequence 6, Appli
c 156	16	0.5	1514	4	US-08-946-165A-219	Sequence 219, App	c 229	16	0.5	3636	4	US-09-090-535-7	Sequence 7, Appli
c 157	16	0.5	1636	4	US-09-117-853-7	Sequence 7, Appli	c 230	16	0.5	3722	4	US-09-058-947A-1	Sequence 1, Appli
c 158	16	0.5	1642	4	US-09-117-853-5	Sequence 5, Appli	c 231	16	0.5	3722	4	US-09-058-947A-1	Sequence 1, Appli
c 159	16	0.5	1642	4	US-09-117-853-9	Sequence 9, Appli	c 232	16	0.5	3957	1	US-07-689-008-5	Sequence 5, Appli
c 160	16	0.5	1643	4	US-09-117-853-3	Sequence 3, Appli	c 233	16	0.5	4059	4	US-09-500-123-11	Sequence 11, Appl
c 161	16	0.5	1669	4	US-08-984-709A-51	Sequence 51, Appl	c 234	16	0.5	4130	4	US-09-657-452A-10	Sequence 10, Appl
c 162	16	0.5	1755	1	US-07-912-900-29	Sequence 29, App	c 235	16	0.5	4157	2	US-08-162-146-2	Sequence 2, Appli
c 163	16	0.5	1755	1	US-08-285-309-29	Sequence 29, Appl	c 236	16	0.5	4157	4	US-09-314-127-2	Sequence 2, Appli
c 164	16	0.5	1755	2	US-08-502-046-29	Sequence 29, Appl	c 237	16	0.5	4161	3	US-08-790-517-1	Sequence 1, Appli
c 165	16	0.5	1761	4	US-09-404-879A-387	Sequence 387, App	c 238	16	0.5	4161	3	US-08-790-517-19	Sequence 19, Appl
c 166	16	0.5	1796	4	US-09-276-531-113	Sequence 113, App	c 239	16	0.5	4181	1	US-07-670-611-1	Sequence 1, Appli
c 167	16	0.5	1807	4	US-09-058-947A-2	Sequence 2, Appli	c 240	16	0.5	4181	1	US-08-220-674-1	Sequence 1, Appli
c 168	16	0.5	1812	1	US-07-912-900-28	Sequence 28, Appl	c 241	16	0.5	4181	1	US-08-445-186-1	Sequence 1, Appli
c 169	16	0.5	1812	1	US-08-285-309-28	Sequence 28, Appl	c 242	16	0.5	4181	1	US-08-446-549-1	Sequence 1, Appli
c 170	16	0.5	1812	1	US-08-313-075A-37	Sequence 37, Appl	c 243	16	0.5	4181	2	US-08-446-550-1	Sequence 1, Appli
c 171	16	0.5	1812	2	US-08-502-046-28	Sequence 28, Appl	c 244	16	0.5	4258	3	US-07-765-830A-5	Sequence 5, Appli
c 172	16	0.5	1821	4	US-09-537-682-2	Sequence 2, Appli	c 245	16	0.5	4335	4	US-08-974-549A-6	Sequence 6, Appli
c 173	16	0.5	1824	3	US-08-606-505B-1	Sequence 1, Appli	c 246	16	0.5	4337	3	US-09-187-049-1	Sequence 1, Appli

247	16	0.5	4550	4	US-09-338-907-182	Sequence 182, App	c 320	15	0.5	33	4	US-09-424-620B-22	Sequence 22, Appl
248	16	0.5	4550	4	US-09-218-207-182	Sequence 182, App	c 321	15	0.5	132	3	US-08-866-340-8	Sequence 8, Appl
249	16	0.5	4566	1	US-08-484-101B-37	Sequence 37, Appl	c 322	15	0.5	173	4	US-09-020-956-147	Sequence 147, App
250	16	0.5	4567	4	US-08-714-524B-37	Sequence 37, Appl	c 323	15	0.5	173	4	US-09-030-607-147	Sequence 147, App
251	16	0.5	4581	4	US-08-961-527-125	Sequence 125, App	c 324	15	0.5	173	4	US-09-605-785-147	Sequence 147, App
252	16	0.5	4940	1	US-08-484-105-1	Sequence 1, Appl	c 325	15	0.5	173	4	US-09-439-313-147	Sequence 147, App
253	16	0.5	4940	1	US-08-484-106-1	Sequence 1, Appl	c 326	15	0.5	173	4	US-09-352-616A-147	Sequence 147, App
254	16	0.5	5089	6	5177197-31	Patent No. 5177197	c 327	15	0.5	173	4	US-09-332-149A-147	Sequence 147, App
255	16	0.5	5111	4	US-09-004-838-118	Sequence 118, App	c 328	15	0.5	203	1	US-08-222-177A-7	Sequence 7, Appl
256	16	0.5	5247	1	US-08-920-812-15	Sequence 15, App	c 329	15	0.5	203	1	US-08-466-033-19	Sequence 19, Appl
257	16	0.5	5247	1	US-08-920-827-15	Sequence 15, App	c 330	15	0.5	203	1	US-08-444-733-19	Sequence 19, Appl
258	16	0.5	5247	1	US-08-921-177-15	Sequence 15, App	c 331	15	0.5	203	2	US-08-464-134-19	Sequence 19, Appl
259	16	0.5	5247	1	US-08-362-577C-15	Sequence 15, App	c 332	15	0.5	203	2	US-08-461-361-19	Sequence 19, Appl
260	16	0.5	5247	2	US-09-820-828-15	Sequence 15, App	c 333	15	0.5	203	2	US-08-485-910-19	Sequence 19, Appl
261	16	0.5	5402	4	US-09-221-017B-194	Sequence 194, App	c 334	15	0.5	203	5	PCT-US95-06266-19	Sequence 19, Appl
262	16	0.5	6463	2	US-08-962-284-3	Sequence 3, Appl	c 335	15	0.5	207	3	US-09-012-515A-25	Sequence 25, Appl
263	16	0.5	6755	3	US-08-931-999-4	Sequence 4, Appl	c 336	15	0.5	207	3	US-08-360-144A-25	Sequence 25, Appl
264	16	0.5	6822	4	US-09-426-998-3	Sequence 3, Appl	c 337	15	0.5	207	4	US-09-012-504A-25	Sequence 25, Appl
265	16	0.5	7082	4	US-09-362-831-1	Sequence 1, Appl	c 338	15	0.5	207	5	PCT-US95-06722-25	Sequence 25, Appl
266	16	0.5	7125	1	US-07-745-206A-1	Sequence 1, Appl	c 339	15	0.5	210	4	US-09-134-001C-1661	Sequence 1661, App
267	16	0.5	7125	2	US-08-311-363-1	Sequence 1, Appl	c 340	15	0.5	227	4	US-08-991-789A-183	Sequence 183, App
268	16	0.5	7635	1	US-08-455-543A-1	Sequence 1, Appl	c 341	15	0.5	227	4	US-09-062-451-183	Sequence 183, App
269	16	0.5	7635	1	US-08-455-543A-23	Sequence 23, Appl	c 342	15	0.5	227	4	US-09-598-326-183	Sequence 183, App
270	16	0.5	7635	2	US-08-193-078B-1	Sequence 1, Appl	c 343	15	0.5	237	1	US-08-466-033-3	Sequence 3, Appl
271	16	0.5	7635	2	US-08-193-078B-29	Sequence 29, Appl	c 344	15	0.5	237	1	US-08-444-733-3	Sequence 3, Appl
272	16	0.5	7635	2	US-08-223-305C-1	Sequence 1, Appl	c 345	15	0.5	237	2	US-08-464-134-3	Sequence 3, Appl
273	16	0.5	7635	2	US-08-223-305C-23	Sequence 23, Appl	c 346	15	0.5	237	2	US-08-461-361-3	Sequence 3, Appl
274	16	0.5	7635	2	US-08-149-097D-1	Sequence 1, Appl	c 347	15	0.5	237	2	US-08-611-757-106	Sequence 106, App
275	16	0.5	7635	3	US-08-949-386-1	Sequence 1, Appl	c 348	15	0.5	237	2	US-08-485-910-3	Sequence 3, Appl
276	16	0.5	7635	3	US-08-450-562-1	Sequence 1, Appl	c 349	15	0.5	237	5	PCT-US95-05980-106	Sequence 106, App
277	16	0.5	7635	4	US-08-984-709A-1	Sequence 1, Appl	c 350	15	0.5	237	5	PCT-US95-06266-3	Sequence 3, Appl
278	16	0.5	7635	4	US-08-450-272-1	Sequence 1, Appl	c 351	15	0.5	240	1	US-08-222-177A-32	Sequence 32, Appl
279	16	0.5	7741	4	US-09-426-998-4	Sequence 4, Appl	c 352	15	0.5	249	1	US-09-103-875-13	Sequence 13, Appl
280	16	0.5	7832	4	US-09-004-838-94	Sequence 94, Appl	c 353	15	0.5	255	1	US-08-618-164-6	Sequence 6, Appl
281	16	0.5	7898	4	US-08-984-709A-49	Sequence 49, Appl	c 354	15	0.5	284	4	US-09-030-607-211	Sequence 211, App
282	16	0.5	8651	4	US-08-961-527-181	Sequence 181, App	c 355	15	0.5	284	4	US-09-605-785-211	Sequence 211, App
283	16	0.5	9540	1	US-07-689-008-1	Sequence 1, Appl	c 356	15	0.5	264	4	US-09-439-313-211	Sequence 211, App
284	16	0.5	10380	4	US-09-077-354B-3	Sequence 3, Appl	c 357	15	0.5	264	4	US-09-352-616A-211	Sequence 211, App
285	16	0.5	11459	4	US-09-454-721A-3	Sequence 3, Appl	c 358	15	0.5	264	4	US-09-232-149A-211	Sequence 211, App
286	16	0.5	12597	4	US-09-705-299-12	Sequence 12, Appl	c 359	15	0.5	267	3	US-09-188-930-72	Sequence 72, Appl
287	16	0.5	12847	1	US-08-550-715-1	Sequence 1, Appl	c 360	15	0.5	268	1	US-08-466-033-33	Sequence 33, Appl
288	16	0.5	14602	1	US-08-597-236-1	Sequence 1, Appl	c 361	15	0.5	268	1	US-08-444-733-33	Sequence 33, Appl
289	16	0.5	14602	1	US-08-746-682A-1	Sequence 1, Appl	c 362	15	0.5	268	2	US-08-464-134-33	Sequence 33, Appl
290	16	0.5	16836	4	US-09-147-236-1	Sequence 1, Appl	c 363	15	0.5	268	2	US-08-461-361-33	Sequence 33, Appl
291	16	0.5	16836	4	US-09-147-236-10	Sequence 10, Appl	c 364	15	0.5	268	2	US-08-485-910-33	Sequence 33, Appl
292	16	0.5	17606	4	US-08-943-731-4	Sequence 4, Appl	c 365	15	0.5	279	1	US-08-466-033-68	Sequence 68, Appl
293	16	0.5	18073	4	US-09-078-294-12	Sequence 12, Appl	c 366	15	0.5	279	1	US-08-444-733-68	Sequence 68, Appl
294	16	0.5	19011	1	US-08-310-356-36	Sequence 36, Appl	c 367	15	0.5	279	2	US-08-461-361-68	Sequence 68, Appl
295	16	0.5	19557	5	PCT-US92-06300-1	Sequence 1, Appl	c 368	15	0.5	279	2	US-08-461-361-68	Sequence 68, Appl
296	16	0.5	20598	4	US-09-593-995-10	Sequence 10, Appl	c 369	15	0.5	279	2	US-08-485-910-68	Sequence 68, Appl
297	16	0.5	22846	2	US-08-469-461-3	Sequence 3, Appl	c 370	15	0.5	279	4	US-09-506-729-30	Sequence 30, Appl
298	16	0.5	22846	3	US-07-890-609-3	Sequence 3, Appl	c 371	15	0.5	279	5	PCT-US95-06266-52	Sequence 52, Appl
299	16	0.5	24183	4	US-08-943-731-3	Sequence 3, Appl	c 372	15	0.5	282	1	US-08-466-033-66	Sequence 66, Appl
300	16	0.5	29604	3	US-08-781-891-207	Sequence 207, App	c 373	15	0.5	282	1	US-08-444-733-66	Sequence 66, Appl
301	16	0.5	32768	4	US-08-961-527-71	Sequence 71, App	c 374	15	0.5	282	2	US-08-464-134-66	Sequence 66, Appl
302	16	0.5	62804	4	US-09-800-960-3	Sequence 3, Appl	c 375	15	0.5	282	2	US-08-461-361-66	Sequence 66, Appl
303	16	0.5	72928	3	US-09-009-913-1	Sequence 1, Appl	c 376	15	0.5	282	2	US-08-485-910-66	Sequence 66, Appl
304	16	0.5	84495	4	US-09-797-906-3	Sequence 3, Appl	c 377	15	0.5	282	5	PCT-US95-06266-50	Sequence 50, Appl
305	16	0.5	98844	4	US-09-791-211-10	Sequence 10, Appl	c 378	15	0.5	291	1	US-08-171-385-24	Sequence 24, Appl
306	16	0.5	111282	4	US-09-754-250-3	Sequence 3, Appl	c 379	15	0.5	291	3	US-08-361-441B-24	Sequence 24, Appl
307	16	0.5	162450	4	US-09-345-882-1	Sequence 1, Appl	c 380	15	0.5	293	1	US-07-781-254A-23	Sequence 23, Appl
308	15	0.5	17	3	US-08-945-654-4	Sequence 4, Appl	c 381	15	0.5	297	4	US-09-134-001C-1862	Sequence 1862, App
309	15	0.5	20	4	US-09-487-445-67	Sequence 67, Appl	c 382	15	0.5	302	4	US-08-638-931-63	Sequence 63, Appl
310	15	0.5	20	4	US-09-657-481A-65	Sequence 65, App	c 383	15	0.5	310	4	US-09-404-879A-81	Sequence 81, Appl
311	15	0.5	24	4	US-09-103-875-87	Sequence 87, App	c 384	15	0.5	310	4	US-09-404-879A-308	Sequence 308, App
312	15	0.5	24	4	US-09-103-875-88	Sequence 88, App	c 385	15	0.5	317	4	US-08-991-789A-75	Sequence 75, Appl
313	15	0.5	29	3	US-09-029-819-13	Sequence 13, Appl	c 386	15	0.5	317	4	US-09-062-451-75	Sequence 75, Appl
314	15	0.5	30	4	US-09-264-693-7	Sequence 7, Appl	c 387	15	0.5	317	4	US-09-598-326-75	Sequence 75, Appl
315	15	0.5	32	1	US-08-453-862-5	Sequence 5, Appl	c 388	15	0.5	323	4	US-08-638-931-64	Sequence 64, Appl
316	15	0.5	32	2	US-08-452-734A-5	Sequence 5, Appl	c 389	15	0.5	325	4	US-08-638-931-53	Sequence 53, Appl
317	15	0.5	32	4	US-08-176-401B-5	Sequence 5, Appl	c 390	15	0.5	325	1	US-07-745-382-21	Sequence 21, Appl
318	15	0.5	33	4	US-09-424-620B-10	Sequence 10, Appl	c 391	15	0.5	327	1	US-07-921-848-21	Sequence 21, Appl
319	15	0.5	33	4	US-09-424-620B-16	Sequence 16, Appl	c 392	15	0.5	327	1	US-08-165-301A-21	Sequence 21, Appl

c 393	15	0.5	327	3	US-08-810-436-21	Sequence 21, Appl	c 466	15	0.5	450	3	US-09-032-894-16	Sequence 16, Appl
c 394	15	0.5	327	4	US-09-166-966E-6	Sequence 6, Appl	c 467	15	0.5	450	4	US-09-031-626-16	Sequence 16, Appl
c 395	15	0.5	327	5	PCT-US94-14179-21	Sequence 21, Appl	c 468	15	0.5	452	1	US-08-466-033-115	Sequence 115, App
c 396	15	0.5	328	1	US-08-455-550-5	Sequence 5, Appl	c 469	15	0.5	452	2	US-08-444-733-115	Sequence 115, App
c 397	15	0.5	330	1	US-08-466-033-90	Sequence 90, Appl	c 470	15	0.5	452	2	US-08-464-134-115	Sequence 115, App
c 398	15	0.5	330	2	US-08-444-733-90	Sequence 90, Appl	c 471	15	0.5	452	2	US-08-461-361-115	Sequence 115, App
c 399	15	0.5	330	2	US-08-464-134-90	Sequence 90, Appl	c 472	15	0.5	452	2	US-08-485-910-115	Sequence 115, App
c 400	15	0.5	330	2	US-08-461-361-90	Sequence 90, Appl	c 473	15	0.5	452	2	US-09-625-040-2	Sequence 2, Appl
c 401	15	0.5	330	2	US-08-485-910-90	Sequence 90, Appl	c 474	15	0.5	452	5	PCT-US95-06266-96	Sequence 96, Appl
c 402	15	0.5	330	4	US-09-134-001C-1138	Sequence 1138, Ap	c 475	15	0.5	455	1	US-08-843-521-3	Sequence 3, Appl
c 403	15	0.5	330	5	PCT-US95-06266-74	Sequence 74, Appl	c 476	15	0.5	455	4	US-09-012-871-3	Sequence 3, Appl
c 404	15	0.5	334	1	US-08-594-031-170	Sequence 170, App	c 477	15	0.5	458	2	US-08-486-663A-15	Sequence 15, Appl
c 405	15	0.5	336	4	US-08-638-931-1	Sequence 1, Appl	c 478	15	0.5	458	2	US-08-247-904B-15	Sequence 15, Appl
c 406	15	0.5	336	4	US-08-638-931-26	Sequence 26, Appl	c 479	15	0.5	458	3	US-08-767-942A-16	Sequence 16, Appl
c 407	15	0.5	336	4	US-08-638-931-27	Sequence 27, Appl	c 480	15	0.5	459	3	US-09-358-580-11	Sequence 11, Appl
c 408	15	0.5	336	4	US-08-638-931-28	Sequence 28, Appl	c 481	15	0.5	468	4	US-09-370-838-133	Sequence 133, App
c 409	15	0.5	336	4	US-08-638-931-29	Sequence 29, Appl	c 482	15	0.5	470	3	US-08-763-332-195	Sequence 195, App
c 410	15	0.5	336	4	US-08-638-931-32	Sequence 32, Appl	c 483	15	0.5	470	4	US-09-448-894-195	Sequence 195, App
c 411	15	0.5	336	4	US-08-638-931-33	Sequence 33, Appl	c 484	15	0.5	479	4	US-09-221-017B-652	Sequence 652, App
c 412	15	0.5	336	4	US-08-638-931-36	Sequence 36, Appl	c 485	15	0.5	483	4	US-09-171-461-37	Sequence 37, Appl
c 413	15	0.5	336	4	US-08-638-931-37	Sequence 37, Appl	c 486	15	0.5	484	4	US-09-370-838-276	Sequence 276, App
c 414	15	0.5	336	4	US-08-638-931-38	Sequence 38, Appl	c 487	15	0.5	494	4	US-09-221-017B-529	Sequence 529, App
c 415	15	0.5	336	4	US-08-638-931-40	Sequence 40, Appl	c 488	15	0.5	497	4	US-09-484-970B-76	Sequence 76, Appl
c 416	15	0.5	336	4	US-08-638-931-41	Sequence 41, Appl	c 489	15	0.5	500	1	US-07-753-462-1	Sequence 1, Appl
c 417	15	0.5	336	4	US-08-638-931-44	Sequence 44, Appl	c 490	15	0.5	500	1	US-08-199-317-1	Sequence 1, Appl
c 418	15	0.5	336	4	US-08-638-931-46	Sequence 46, Appl	c 491	15	0.5	500	4	US-09-147-751-3	Sequence 3, Appl
c 419	15	0.5	336	4	US-08-638-931-47	Sequence 47, Appl	c 492	15	0.5	501	4	US-09-741-243C-3	Sequence 3, Appl
c 420	15	0.5	340	4	US-08-638-931-62	Sequence 62, Appl	c 493	15	0.5	506	4	US-08-916-576B-10	Sequence 10, Appl
c 421	15	0.5	342	4	US-08-638-931-54	Sequence 54, Appl	c 494	15	0.5	507	4	US-09-257-894-5	Sequence 5, Appl
c 422	15	0.5	347	1	US-08-171-385-13	Sequence 13, Appl	c 495	15	0.5	514	6	5405952-3	Patent No. 5405952
c 423	15	0.5	347	3	US-08-361-441B-13	Sequence 13, Appl	c 496	15	0.5	536	3	US-09-040-508-3	Sequence 3, Appl
c 424	15	0.5	348	1	US-08-618-164-5	Sequence 5, Appl	c 497	15	0.5	536	4	US-09-500-654-3	Sequence 3, Appl
c 425	15	0.5	348	4	US-08-638-931-57	Sequence 57, Appl	c 498	15	0.5	543	4	US-09-221-017B-681	Sequence 681, App
c 426	15	0.5	349	4	US-08-638-931-55	Sequence 55, Appl	c 499	15	0.5	546	2	US-08-477-493-2	Sequence 2, Appl
c 427	15	0.5	350	4	US-08-638-931-49	Sequence 49, Appl	c 500	15	0.5	546	4	US-09-788-070-3	Sequence 3, Appl
c 428	15	0.5	350	4	US-08-638-931-66	Sequence 66, Appl	c 501	15	0.5	565	4	US-09-643-597-137	Sequence 137, App
c 429	15	0.5	353	4	US-09-242-901-21	Sequence 21, Appl	c 502	15	0.5	570	1	US-08-466-033-37	Sequence 37, Appl
c 430	15	0.5	354	2	US-08-958-201-1	Sequence 1, Appl	c 503	15	0.5	570	2	US-08-464-733-37	Sequence 37, Appl
c 431	15	0.5	354	2	US-08-958-201-3	Sequence 3, Appl	c 504	15	0.5	570	2	US-08-464-134-37	Sequence 37, Appl
c 432	15	0.5	354	4	US-08-638-931-60	Sequence 60, Appl	c 505	15	0.5	570	2	US-08-461-361-37	Sequence 37, Appl
c 433	15	0.5	359	4	US-08-638-931-51	Sequence 51, Appl	c 506	15	0.5	570	2	US-08-485-910-37	Sequence 37, Appl
c 434	15	0.5	360	4	US-08-638-931-67	Sequence 67, Appl	c 507	15	0.5	570	4	US-09-328-111-91	Sequence 91, Appl
c 435	15	0.5	360	4	US-09-011-769A-87	Sequence 87, Appl	c 508	15	0.5	573	5	PCT-US95-06266-28	Sequence 28, Appl
c 436	15	0.5	362	3	US-09-026-343-11	Sequence 11, Appl	c 509	15	0.5	573	2	US-08-286-819A-20	Sequence 20, Appl
c 437	15	0.5	362	4	US-08-638-931-52	Sequence 52, Appl	c 510	15	0.5	573	3	US-08-980-357-20	Sequence 20, Appl
c 438	15	0.5	362	4	US-09-362-871-11	Sequence 11, Appl	c 511	15	0.5	576	3	US-08-465-375-3	Sequence 3, Appl
c 439	15	0.5	364	1	US-08-466-033-50	Sequence 50, Appl	c 512	15	0.5	587	4	US-09-166-966E-1	Sequence 1, Appl
c 440	15	0.5	364	1	US-08-444-733-50	Sequence 50, Appl	c 513	15	0.5	589	4	US-09-328-111-149	Sequence 149, App
c 441	15	0.5	364	2	US-08-464-134-50	Sequence 50, Appl	c 514	15	0.5	597	4	US-09-623-040-3	Sequence 3, Appl
c 442	15	0.5	364	2	US-08-461-361-50	Sequence 50, Appl	c 515	15	0.5	608	4	US-09-328-111-655	Sequence 655, App
c 443	15	0.5	364	2	US-08-485-910-50	Sequence 50, Appl	c 516	15	0.5	610	4	US-09-812-484-27	Sequence 27, Appl
c 444	15	0.5	364	5	PCT-US95-06266-34	Sequence 34, Appl	c 517	15	0.5	613	4	US-09-442-143A-6	Sequence 6, Appl
c 445	15	0.5	370	2	US-08-457-752-1	Sequence 1, Appl	c 518	15	0.5	621	4	US-09-328-111-204	Sequence 204, App
c 446	15	0.5	374	4	US-08-638-931-48	Sequence 48, Appl	c 519	15	0.5	635	1	US-08-644-664B-7	Sequence 7, Appl
c 447	15	0.5	374	4	US-08-638-931-61	Sequence 61, Appl	c 520	15	0.5	635	2	US-09-098-789-5	Sequence 5, Appl
c 448	15	0.5	390	1	US-08-203-196-5	Sequence 5, Appl	c 521	15	0.5	654	4	US-09-328-111-256	Sequence 256, App
c 449	15	0.5	390	5	PCT-US95-01976-5	Sequence 5, Appl	c 522	15	0.5	656	4	US-09-404-879A-313	Sequence 313, App
c 450	15	0.5	402	1	US-08-466-033-159	Sequence 159, App	c 523	15	0.5	657	4	US-09-385-982-344	Sequence 344, App
c 451	15	0.5	402	1	US-08-444-733-159	Sequence 159, App	c 524	15	0.5	660	4	US-09-373-750-2	Sequence 2, Appl
c 452	15	0.5	402	2	US-08-464-134-159	Sequence 159, App	c 525	15	0.5	661	4	US-08-943-731-186	Sequence 186, App
c 453	15	0.5	402	2	US-08-461-361-159	Sequence 159, App	c 526	15	0.5	684	4	US-09-328-111-306	Sequence 306, App
c 454	15	0.5	402	2	US-08-485-910-159	Sequence 159, App	c 527	15	0.5	691	3	US-08-933-750C-57	Sequence 57, Appl
c 455	15	0.5	406	4	US-09-060-756-563	Sequence 563, App	c 528	15	0.5	691	3	US-09-234-613-57	Sequence 57, Appl
c 456	15	0.5	427	4	US-08-615-192A-128	Sequence 128, App	c 529	15	0.5	691	4	US-09-347-001-5	Sequence 5, Appl
c 457	15	0.5	430	2	US-08-611-757-104	Sequence 104, App	c 530	15	0.5	696	4	US-08-998-416-1134	Sequence 1134, Ap
c 458	15	0.5	430	5	PCT-US95-05980-104	Sequence 104, App	c 531	15	0.5	697	4	US-09-328-111-103	Sequence 103, App
c 459	15	0.5	436	4	US-09-397-787-253	Sequence 253, App	c 532	15	0.5	702	4	US-08-858-207A-211	Sequence 211, App
c 460	15	0.5	439	4	US-09-397-787-273	Sequence 273, App	c 533	15	0.5	705	4	US-09-134-001C-358	Sequence 358, App
c 461	15	0.5	441	1	US-07-781-254A-8	Sequence 8, Appl	c 534	15	0.5	717	4	US-09-124-238A-7	Sequence 7, Appl
c 462	15	0.5	441	2	US-08-975-316-60	Sequence 60, Appl	c 535	15	0.5	717	4	US-09-721-975-7	Sequence 7, Appl
c 463	15	0.5	441	4	US-09-615-192A-60	Sequence 60, Appl	c 536	15	0.5	722	4	US-08-998-416-1095	Sequence 1095, App
c 464	15	0.5	450	2	US-08-890-980-16	Sequence 16, Appl	c 537	15	0.5	745	4	US-09-328-111-693	Sequence 683, App
c 465	15	0.5	450	3	US-08-890-979-16	Sequence 16, Appl	c 538	15	0.5				

539	15	0.5	755	4	US-09-198-119C-80	Sequence 80, Appl	c 612	15	0.5	1116	2	US-08-805-965-4	Sequence 4, Appl
540	15	0.5	763	4	US-09-221-017B-723	Sequence 723, App	c 613	15	0.5	1116	4	US-09-221-017B-125	Sequence 125, App
c 541	15	0.5	773	4	US-09-237-357-47	Sequence 47, Appl	c 614	15	0.5	1121	1	US-08-086-410-36	Sequence 36, Appl
542	15	0.5	775	3	US-09-124-476-1	Sequence 1, Appl	c 615	15	0.5	1121	1	US-08-314-586-39	Sequence 39, Appl
543	15	0.5	775	4	US-09-577-796A-1	Sequence 1, Appl	616	15	0.5	1122	1	US-08-375-962B-10	Sequence 10, Appl
544	15	0.5	793	4	US-09-198-119C-90	Sequence 90, Appl	617	15	0.5	1122	2	US-08-562-114B-10	Sequence 10, Appl
545	15	0.5	795	3	US-08-969-644-15	Sequence 15, Appl	618	15	0.5	1122	4	US-08-729-594A-10	Sequence 10, Appl
546	15	0.5	795	3	US-08-444-189-15	Sequence 15, Appl	619	15	0.5	1122	4	US-09-134-001C-1192	Sequence 1192, App
547	15	0.5	795	4	US-08-468-544-15	Sequence 15, Appl	620	15	0.5	1122	4	US-08-937-993-10	Sequence 10, Appl
548	15	0.5	807	1	US-08-431-080-21	Sequence 21, Appl	621	15	0.5	1123	1	US-08-700-626-2	Sequence 2, Appl
c 549	15	0.5	807	1	US-08-431-080-31	Sequence 31, Appl	622	15	0.5	1128	2	US-08-562-114B-14	Sequence 14, Appl
550	15	0.5	807	2	US-08-938-534-21	Sequence 21, Appl	623	15	0.5	1128	4	US-08-729-594A-14	Sequence 14, Appl
c 551	15	0.5	807	2	US-08-938-534-31	Sequence 31, Appl	624	15	0.5	1128	4	US-09-880-427-5	Sequence 5, Appl
552	15	0.5	807	4	US-09-345-294-21	Sequence 21, Appl	625	15	0.5	1128	4	US-09-306-538B-5	Sequence 5, Appl
c 553	15	0.5	807	4	US-09-345-294-31	Sequence 31, Appl	626	15	0.5	1128	4	US-09-134-001C-2242	Sequence 2242, App
554	15	0.5	832	4	US-09-198-119C-82	Sequence 82, Appl	627	15	0.5	1128	4	US-08-937-993-14	Sequence 14, Appl
555	15	0.5	833	2	US-08-837-029-1	Sequence 1, Appl	c 628	15	0.5	1137	1	US-08-706-214-2	Sequence 2, Appl
556	15	0.5	846	2	US-08-179-557-32	Sequence 32, Appl	c 629	15	0.5	1140	2	US-08-698-805-5	Sequence 5, Appl
c 557	15	0.5	863	1	US-08-592-126-71	Sequence 71, Appl	c 630	15	0.5	1168	4	US-09-484-970B-89	Sequence 89, Appl
c 558	15	0.5	870	4	US-09-360-017-2	Sequence 2, Appl	c 631	15	0.5	1176	4	US-09-134-001C-853	Sequence 853, App
c 559	15	0.5	898	1	US-08-419-078-3	Sequence 3, Appl	c 632	15	0.5	1183	1	US-08-188-582-25	Sequence 25, Appl
c 560	15	0.5	898	1	US-08-726-883-3	Sequence 3, Appl	c 633	15	0.5	1183	1	US-08-646-715-25	Sequence 25, Appl
c 561	15	0.5	900	1	US-08-459-264-1	Sequence 1, Appl	c 634	15	0.5	1197	4	US-09-134-001C-1516	Sequence 1516, App
c 562	15	0.5	900	1	US-08-459-263-1	Sequence 1, Appl	c 635	15	0.5	1206	1	US-08-318-947A-1	Sequence 1, Appl
c 563	15	0.5	906	1	US-07-920-519-3	Sequence 3, Appl	c 636	15	0.5	1206	2	US-08-795-303-1	Sequence 1, Appl
c 564	15	0.5	906	1	US-07-920-519-4	Sequence 4, Appl	637	15	0.5	1221	2	US-08-934-846-3	Sequence 3, Appl
c 565	15	0.5	906	1	US-07-920-519-6	Sequence 6, Appl	638	15	0.5	1221	2	US-09-238-557-3	Sequence 3, Appl
c 566	15	0.5	906	1	US-08-314-586-3	Sequence 3, Appl	c 639	15	0.5	1227	2	US-08-683-007A-1	Sequence 1, Appl
c 567	15	0.5	906	1	US-08-314-586-4	Sequence 4, Appl	640	15	0.5	1230	4	US-08-940-424-1	Sequence 1, Appl
c 568	15	0.5	906	1	US-08-314-586-6	Sequence 6, Appl	c 641	15	0.5	1235	4	US-08-642-274D-36	Sequence 36, Appl
c 569	15	0.5	906	3	US-08-115-753-31	Sequence 31, Appl	c 642	15	0.5	1235	4	US-08-952-014C-36	Sequence 36, Appl
c 570	15	0.5	906	4	US-09-347-878-57	Sequence 57, Appl	c 643	15	0.5	1240	1	US-08-103-998-1	Sequence 1, Appl
c 571	15	0.5	913	2	US-08-975-316-61	Sequence 61, Appl	644	15	0.5	1242	5	PCT-US91-00909-3	Sequence 3, Appl
c 572	15	0.5	913	4	US-09-615-192B-61	Sequence 61, Appl	645	15	0.5	1254	2	US-08-934-846-1	Sequence 1, Appl
c 573	15	0.5	920	1	US-07-920-519-36	Sequence 36, Appl	646	15	0.5	1254	4	US-09-238-557-1	Sequence 1, Appl
c 574	15	0.5	920	1	US-08-314-586-36	Sequence 36, Appl	647	15	0.5	1254	5	PCT-US91-00909-1	Sequence 1, Appl
575	15	0.5	930	4	US-09-134-001C-202	Sequence 202, App	648	15	0.5	1261	3	US-08-961-083-25	Sequence 25, Appl
576	15	0.5	973	3	US-09-013-881-16	Sequence 16, Appl	c 649	15	0.5	1262	4	US-07-715-751B-3	Sequence 3, Appl
c 577	15	0.5	973	3	US-09-013-881-16	Sequence 16, Appl	650	15	0.5	1262	4	US-09-359-161-1	Sequence 1, Appl
578	15	0.5	980	1	US-08-452-267-1	Sequence 1, Appl	651	15	0.5	1277	1	US-08-376-427B-1	Sequence 1, Appl
579	15	0.5	980	3	US-09-123-644-1	Sequence 1, Appl	652	15	0.5	1277	2	US-08-356-060A-1	Sequence 1, Appl
580	15	0.5	993	1	US-08-466-033-165	Sequence 165, App	653	15	0.5	1277	4	US-08-460-900C-1	Sequence 1, Appl
581	15	0.5	993	3	US-08-444-733-165	Sequence 165, App	654	15	0.5	1277	4	US-08-674-509B-1	Sequence 1, Appl
582	15	0.5	993	2	US-08-464-134-165	Sequence 165, App	655	15	0.5	1277	4	US-08-954-698-1	Sequence 1, Appl
583	15	0.5	993	2	US-08-461-361-165	Sequence 165, App	656	15	0.5	1277	4	US-08-957-874-1	Sequence 1, Appl
584	15	0.5	993	2	US-08-485-910-165	Sequence 165, App	657	15	0.5	1277	4	US-09-325-256-5	Sequence 5, Appl
585	15	0.5	1001	4	US-09-641-638-82	Sequence 82, Appl	c 658	15	0.5	1278	4	US-09-134-001C-58	Sequence 58, Appl
c 586	15	0.5	1001	4	US-09-641-638-209	Sequence 209, App	c 659	15	0.5	1286	2	US-08-807-200-3	Sequence 3, Appl
587	15	0.5	1002	4	US-09-625-040-4	Sequence 4, Appl	c 660	15	0.5	1286	4	US-09-001-777-3	Sequence 3, Appl
c 588	15	0.5	1002	4	US-09-641-638-583	Sequence 583, App	661	15	0.5	1287	4	US-08-845-258-11	Sequence 11, Appl
c 589	15	0.5	1002	4	US-09-641-638-594	Sequence 594, App	662	15	0.5	1287	4	US-08-990-571-11	Sequence 11, Appl
c 590	15	0.5	1005	2	US-08-844-312-3	Sequence 3, Appl	663	15	0.5	1287	4	US-08-723-142A-11	Sequence 11, Appl
c 591	15	0.5	1007	4	US-09-247-155-81	Sequence 81, Appl	664	15	0.5	1287	4	US-09-528-784A-11	Sequence 11, Appl
592	15	0.5	1008	4	US-09-095-117-1	Sequence 1, Appl	665	15	0.5	1290	1	US-08-638-911A-55	Sequence 55, Appl
593	15	0.5	1008	4	US-09-095-117-3	Sequence 3, Appl	666	15	0.5	1290	2	US-08-844-312-1	Sequence 1, Appl
c 594	15	0.5	1009	4	US-09-291-922-15	Sequence 15, Appl	c 667	15	0.5	1301	4	US-08-983-502-19	Sequence 19, Appl
595	15	0.5	1011	1	US-08-466-033-161	Sequence 161, App	c 668	15	0.5	1301	5	PCT-US96-10521-19	Sequence 19, Appl
596	15	0.5	1011	2	US-08-444-733-161	Sequence 161, App	669	15	0.5	1302	4	US-09-255-368-5	Sequence 5, Appl
597	15	0.5	1011	2	US-08-464-134-161	Sequence 161, App	670	15	0.5	1320	4	US-09-370-838-22	Sequence 22, Appl
598	15	0.5	1011	2	US-08-461-361-161	Sequence 161, App	c 671	15	0.5	1322	1	US-08-419-078-1	Sequence 1, Appl
599	15	0.5	1011	2	US-08-485-910-161	Sequence 161, App	c 672	15	0.5	1322	1	US-08-726-883-1	Sequence 1, Appl
c 600	15	0.5	1013	1	US-07-920-519-30	Sequence 30, Appl	c 673	15	0.5	1322	4	US-09-579-236-3	Sequence 3, Appl
c 601	15	0.5	1013	1	US-08-086-410-23	Sequence 23, Appl	c 674	15	0.5	1323	4	US-08-983-502-15	Sequence 15, Appl
c 602	15	0.5	1013	1	US-08-314-586-30	Sequence 30, Appl	c 675	15	0.5	1323	5	PCT-US96-10521-15	Sequence 15, Appl
c 603	15	0.5	1037	2	US-08-824-405-1	Sequence 1, Appl	676	15	0.5	1328	4	US-09-370-838-24	Sequence 24, Appl
c 604	15	0.5	1038	1	US-07-661-610C-13	Sequence 13, Appl	c 677	15	0.5	1330	2	US-08-807-200-1	Sequence 1, Appl
605	15	0.5	1046	1	US-08-361-467B-4	Sequence 4, Appl	c 678	15	0.5	1330	4	US-09-001-777-1	Sequence 27, Appl
606	15	0.5	1046	1	US-08-484-332C-4	Sequence 4, Appl	679	15	0.5	1331	4	US-09-370-838-27	Sequence 27, Appl
607	15	0.5	1065	2	US-08-512-955-1	Sequence 1, Appl	680	15	0.5	1333	4	US-09-370-838-28	Sequence 28, Appl
608	15	0.5	1073	3	US-08-311-423-1	Sequence 1, Appl	c 681	15	0.5	1334	4	US-08-922-957-2	Sequence 2, Appl
609	15	0.5	1079	1	US-08-270-583-1	Sequence 1, Appl	c 682	15	0.5	1335	3	US-08-714-918-94	Sequence 94, Appl
610	15	0.5	1079	1	US-08-783-889A-1	Sequence 1, Appl	c 683	15	0.5	1335	4	US-09-265-315-94	Sequence 94, Appl
611	15	0.5	1102	3	US-09-067-089-1	Sequence 1, Appl	c 684	15	0.5	1335	4	US-09-265-315-94	Sequence 94, Appl

c 685	15	0.5	1335	4	US-09-266-417-94	Sequence 94, Appl	c 758	15	0.5	1615	3	US-09-040-508-1	Sequence 1, Appl1
c 686	15	0.5	1335	4	US-09-740-028A-1	Sequence 1, Appl1	c 759	15	0.5	1615	4	US-09-500-654-1	Sequence 1, Appl1
687	15	0.5	1339	4	US-09-556-877-64	Sequence 64, Appl	c 760	15	0.5	1617	4	US-09-444-336-4	Sequence 4, Appl1
688	15	0.5	1339	4	US-09-620-412C-64	Sequence 64, Appl	761	15	0.5	1620	4	US-09-124-238A-32	Sequence 32, Appl
689	15	0.5	1344	1	US-08-844-010-1	Sequence 1, Appl1	762	15	0.5	1620	4	US-09-721-975-32	Sequence 32, Appl
690	15	0.5	1344	1	US-08-341-456A-10	Sequence 10, Appl	c 763	15	0.5	1624	2	US-08-464-517-35	Sequence 35, Appl
691	15	0.5	1344	2	US-08-478-414A-10	Sequence 10, Appl	c 764	15	0.5	1624	2	US-08-246-361A-35	Sequence 35, Appl
692	15	0.5	1344	2	US-08-325-240A-10	Sequence 10, Appl	c 765	15	0.5	1624	3	US-08-463-772-35	Sequence 35, Appl
693	15	0.5	1344	3	US-09-012-873-1	Sequence 1, Appl1	c 766	15	0.5	1624	5	PCT-US93-05000-35	Sequence 35, Appl
694	15	0.5	1344	3	US-08-898-982-10	Sequence 10, Appl	767	15	0.5	1626	4	US-09-158-767-14	Sequence 14, Appl
695	15	0.5	1344	4	US-09-371-261-10	Sequence 10, Appl	c 768	15	0.5	1631	1	US-08-583-318-4	Sequence 4, Appl1
c 696	15	0.5	1355	2	US-08-618-408B-3	Sequence 3, Appl1	769	15	0.5	1634	4	US-09-126-420A-2	Sequence 2, Appl1
c 697	15	0.5	1355	4	US-09-370-838-31	Sequence 31, Appl	770	15	0.5	1636	4	US-09-117-853-7	Sequence 7, Appl1
c 698	15	0.5	1360	4	US-08-858-207A-65	Sequence 65, Appl	771	15	0.5	1642	4	US-09-117-853-5	Sequence 5, Appl1
c 699	15	0.5	1377	1	US-08-638-911A-38	Sequence 38, Appl	772	15	0.5	1642	4	US-09-117-853-9	Sequence 9, Appl1
c 700	15	0.5	1378	1	US-08-592-126-72	Sequence 72, Appl	773	15	0.5	1643	3	US-09-117-853-3	Sequence 3, Appl1
701	15	0.5	1382	1	US-08-350-325A-6	Sequence 6, Appl1	c 774	15	0.5	1644	3	US-08-852-782-1	Sequence 1, Appl1
702	15	0.5	1382	5	PCT-US94-03856-6	Sequence 6, Appl1	775	15	0.5	1644	4	US-09-124-238A-9	Sequence 9, Appl1
703	15	0.5	1383	1	US-08-484-044-1	Sequence 4, Appl1	776	15	0.5	1644	4	US-09-721-975-9	Sequence 9, Appl1
c 704	15	0.5	1393	4	US-09-147-751-4	Sequence 4, Appl1	c 777	15	0.5	1653	4	US-09-741-243C-1	Sequence 1, Appl1
705	15	0.5	1401	4	US-09-134-001C-183	Sequence 183, App	778	15	0.5	1665	4	US-09-124-238A-33	Sequence 33, Appl
706	15	0.5	1404	4	US-09-134-001C-398	Sequence 398, App	779	15	0.5	1665	4	US-09-721-975-33	Sequence 33, Appl
c 707	15	0.5	1408	1	US-08-447-554-3	Sequence 3, Appl1	c 780	15	0.5	1673	4	US-09-381-843-6	Sequence 6, Appl1
c 708	15	0.5	1408	1	US-08-448-160-3	Sequence 3, Appl1	781	15	0.5	1689	4	US-09-124-238A-22	Sequence 22, Appl
709	15	0.5	1408	2	US-08-632-470-40	Sequence 40, Appl	782	15	0.5	1689	4	US-09-721-975-22	Sequence 22, Appl
c 710	15	0.5	1412	4	US-09-615-192A-129	Sequence 129, App	783	15	0.5	1709	4	PCT-US91-04274A-2	Sequence 2, Appl1
711	15	0.5	1420	3	US-08-358-171-1	Sequence 1, Appl1	c 784	15	0.5	1720	4	US-08-936-165A-188	Sequence 188, App
712	15	0.5	1420	3	US-09-090-947-1	Sequence 1, Appl1	c 785	15	0.5	1720	4	US-09-227-357-139	Sequence 139, App
713	15	0.5	1427	2	US-08-632-470-27	Sequence 27, Appl	786	15	0.5	1728	3	US-08-913-805A-1	Sequence 1, Appl1
714	15	0.5	1430	2	US-08-204-288-4	Sequence 4, Appl1	787	15	0.5	1728	4	US-09-442-629-1	Sequence 1, Appl1
715	15	0.5	1432	2	US-08-632-470-25	Sequence 25, Appl	788	15	0.5	1730	3	US-09-222-817-11	Sequence 11, Appl
716	15	0.5	1432	2	US-08-632-470-32	Sequence 32, Appl	789	15	0.5	1730	3	US-09-222-817-13	Sequence 13, Appl
717	15	0.5	1436	2	US-08-632-470-34	Sequence 34, Appl	790	15	0.5	1730	4	US-09-222-786-11	Sequence 11, Appl
718	15	0.5	1438	2	US-08-632-470-24	Sequence 24, Appl	791	15	0.5	1730	4	US-09-222-786-13	Sequence 13, Appl
719	15	0.5	1439	2	US-08-632-470-31	Sequence 31, Appl	792	15	0.5	1737	4	US-09-126-420A-1	Sequence 1, Appl1
720	15	0.5	1439	2	US-08-632-470-42	Sequence 42, Appl	793	15	0.5	1744	4	US-09-221-017B-219	Sequence 219, App
c 721	15	0.5	1440	2	US-08-807-200-11	Sequence 11, Appl	794	15	0.5	1758	4	US-09-370-838-28	Sequence 28, App
722	15	0.5	1440	2	US-08-632-470-23	Sequence 23, Appl	c 795	15	0.5	1785	2	US-08-559-505-3	Sequence 3, Appl1
723	15	0.5	1440	2	US-08-632-470-26	Sequence 26, Appl	c 796	15	0.5	1785	2	US-08-749-907-3	Sequence 3, Appl1
724	15	0.5	1440	2	US-08-632-470-28	Sequence 28, Appl	c 797	15	0.5	1785	4	US-09-241-581B-7	Sequence 7, Appl1
725	15	0.5	1440	2	US-08-632-470-29	Sequence 29, Appl	c 798	15	0.5	1785	5	PCT-US95-07721-7	Sequence 7, Appl1
726	15	0.5	1440	2	US-08-632-470-33	Sequence 33, Appl	c 799	15	0.5	1788	2	US-08-559-505-1	Sequence 1, Appl1
727	15	0.5	1440	2	US-08-632-470-35	Sequence 35, Appl	c 800	15	0.5	1788	2	US-08-749-907-1	Sequence 1, Appl1
728	15	0.5	1440	2	US-08-632-470-36	Sequence 36, Appl	c 801	15	0.5	1788	4	US-09-241-581B-3	Sequence 3, Appl1
729	15	0.5	1440	2	US-08-632-470-39	Sequence 39, Appl	c 802	15	0.5	1788	4	US-08-265-428-3	Sequence 3, Appl1
730	15	0.5	1440	2	US-08-632-470-39	Sequence 39, Appl	c 803	15	0.5	1788	5	PCT-US95-07721-3	Sequence 3, Appl1
731	15	0.5	1440	2	US-08-632-470-41	Sequence 41, Appl	c 804	15	0.5	1812	4	US-09-008-097-3	Sequence 3, Appl1
732	15	0.5	1440	2	US-08-632-470-43	Sequence 43, Appl	805	15	0.5	1814	2	US-08-483-151-1	Sequence 1, Appl1
733	15	0.5	1440	2	US-08-632-470-46	Sequence 46, Appl	806	15	0.5	1814	5	PCT-US96-06427-1	Sequence 1, Appl1
c 734	15	0.5	1440	3	US-08-852-782-2	Sequence 2, Appl1	c 807	15	0.5	1825	2	US-08-890-980-3	Sequence 3, Appl1
c 735	15	0.5	1440	4	US-09-001-777-11	Sequence 11, Appl	c 808	15	0.5	1825	3	US-08-890-979-3	Sequence 3, Appl1
736	15	0.5	1441	2	US-08-632-470-38	Sequence 38, Appl	c 809	15	0.5	1825	3	US-09-032-894-3	Sequence 3, Appl1
737	15	0.5	1442	2	US-08-632-470-30	Sequence 30, Appl	c 810	15	0.5	1825	4	US-09-031-626-3	Sequence 3, Appl1
c 738	15	0.5	1443	4	US-08-983-502-33	Sequence 33, Appl	c 811	15	0.5	1827	2	US-08-737-371A-3	Sequence 3, Appl1
c 739	15	0.5	1443	5	PCT-US96-10521-33	Sequence 33, Appl	812	15	0.5	1827	4	US-09-310-275-1	Sequence 1, Appl1
740	15	0.5	1448	4	US-09-625-040-1	Sequence 1, Appl1	c 813	15	0.5	1827	5	PCT-US95-05853-3	Sequence 3, Appl1
741	15	0.5	1450	3	US-09-108-020-15	Sequence 15, Appl	c 814	15	0.5	1840	3	US-08-399-696-126	Sequence 126, App
742	15	0.5	1458	2	US-08-632-470-45	Sequence 45, Appl	c 815	15	0.5	1846	3	US-09-173-581-15	Sequence 15, Appl
743	15	0.5	1488	4	US-09-124-238A-8	Sequence 8, Appl1	c 816	15	0.5	1846	4	US-09-420-915-15	Sequence 15, Appl
744	15	0.5	1488	4	US-09-721-975-8	Sequence 8, Appl1	c 817	15	0.5	1849	1	US-08-399-696-3	Sequence 3, Appl1
c 745	15	0.5	1493	4	US-09-561-756-25	Sequence 25, Appl	818	15	0.5	1853	4	US-08-952-061-1	Sequence 1, Appl1
746	15	0.5	1493	4	US-09-227-721-25	Sequence 25, Appl	c 819	15	0.5	1855	3	US-08-961-083-71	Sequence 71, Appl
747	15	0.5	1508	2	US-08-632-470-44	Sequence 44, Appl	c 820	15	0.5	1856	1	US-08-706-214-1	Sequence 1, Appl1
748	15	0.5	1512	4	US-09-134-001C-643	Sequence 643, App	c 821	15	0.5	1859	4	US-09-724-864-22	Sequence 22, Appl
c 749	15	0.5	1530	4	US-09-444-336-3	Sequence 3, Appl1	822	15	0.5	1860	4	US-09-178-252-19	Sequence 19, Appl
750	15	0.5	1533	5	PCT-US91-04274A-1	Sequence 1, Appl1	c 823	15	0.5	1863	1	US-07-781-254A-4	Sequence 4, Appl1
751	15	0.5	1535	4	US-09-668-680-12	Sequence 12, Appl	c 824	15	0.5	1863	1	US-07-781-254A-5	Sequence 5, Appl1
c 752	15	0.5	1582	4	US-09-210-422-4	Sequence 4, Appl1	825	15	0.5	1880	2	US-08-845-161A-3	Sequence 3, Appl1
753	15	0.5	1588	4	US-08-617-785-7	Sequence 7, Appl1	826	15	0.5	1880	4	US-09-270-751-3	Sequence 3, Appl1
754	15	0.5	1594	2	US-08-933-750C-61	Sequence 61, Appl	827	15	0.5	1880	4	US-09-168-218B-2	Sequence 2, Appl1
755	15	0.5	1594	3	US-09-234-613-61	Sequence 61, Appl	c 828	15	0.5	1881	6	5268290-1	Sequence 2, Appl1
756	15	0.5	1597	1	US-08-166-316-1	Sequence 1, Appl1	c 829	15	0.5	1881	6	5268290-1	Sequence 2, Appl1
c 757	15	0.5	1600	1	US-08-631-427A-6	Sequence 6, Appl1	c 830	15	0.5	1883	1	US-08-665-220-3	Sequence 3, Appl1
										1883	4	US-09-487-445-3	Sequence 3, Appl1

c 831	15	0.5	1883	4	US-09-291-692-3	Sequence 3, Appli Patent No. RE34,60	904	15	0.5	2287	4	US-09-528-784A-8	Sequence 8, Appli
c 832	15	0.5	1897	6	RE34606-5	Sequence 8, Appli	c 905	15	0.5	2309	4	US-09-091-725-9	Sequence 9, Appli
c 833	15	0.5	1910	1	US-09-071-709-8	Sequence 8, Appli	c 906	15	0.5	2322	4	US-08-618-164-1	Sequence 1, Appli
c 834	15	0.5	1910	4	US-09-221-017B-234	Sequence 234, App	c 907	15	0.5	2350	1	US-08-843-521-1	Sequence 1, Appli
c 835	15	0.5	1911	1	US-08-258-420-8	Sequence 8, Appli	c 908	15	0.5	2350	4	US-09-012-871-1	Sequence 1, Appli
c 836	15	0.5	1915	1	US-08-496-855A-5	Sequence 5, Appli	c 909	15	0.5	2360	1	US-08-039-364-1	Sequence 1, Appli
c 837	15	0.5	1915	2	US-08-466-589-11	Sequence 11, Appl	c 910	15	0.5	2360	4	US-09-158-710-1	Sequence 1, Appli
c 838	15	0.5	1915	2	US-08-700-636-11	Sequence 11, Appl	c 911	15	0.5	2375	1	US-08-468-855-9	Sequence 9, Appli
c 839	15	0.5	1915	3	US-08-467-574-11	Sequence 11, Appl	c 912	15	0.5	2375	1	US-08-468-855-9	Sequence 9, Appli
c 840	15	0.5	1915	4	US-09-217-345-11	Sequence 11, Appl	c 913	15	0.5	2375	1	US-08-310-357-9	Sequence 9, Appli
c 841	15	0.5	1915	4	US-08-487-596-17	Sequence 17, Appl	c 914	15	0.5	2375	1	US-08-468-852-9	Sequence 9, Appli
c 842	15	0.5	1920	2	US-08-855-714-1	Sequence 1, Appli	c 915	15	0.5	2375	2	US-08-468-857-9	Sequence 9, Appli
c 843	15	0.5	1934	4	US-09-579-236-1	Sequence 1, Appli	c 916	15	0.5	2381	2	US-08-736-770-4	Sequence 4, Appli
c 844	15	0.5	1953	3	US-08-826-246-1	Sequence 1, Appli	c 917	15	0.5	2388	1	US-08-638-911A-56	Sequence 56, Appl
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c 846	15	0.5	1953	3	US-09-126-640-1	Sequence 1, Appli	c 919	15	0.5	2389	2	US-08-460-507-2	Sequence 2, Appli
c 847	15	0.5	1953	4	US-08-925-588-1	Sequence 1, Appli	c 920	15	0.5	2415	4	US-08-989-299-3	Sequence 3, Appli
c 848	15	0.5	1953	4	US-09-288-292A-1	Sequence 1, Appli	c 921	15	0.5	2430	2	US-08-488-199-3	Sequence 3, Appli
c 849	15	0.5	1962	1	US-08-399-696-1	Sequence 1, Appli	c 922	15	0.5	2431	3	US-08-985-526-35	Sequence 35, Appl
c 850	15	0.5	1964	4	US-09-117-853-1	Sequence 1, Appli	c 923	15	0.5	2435	4	US-09-484-970B-134	Sequence 134, App
c 851	15	0.5	1965	1	US-08-258-420-9	Sequence 9, Appli	c 924	15	0.5	2472	4	US-09-626-589-6	Sequence 6, Appli
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c 853	15	0.5	2001	3	US-08-850-961-13	Sequence 13, Appl	c 926	15	0.5	2481	2	US-08-937-931-7	Sequence 7, Appli
c 854	15	0.5	2001	4	US-09-479-776-13	Sequence 13, Appl	c 927	15	0.5	2481	4	US-09-285-502-7	Sequence 7, Appli
c 855	15	0.5	2001	4	US-09-315-127-10	Sequence 10, Appl	c 928	15	0.5	2481	4	US-09-709-126-7	Sequence 7, Appli
c 856	15	0.5	2002	4	US-09-315-127-7	Sequence 7, Appli	c 929	15	0.5	2481	4	US-09-871-385A-7	Sequence 7, Appli
c 857	15	0.5	2009	4	US-09-380-061B-17	Sequence 17, Appl	c 930	15	0.5	2492	3	US-08-695-191-3	Sequence 3, Appli
c 858	15	0.5	2010	4	US-08-487-183A-15	Sequence 15, Appl	c 931	15	0.5	2492	3	US-08-682-080-3	Sequence 3, Appli
c 859	15	0.5	2019	4	US-09-160-494-3	Sequence 3, Appli	c 932	15	0.5	2555	2	US-08-960-022-15	Sequence 15, Appl
c 860	15	0.5	2031	2	US-08-933-750C-53	Sequence 53, Appl	c 933	15	0.5	2556	3	US-08-699-103B-9	Sequence 9, Appli
c 861	15	0.5	2031	3	US-09-234-613-53	Sequence 53, Appl	c 934	15	0.5	2556	4	US-09-229-059-9	Sequence 9, Appli
c 862	15	0.5	2042	2	US-08-933-821-16	Sequence 16, Appl	c 935	15	0.5	2566	4	US-09-270-542-124	Sequence 124, App
c 863	15	0.5	2042	3	US-08-934-494-5	Sequence 5, Appli	c 936	15	0.5	2575	1	US-08-135-511-33	Sequence 33, Appl
c 864	15	0.5	2042	3	US-08-960-507-16	Sequence 16, Appl	c 937	15	0.5	2575	1	US-08-483-852-10	Sequence 10, Appl
c 865	15	0.5	2042	3	US-09-143-068-5	Sequence 5, Appli	c 938	15	0.5	2575	1	US-08-361-458-5	Sequence 5, Appli
c 866	15	0.5	2042	4	US-09-143-707-5	Sequence 5, Appli	c 939	15	0.5	2575	1	US-08-477-953-13	Sequence 13, Appl
c 867	15	0.5	2042	4	US-09-202-089-5	Sequence 5, Appli	c 940	15	0.5	2575	2	US-08-187-453-30	Sequence 30, Appl
c 868	15	0.5	2042	4	US-09-136-828-16	Sequence 16, Appl	c 941	15	0.5	2575	2	US-08-477-952-10	Sequence 10, Appl
c 869	15	0.5	2042	4	US-09-332-928A-16	Sequence 16, Appl	c 942	15	0.5	2581	4	US-09-363-708-1	Sequence 1, Appli
c 870	15	0.5	2042	4	US-09-511-133-5	Sequence 5, Appli	c 943	15	0.5	2599	2	US-08-239-276-7	Sequence 7, Appli
c 871	15	0.5	2042	4	US-09-136-801-16	Sequence 16, Appl	c 944	15	0.5	2599	2	US-08-468-579B-7	Sequence 7, Appli
c 872	15	0.5	2042	4	US-09-332-929-16	Sequence 16, Appl	c 945	15	0.5	2599	3	US-08-468-577B-7	Sequence 7, Appli
c 873	15	0.5	2042	4	US-09-690-169-5	Sequence 5, Appli	c 946	15	0.5	2617	1	US-08-430-024-1	Sequence 1, Appli
c 874	15	0.5	2042	4	US-09-511-631-5	Sequence 5, Appli	c 947	15	0.5	2617	1	US-08-782-009-1	Sequence 1, Appli
c 875	15	0.5	2087	4	US-09-257-894-9	Sequence 9, Appli	c 948	15	0.5	2619	3	US-09-017-302-1	Sequence 1, Appli
c 876	15	0.5	2111	1	US-08-528-255A-2	Sequence 2, Appli	c 949	15	0.5	2619	4	US-08-983-502-17	Sequence 17, App
c 877	15	0.5	2111	4	US-08-717-365-2	Sequence 2, Appli	c 950	15	0.5	2619	5	PCT-US96-10521-17	Sequence 17, Appl
c 878	15	0.5	2136	2	US-09-276-531-22	Sequence 22, Appl	c 951	15	0.5	2630	2	US-08-890-980-1	Sequence 1, Appli
c 879	15	0.5	2165	4	US-09-257-894-8	Sequence 8, Appli	c 952	15	0.5	2630	3	US-08-890-979-1	Sequence 1, Appli
c 880	15	0.5	2180	2	US-09-003-217-1	Sequence 3, Appli	c 953	15	0.5	2630	4	US-09-032-894-1	Sequence 1, Appli
c 881	15	0.5	2180	4	US-09-218-942-1	Sequence 1, Appli	c 954	15	0.5	2630	4	US-09-031-626-1	Sequence 1, Appli
c 882	15	0.5	2181	4	US-09-158-767-10	Sequence 10, Appl	c 955	15	0.5	2643	2	US-08-961-527-277	Sequence 277, App
c 883	15	0.5	2181	4	US-09-196-390-1	Sequence 1, Appli	c 956	15	0.5	2649	4	US-08-718-964-1	Sequence 1, Appli
c 884	15	0.5	2239	4	US-09-084-079-4	Sequence 4, Appli	c 957	15	0.5	2649	2	US-09-059-964A-1	Sequence 1, Appli
c 885	15	0.5	2243	3	US-08-890-853-1	Sequence 1, Appli	c 958	15	0.5	2649	2	US-08-842-341-1	Sequence 1, Appli
c 886	15	0.5	2268	4	US-09-099-125A-1	Sequence 1, Appli	c 959	15	0.5	2665	4	US-09-257-894-1	Sequence 1, Appli
c 887	15	0.5	2268	2	US-09-099-124A-1	Sequence 1, Appli	c 960	15	0.5	2675	1	US-08-070-165F-5	Sequence 5, Appli
c 888	15	0.5	2268	2	US-09-197-008-1	Sequence 1, Appli	c 961	15	0.5	2675	2	US-08-885-418-5	Sequence 5, Appli
c 889	15	0.5	2268	4	US-09-032-476-1	Sequence 1, Appli	c 962	15	0.5	2681	1	US-08-070-165F-9	Sequence 9, Appli
c 890	15	0.5	2268	4	US-08-890-854-1	Sequence 1, Appli	c 963	15	0.5	2681	2	US-08-885-418-9	Sequence 9, Appli
c 891	15	0.5	2268	4	US-09-023-324-1	Sequence 1, Appli	c 964	15	0.5	2725	3	US-08-941-445A-14	Sequence 14, Appl
c 892	15	0.5	2271	4	US-08-910-820-8	Sequence 8, Appli	c 965	15	0.5	2731	3	US-08-699-103B-11	Sequence 11, Appl
c 893	15	0.5	2271	4	US-09-232-191-10	Sequence 10, Appl	c 966	15	0.5	2731	4	US-09-229-059-11	Sequence 11, Appl
c 894	15	0.5	2277	4	US-09-232-200-10	Sequence 10, Appl	c 967	15	0.5	2736	4	US-08-617-785-1	Sequence 1, Appli
c 895	15	0.5	2277	4	US-09-232-200-72	Sequence 72, Appl	c 968	15	0.5	2745	4	US-08-617-785-11	Sequence 11, Appl
c 896	15	0.5	2277	4	US-09-232-197-10	Sequence 10, Appl	c 969	15	0.5	2766	4	US-08-617-785-13	Sequence 13, Appl
c 897	15	0.5	2277	4	US-09-232-197-72	Sequence 72, Appl	c 970	15	0.5	2802	1	US-08-215-805A-79	Sequence 79, Appl
c 898	15	0.5	2277	4	US-09-232-201-10	Sequence 10, Appl	c 971	15	0.5	2848	2	US-08-805-918-1	Sequence 1, Appli
c 899	15	0.5	2277	4	US-09-232-201-72	Sequence 72, Appl	c 972	15	0.5	2853	4	US-09-221-017B-843	Sequence 843, App
c 900	15	0.5	2277	4	US-08-845-258-8	Sequence 8, Appli	c 973	15	0.5	2882	1	US-08-424-567-1	Sequence 1, Appli
c 901	15	0.5	2287	4	US-08-990-571-8	Sequence 8, Appli	c 974	15	0.5	2882	2	US-08-711-928-1	Sequence 1, Appli
c 902	15	0.5	2287	4	US-08-723-142A-8	Sequence 8, Appli	c 975	15	0.5	2882	4	US-08-724-394A-12	Sequence 12, Appl
c 903	15	0.5	2287	4			c 976	15	0.5	2882	4	US-09-184-937-1	Sequence 1, Appli

c 977 15 0.5 2887 4 US-08-983-502-14
c 978 15 0.5 2887 5 PCT-US96-10521-14
c 979 15 0.5 2923 1 US-08-480-449-1
c 980 15 0.5 2923 2 US-08-660-542-1
c 981 15 0.5 2923 4 US-08-479-603-1
c 982 15 0.5 2927 4 US-09-232-878-5
c 983 15 0.5 2931 4 US-09-168-629-14
c 984 15 0.5 2935 4 US-09-480-921B-27
c 985 15 0.5 2965 2 US-08-460-570-1
c 986 15 0.5 2965 2 US-08-460-570-2
c 987 15 0.5 2965 3 US-08-286-870A-1
c 988 15 0.5 2965 3 US-08-286-870A-2
c 989 15 0.5 2997 1 US-08-453-862-1
c 990 15 0.5 2997 2 US-08-452-734A-1
c 991 15 0.5 2997 4 US-08-176-401B-1
c 992 15 0.5 2997 5 PCT-US94-14989-1
c 993 15 0.5 3014 4 US-09-268-480-14
c 994 15 0.5 3019 4 US-09-359-161-2
c 995 15 0.5 3060 2 US-08-560-398-1
c 996 15 0.5 3070 1 US-08-428-732-3
c 997 15 0.5 3083 1 US-08-346-849-1
c 998 15 0.5 3083 2 US-08-293-284A-1
c 999 15 0.5 3105 4 US-08-542-635-1
1000 15 0.5 3207 1 US-07-946-497-1

ALIGNMENTS

RESULT 1
US-09-071-035-425
; Sequence 425, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 425:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 888 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

US-09-071-035-425
Query Match 0.6%; Score 18; DB 4; Length 888;
Best Local Similarity 100.0%; Pred. No. 60;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2492 GCTTGTCTGCAATGCAG 2509
|||||
Db 110 GCTTGTCTGCAATGCAG 127
RESULT 2
US-08-870-518-34
; Sequence 34, Application US/08870518
; Patent No. 5925566
; GENERAL INFORMATION:
; APPLICANT: Davis, Roger J.
; APPLICANT: Galcheva-Cargova, Zoya
; TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX
; TITLE OF INVENTION: PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/870,518
; FILING DATE: 06-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,219
; FILING DATE: 06-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, Peter J.
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04020/102001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1094 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-870-518-34
Query Match 0.6%; Score 18; DB 2; Length 1094;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 731 TTTTCCTTCTTGATGGCT 748
|||||
Db 755 TTTTCCTTCTTGATGGCT 772
RESULT 3
US-08-747-221B-16/c
; Sequence 16, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation

STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
FILING DATE: NO. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1515 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1515
FEATURE:
NAME/KEY: Asx = Asn or Asp
LOCATION: 298
US-08-747-221B-16

Query Match 0.6%; Score 18; DB 3; Length 1515;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAATTCAGAAATCC 984
|||||
Db 363 CTCCAATTCAGAAATCC 346

RESULT 4
US-08-747-221B-17
Sequence 17, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
FILING DATE: NO. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1515 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-747-221B-17

Query Match 0.6%; Score 18; DB 3; Length 1515;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAATTCAGAAATCC 984
|||||
Db 1153 CTCCAATTCAGAAATCC 1170

RESULT 5
US-09-005-051-16/c
Sequence 16, Application US/09005051
Patent No. 6291222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
FILING DATE: NO. 6291222ember 12, 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: NO. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1515 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1515
FEATURE:
NAME/KEY: Asx = Asn or Asp

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; LOCATION: 298
US-09-005-051-16

Query Match          0.6%; Score 18; DB 4; Length 1515;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
|||||
Db 363 CTCCAAAATTCAGAAATCC 346

RESULT 6
US-09-005-051-17
; Sequence 17, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1515 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-005-051-17

Query Match          0.6%; Score 18; DB 4; Length 1515;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
|||||
Db 1153 CTCCAAAATTCAGAAATCC 1170

RESULT 7
5213972-6/c
; Patent No. 5213972
; APPLICANT: MCCANDLISS, RUSSELL J.; ANDERSON, DAVID M.
; TITLE OF INVENTION: FERMENTATION PROCESS FOR THE PRODUCTION
; OF PYRIMIDINE DEOXYRIBONUCLEOSIDES

; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/448,158
; FILING DATE: 08-DEC-1989
; SEQ ID NO: 6;
; LENGTH: 1611
5213972-6

Query Match          0.6%; Score 18; DB 6; Length 1611;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 AGGATTTAAAGGACTTGT 325
|||||
Db 979 AGGATTTAAAGGACTTGT 962

RESULT 8
US-08-747-221B-60/c
; Sequence 60, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1650 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1650
; FEATURE:
; NAME/KEY: Asx = Asn or Asp
; LOCATION: 433
US-08-747-221B-60

Query Match          0.6%; Score 18; DB 3; Length 1650;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
|||||
Db 498 CTCCAAAATTCAGAAATCC 481
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RESULT 9
US-08-747-221B-61
; Sequence 61, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1650 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-747-221B-61

Query Match 0.6%; Score 18; DB 3; Length 1650;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAATTGAGAAATCC 984
|||||
Db 1153 CTCCAATTGAGAAATCC 1170

RESULT 10
US-09-005-051-60/c
; Sequence 60, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1650 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-005-051-60

Query Match 0.6%; Score 18; DB 4; Length 1650;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAATTGAGAAATCC 984
|||||
Db 498 CTCCAATTGAGAAATCC 481

RESULT 11
US-09-005-051-61
; Sequence 61, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1650 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-005-051-60

NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 1650 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-005-051-61

Query Match 0.6%; Score 18; DB 4; Length 1650;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCGAATTCAGAAATCC 984
|||||
DB 1153 CTCGAATTCAGAAATCC 1170

RESULT 12
US-08-857-213-2/C
Sequence 2, Application US/08857213
Patent No. 6034290
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN VESICLE BINDING PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,213
FILING DATE: Herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0297 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1721 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: FIBRNGT01
CLONE: 148415
US-08-857-213-2

Query Match 0.6%; Score 18; DB 3; Length 1721;

Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATTTTCATAAAGGAC 18
|||||
DB 1538 ATGAATTTTCATAAAGGAC 1521

RESULT 13
US-08-139-937-11
Sequence 11, Application US/08139937
Patent No. 5821070
GENERAL INFORMATION:
APPLICANT: LEE, WEN-HWA
APPLICANT: SHAN, BEI
TITLE OF INVENTION: CELLULAR GENES ENCODING
TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/139,937
FILING DATE: 20-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/979,156
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CJ 9370
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-139-937-11

Query Match 0.6%; Score 18; DB 1; Length 1800;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2796 AAAGAACCCCTCTGAAAAA 2813
|||||
DB 307 AAAGAACCCCTCTGAAAAA 324

RESULT 14
PCT-US93-11310-11
Sequence 11, Application PC/TUS9311310
GENERAL INFORMATION:
APPLICANT: BOARD OF REGENTS OF THE UNIVERSITY OF TEXAS SYSTEM
TITLE OF INVENTION: CELLULAR GENES ENCODING
TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE

CTY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11310
FILING DATE: 19-NOV-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: FP-CJ 9790
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US93-11310-11

Query Match 0.6%; Score 18; DB 5; Length 1800;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2796 AAGAACCCTCTGAAAAA 2813
|||||
Db 307 AAGAACCCTCTGAAAAA 324

RESULT 15
US-09-079-955-10
Sequence 10, Application US/09079955A
Patent No. 6465209
GENERAL INFORMATION:
APPLICANT: Alexander Blinkovsky
APPLICANT: Kimberly Brown
APPLICANT: Elizabeth Golightly
APPLICANT: Tony Byun
APPLICANT: Thomas Mathiasen
APPLICANT: Lene V. Kofoed
APPLICANT: Mikio Fujii
APPLICANT: Chigusa Shizuoka
TITLE OF INVENTION: Methods For Producing Protein
FILE REFERENCE: 5253.500-US
CURRENT APPLICATION NUMBER: US/09/079,955A
CURRENT FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 1926
TYPE: DNA
ORGANISM: Sphingomonas capsulata
US-09-079-955-10

Query Match 0.6%; Score 18; DB 4; Length 1926;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2092 GCTGGTGTGCTGAAGC 2109
|||||
Db 1242 GCTGGTGTGCTGAAGC 1259

RESULT 16
US-08-747-221B-13/c
Sequence 13, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1982 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 31..1517
FEATURE:
NAME/KEY: Asx = Asn or Asp
LOCATION: 300
US-08-747-221B-13

Query Match 0.6%; Score 18; DB 3; Length 1982;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAATTCAGAAATCC 984
|||||
Db 365 CTCCAAATTCAGAAATCC 348

RESULT 17
US-08-747-221B-15
Sequence 15, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins

```
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1982 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
;
; US-08-747-221B-15
;
; Query Match 0.6%; Score 18; DB 3; Length 1982;
; Best Local Similarity 100.0%; Pred. No. 61;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 967 CTCCAAAATTCAGAAATCC 984
; Db 1618 CTCCAAAATTCAGAAATCC 1635
;
; RESULT 18
; US-09-005-051-13/c
; Sequence 13, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
```

```
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1982 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1517
; FEATURE:
; NAME/KEY: Asx = Asn or Asp
; LOCATION: 300
;
; US-09-005-051-13
;
; Query Match 0.6%; Score 18; DB 4; Length 1982;
; Best Local Similarity 100.0%; Pred. No. 61;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 967 CTCCAAAATTCAGAAATCC 984
; Db 365 CTCCAAAATTCAGAAATCC 348
;
; RESULT 19
; US-09-005-051-15
; Sequence 15, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1982 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
;
; US-09-005-051-15
;
; Query Match 0.6%; Score 18; DB 4; Length 1982;
; Best Local Similarity 100.0%; Pred. No. 61;
```

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 967 CTCGAAATTCAGAAATCC 984
|||||
Db 1618 CTCGAAATTCAGAAATCC 1635

RESULT 20

US-08-747-221B-57/c
; Sequence 57, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2144 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 30..1682
; FEATURE:
; NAME/KEY: Asx = Asn or Asp
; LOCATION: 462
US-08-747-221B-57

Query Match 0.6%; Score 18; DB 3; Length 2144;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 967 CTCGAAATTCAGAAATCC 984
|||||
Db 527 CTCGAAATTCAGAAATCC 510

RESULT 21

US-08-747-221B-59
; Sequence 59, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid

; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2144 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-747-221B-59

Query Match 0.6%; Score 18; DB 3; Length 2144;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 967 CTCGAAATTCAGAAATCC 984
|||||
Db 1618 CTCGAAATTCAGAAATCC 1635

RESULT 22

US-09-005-051-57/c
; Sequence 57, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221

```
; FILING DATE: NO. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2144 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 30..1682
; FEATURE:
; NAME/KEY: Asx = Asn or Asp
; LOCATION: 462
; US-09-005-051-57

Query Match 0.6%; Score 18; DB 4; Length 2144;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
|||||
Db 527 CTCCAAAATTCAGAAATCC 510

RESULT 23
US-09-005-051-59
; Sequence 59, Application US/09005051
; Patent No. 6291222
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heaska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,051
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/747,221
; FILING DATE: No. 6291222ember 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2144 nucleotides
; TYPE: nucleic acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-09-005-051-59

Query Match 0.6%; Score 18; DB 4; Length 2144;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 967 CTCCAAAATTCAGAAATCC 984
|||||
Db 1618 CTCCAAAATTCAGAAATCC 1635

RESULT 24
US-09-192-104-1
; Sequence 1, Application US/09192104B
; Patent No. 6184020
; GENERAL INFORMATION:
; APPLICANT: Alexander Blinkovsky
; APPLICANT: Tony Byun
; APPLICANT: Alan V. Klotz
; APPLICANT: Alan Sloma
; APPLICANT: Maria Tang
; APPLICANT: Mikio Fujii
; APPLICANT: Chigusa Marumoto
; APPLICANT: Lene Venke Kofod
; TITLE OF INVENTION: Polypeptides Having Amino-peptidase
; TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5379.200-US
; CURRENT APPLICATION NUMBER: US/09/192,104B
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/069719
; EARLIER FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: 1465/97
; EARLIER FILING DATE: 1997-12-16
; EARLIER APPLICATION NUMBER: PA 1998 00670
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3000
; TYPE: DNA
; ORGANISM: Sphingomonas
; US-09-192-104-1

Query Match 0.6%; Score 18; DB 4; Length 3000;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2092 GCTGGTGTGGCTGGAAGC 2109
|||||
Db 1911 GCTGGTGTGGCTGGAAGC 1928

RESULT 25
US-09-543-446-1
; Sequence 1, Application US/09543446
; Patent No. 6303360
; GENERAL INFORMATION:
; APPLICANT: Alexander Blinkovsky
; APPLICANT: Tony Byun
; APPLICANT: Alan V. Klotz
; APPLICANT: Alan Sloma
; APPLICANT: Maria Tang
; APPLICANT: Mikio Fujii
; APPLICANT: Chigusa Marumoto
; APPLICANT: Lene Venke Kofod
; TITLE OF INVENTION: Polypeptides Having Amino-peptidase
; TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5379.210-US
; CURRENT APPLICATION NUMBER: US/09/543,446
; CURRENT FILING DATE: 2000-04-05
```

;; EARLIER APPLICATION NUMBER: 60/069719
;; EARLIER FILING DATE: 1997-12-16
;; EARLIER APPLICATION NUMBER: 1465/97
;; EARLIER FILING DATE: 1997-12-16
;; EARLIER APPLICATION NUMBER: PA 1998 00670
;; EARLIER FILING DATE: 1998-03-15
;; EARLIER APPLICATION NUMBER: 09/192,104
;; EARLIER FILING DATE: 1998-11-13
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 3000
;; TYPE: DNA
;; ORGANISM: Spingomonas
US-09-543-446-1

Query Match 0.6%; Score 18; DB 4; Length 3000;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2092 GCTGGTGTGGCTGGAAGC 2109
|||||
Db 1911 GCTGGTGTGGCTGGAAGC 1928

RESULT 26
US-09-518-386B-4/c
; Sequence 4, Application US/09518386B
; Patent No. 6365386
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: OJIMA, Kazuyuki
; TITLE OF INVENTION: SETOGUCHI, Yutaka
; TITLE OF INVENTION: ASTAXANTHIN SYNTHETASE
; FILE REFERENCE: ASTAXANTHIN SYNTHETASE
; CURRENT APPLICATION NUMBER: US/09/518,386B
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: EP 99104668.1
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EP 00101666.6
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 3969
; TYPE: DNA
; ORGANISM: Phaffia rhodozyma
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (517)..(518)
; NAME/KEY: intron
; LOCATION: (784)..(898)
; NAME/KEY: intron
; LOCATION: (1016)..(1087)
; NAME/KEY: intron
; LOCATION: (1180)..(1302)
; NAME/KEY: intron
; LOCATION: (1518)..(1600)
; NAME/KEY: intron
; LOCATION: (1635)..(1723)
; NAME/KEY: intron
; LOCATION: (1867)..(1939)
; NAME/KEY: intron
; LOCATION: (2000)..(2081)
; NAME/KEY: intron
; LOCATION: (2182)..(2257)
; NAME/KEY: intron
; LOCATION: (2355)..(2431)
; NAME/KEY: intron
; LOCATION: (2543)..(2618)
; NAME/KEY: intron
; LOCATION: (2653)..(2742)
; NAME/KEY: intron

;; LOCATION: (2815)..(2962)
;; NAME/KEY: intron
;; LOCATION: (3051)..(3113)
;; NAME/KEY: intron
;; LOCATION: (3172)..(3247)
;; NAME/KEY: intron
;; LOCATION: (3322)..(3398)
;; NAME/KEY: intron
;; LOCATION: (3424)..(3513)
;; NAME/KEY: polyA_site
;; LOCATION: (3865)..(3866)
;; NAME/KEY: intron
;; LOCATION: (653)..(734)
US-09-518-386B-4

Query Match 0.6%; Score 18; DB 4; Length 3969;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 385 AACTTGAAGCACCTTC 402
|||||
Db 1193 AACTTGAAGCACCTTC 1176

RESULT 27
US-08-699-103B-1/c
; Sequence 1, Application US/08699103B
; Patent No. 6107462
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper D.
; APPLICANT: Hampton, Randolph
; TITLE OF INVENTION: GENES AND PROTEINS CONTROLLING
; TITLE OF INVENTION: CHOLESTEROL SYNTHESIS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/699,103B
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,581
; FILING DATE: 17-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D.
; REGISTRATION NUMBER: 31,259
; REFERENCE/DOCKET NUMBER: 09272/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/322-5070
; TELEFAX: 650/854-0875
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-699-103B-1

Query Match 0.6%; Score 18; DB 3; Length 4982;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 CCCTTGGTGAAGATATTG 373

Db 1743 CCCTGGTGAAGATATTG 1726
|||||

RESULT 28

US-09-229-059-1/C
; Sequence 1, Application US/09229059
; Patent No. 633172
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper D.
; APPLICANT: Hampton, Randolph
; TITLE OF INVENTION: GENES AND PROTEINS CONTROLLING
; TITLE OF INVENTION: CHOLESTEROL SYNTHESIS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/229,059
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/699,103
; FILING DATE: 16-AUG-1996
; APPLICATION NUMBER: 60/002,581
; FILING DATE: 17-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D.
; REGISTRATION NUMBER: 31,259
; REFERENCE/DOCKET NUMBER: 09272/005001
; TELEPHONE: 650/322-5070
; TELEFAX: 650/854-0875
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA

US-09-229-059-1
Query Match 0.6%; Score 18; DB 4; Length 4982;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 CCCTGGTGAAGATATTG 373
Db 1743 CCCTGGTGAAGATATTG 1726
|||||

RESULT 29

US-08-801-308-2
; Sequence 2, Application US/08801308
; Patent No. 6368790
; GENERAL INFORMATION:
; APPLICANT: Scott, Robert E.
; TITLE OF INVENTION: CDNA ENCODING P2P PROTEINS AND USE OF
; TITLE OF INVENTION: P2P CDNA-DERIVED ANTIBODIES AND ANTISENSE REAGENTS IN
; TITLE OF INVENTION: DETERMINING THE PROLIFERATIVE POTENTIAL OF NORMAL,
; TITLE OF INVENTION: ABNORMAL AND CANCER CELLS IN ANIMALS AND HUMANS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates, P.C.
; STREET: 230 S. Fifteenth Street, Suite 500

; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,308
; FILING DATE: 18-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 372.6435P
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5173 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-801-308-2

Query Match 0.6%; Score 18; DB 4; Length 5173;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2796 AAGAACCCTCTGAAAAA 2813
Db 3187 AAGAACCCTCTGAAAAA 3204
|||||

RESULT 30

US-09-037-990B-27
; Sequence 27, Application US/09037990B
; Patent No. 6248519
; GENERAL INFORMATION:
; APPLICANT: ENGEL, Stacia R.
; DESCENZO, Richard A.
; MORENZONI, Richard A.
; IRELAN, Nancy A.
; TITLE OF INVENTION: DETECTION OF FERMENTATION-RELATED
; MICROORGANISMS
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,990B
; FILING DATE: 11-Mar-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 29520/30001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-037-990B-27

Query Match 0.6%; Score 17; DB 4; Length 290;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1117 AAAAACAACACAACA 1133
|||||
Db 209 AAAAACAACACAACA 225

RESULT 31
US-08-991-789A-171/c
Sequence 171, Application US/08991789A
Patent No. 6225054
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
Smith, John M.
Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER

NUMBER OF SEQUENCES: 292
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991.789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-08-991-789A-171

Query Match 0.6%; Score 17; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 374 ACATTATTTTAACTTG 390
|||||
Db 35 ACATTATTTTAACTTG 19

RESULT 32
US-09-062-451-171/c
Sequence 171, Application US/09062451
Patent No. 6344550
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
Smith, John M.
Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-171

Query Match 0.6%; Score 17; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 374 ACATTATTTTAACTTG 390
|||||
Db 35 ACATTATTTTAACTTG 19

RESULT 33
US-09-598-326-171/c
Sequence 171, Application US/09598326
Patent No. 6423496
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
Smith, John M.
Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 247
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/598,326
FILING DATE: 20-Jun-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419D1
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-09-598-326-171
Query Match 0.6%; Score 17; DB 4; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 374 ACATTATTTTAACTTG 390
Db 35 ACATTATTTTAACTTG 19
RESULT 34
US-09-037-990B-8
Sequence 8, Application US/09037990B
Patent No. 6248519
GENERAL INFORMATION:
APPLICANT: ENGEL, Stacia R.
DESCENZO, Richard A.
MORENZONI, Richard A.
IRELAN, Nancy A.
TITLE OF INVENTION: DETECTION OF FERMENTATION-RELATED MICROORGANISMS
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,990B
FILING DATE: 11-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 29520/30001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 661 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-037-990B-8
Query Match 0.6%; Score 17; DB 4; Length 661;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1117 AAAACAAACACAAACA 1133
Db 209 AAAACAAACACAAACA 225
RESULT 35
US-08-998-416-818
Sequence 818, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 818:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1520UP
US-08-998-416-818
Query Match 0.6%; Score 17; DB 4; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 460 CTGAATGGCCTCTCGCA 476
      |||||
Db 111 CTGAATGGCCTCTCGCA 127

RESULT 36
US-09-134-001C-621
; Sequence 621, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 621
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-621

Query Match 0.6%; Score 17; DB 4; Length 939;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3040 GTTATTACAGGTGCTTT 3056
      |||||
Db 799 GTTATTACAGGTGCTTT 815

RESULT 37
US-09-221-017B-138
; Sequence 138, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 138:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 963 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORYPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...963
US-09-221-017B-138

Query Match 0.6%; Score 17; DB 4; Length 963;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2310 GGATACATAAAGATGA 2326
      |||||
Db 943 GGATACATAAAGATGA 959

RESULT 38
US-09-134-001C-828
; Sequence 828, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 828
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-828

Query Match 0.6%; Score 17; DB 4; Length 1302;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1728 AGCTTTCTTTCAAGGTA 1744
      |||||
Db 975 AGCTTTCTTTCAAGGTA 991

RESULT 39
US-09-318-443-5/c
; Sequence 5, Application US/09318443
; Patent No. 6197947
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Weinstein, Daniel C.
; TITLE OF INVENTION: TRANSLATION INITIATION FACTOR 4AIIII, AND METHODS OF USE
; FILE REFERENCE: 600-1-211 N
```

; CURRENT APPLICATION NUMBER: US/09/318,443
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-443-5

Query Match 0.6%; Score 17; DB 4; Length 1536;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1339 CAGGAGTACACAGCAGG 1355
|||||

DB 1360 CAGGAGTACACAGCAGG 1344
|||||

RESULT 40

US-08-743-637B-183/c
; Sequence 183, Application US/08743637B
; Patent No. 5994066

GENERAL INFORMATION:

; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.

; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA

; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND

; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED

; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

; NUMBER OF SEQUENCES: 273

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: QUARLES & BRADY

; STREET: 411 EAST WISCONSIN AVENUE

; CITY: MILWAUKEE

; STATE: WISCONSIN

; COUNTRY: USA

; ZIP: 53202-4497

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/743,637B

; FILING DATE: 04-NOV-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/526,840

; FILING DATE: 11-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: BAKER, Jean C.

; REGISTRATION NUMBER: 35,433

; REFERENCE/DOCKET NUMBER: 850586.90012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (414) 277-5000

; TELEFAX: (414) 277-5591

; INFORMATION FOR SEQ ID NO: 183:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1563 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORGANISM: Klebsiella pneumoniae

US-08-743-637B-183

Query Match 0.6%; Score 17; DB 2; Length 1563;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 TCCTGCAGGCTCTTCAG 486
|||||

DB 74 TCCTGCAGGCTCTTCAG 58
|||||

RESULT 41

US-09-318-443-7/c

; Sequence 7, Application US/09318443

; Patent No. 6197947

; GENERAL INFORMATION:

; APPLICANT: Hemmati-Brivanlou, Ali

; APPLICANT: Weinstein, Daniel C.

; TITLE OF INVENTION: TRANSLATION INITIATION FACTOR 4AIII, AND METHODS OF USE

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 600-1-211 N

; CURRENT APPLICATION NUMBER: US/09/318,443

; CURRENT FILING DATE: 1999-05-25

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 1682

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-318-443-7

Query Match 0.6%; Score 17; DB 4; Length 1682;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1339 CAGGAGTACACAGCAGG 1355
|||||

DB 1501 CAGGAGTACACAGCAGG 1485
|||||

RESULT 42

US-09-178-252-26

; Sequence 26, Application US/09178252

; Patent No. 6218188

; GENERAL INFORMATION:

; APPLICANT: Cardineau, Guy A.

; APPLICANT: Stelman, Steven J.

; APPLICANT: Narva, Kenneth E.

; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins

; FILE REFERENCE: MA-714XC2

; CURRENT APPLICATION NUMBER: US/09/178,252

; CURRENT FILING DATE: 1998-10-23

; EARLIER APPLICATION NUMBER: 60/065,215

; EARLIER FILING DATE: 1997-11-12

; EARLIER APPLICATION NUMBER: 60/076,445

; EARLIER FILING DATE: 1998-03-02

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 26

; LENGTH: 1965

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic B.t. toxin gene

US-09-178-252-26

Query Match 0.6%; Score 17; DB 4; Length 1965;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 ACCAACACCATCACCGC 444
|||||

DB 1519 ACCAACACCATCACCGC 1535
|||||

RESULT 43

US-08-960-780-10

; Sequence 10, Application US/08960780

Patent No. 6204435
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeits, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide
SEQUENCES Which Encode These Toxins
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,780
FILING DATE: 30-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA-708
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2035 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 158C2-pt1
US-08-960-780-10

Query Match 0.6%; Score 17; DB 4; Length 2035;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2585 AAGATGGAATGAAGCT 2601
Db 1973 AAGATGGAATGAAGCT 1989

RESULT 44
US-09-073-898-10
Sequence 10, Application US/09073898
Patent No. 6242669
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schmeits, James
APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Muller-Cohn, Judy

APPLICANT: Stamp, Lisa
APPLICANT: Morrill, George
APPLICANT: Finstad-Lee, Stacey
TITLE OF INVENTION: No. 6242669el Pesticidal Toxins and Nucleotide
SEQUENCES Which Encode These Toxins
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,898
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2035 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 158C2-pt1
US-09-073-898-10

Query Match 0.6%; Score 17; DB 4; Length 2035;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2585 AAGATGGAATGAAGCT 2601
Db 1973 AAGATGGAATGAAGCT 1989

RESULT 45
US-09-227-357-31/C
Sequence 31, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08

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; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 2095
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (14)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-31
```

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Query Match          0.6%; Score 17; DB 4; Length 2095;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1117 AAAAAACAAACAAACA 1133
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Db 483 AAAAAACAAACAAACA 467

RESULT 46
US-09-115-446-1/c
; Sequence 1, Application US/09115446
; Patent No. 6165719
; GENERAL INFORMATION:
; APPLICANT: Chandy, George K.
; APPLICANT: Gargus, Jay J.
; APPLICANT: Gutman, George
; APPLICANT: Fantino, Emmanuelle
; APPLICANT: Kalman, Katarin
; TITLE OF INVENTION: hKCA3/KCNN3 SMALL CONDUCTANCE CALCIUM
; TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOSTIC
; FILE REFERENCE: 07306/014001
; CURRENT APPLICATION NUMBER: US/09/115,446
; CURRENT FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: 60/052,556
; EARLIER FILING DATE: 1997-07-15
; EARLIER APPLICATION NUMBER: 60/070,741
; EARLIER FILING DATE: 1998-01-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (287)...(2479)
US-09-115-446-1
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Query Match          0.6%; Score 17; DB 4; Length 2521;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 704 TGCTGCTGAAGCTGCGG 720
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Db 492 TGCTGCTGAAGCTGCGG 476
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RESULT 47
US-09-115-446-5/c
; Sequence 5, Application US/09115446
; Patent No. 6165719
; GENERAL INFORMATION:
; APPLICANT: Chandy, George K.
; APPLICANT: Gargus, Jay J.
; APPLICANT: Gutman, George
; APPLICANT: Fantino, Emmanuelle
; APPLICANT: Kalman, Katarin
; TITLE OF INVENTION: hKCA3/KCNN3 SMALL CONDUCTANCE CALCIUM
; TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOSTIC
; TITLE OF INVENTION: MARKER AND THERAPEUTIC TARGET
; FILE REFERENCE: 07306/014001
; CURRENT APPLICATION NUMBER: US/09/115,446
; CURRENT FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: 60/052,556
; EARLIER FILING DATE: 1997-07-15
; EARLIER APPLICATION NUMBER: 60/070,741
; EARLIER FILING DATE: 1998-01-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2526
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-115-446-5
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Query Match 0.6%; Score 17; DB 4; Length 2526;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 704 TGCTGCTGAAGTGGG 720
Db 497 TGCTGCTGAAGTGGG 481

RESULT 48

US-08-095-737-1/c
; Sequence 1, Application US/08095737
; Patent No. 5487979
; GENERAL INFORMATION:
; APPLICANT: DiFiore, Pier P
; APPLICANT: Fazioli, Francesca
; TITLE OF INVENTION: A Substrate for the Epidermal Growth
; TITLE OF INVENTION: Factor Receptor Kinase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: United States of America
; ZIP: 92660

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/095.737
; FILING DATE: 19930722
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH060.001A
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 21..2709

US-08-095-737-1

Query Match 0.6%; Score 17; DB 1; Length 4165;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2776 ATTTAGTGTCATTTT 2792
Db 4070 ATTTAGTGTCATTTT 4054

RESULT 49

US-08-480-145-1/c
; Sequence 1, Application US/08480145
; Patent No. 5717067
; GENERAL INFORMATION:
; APPLICANT: DiFiore, Pier P
; APPLICANT: Fazioli, Francesca

; TITLE OF INVENTION: A Substrate for the Epidermal Growth
; TITLE OF INVENTION: Factor Receptor Kinase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: United States of America
; ZIP: 92660

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480.145
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/095.737
; FILING DATE: 22-JUL-1993

ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH060.001A
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 21..2709

US-08-480-145-1

Query Match 0.6%; Score 17; DB 1; Length 4165;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2776 ATTTAGTGTCATTTT 2792
Db 4070 ATTTAGTGTCATTTT 4054

RESULT 50

US-08-477-389-1/c
; Sequence 1, Application US/08477389
; Patent No. 5872219
; GENERAL INFORMATION:
; APPLICANT: DiFiore, Pier P
; APPLICANT: Fazioli, Francesca
; TITLE OF INVENTION: A Substrate for the Epidermal Growth
; TITLE OF INVENTION: Factor Receptor Kinase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: United States of America
; ZIP: 92660

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2003, 00:11:05 ; Search time 170 Seconds
(without alignments)
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Title: US-09-697-089-3
Perfect score: 3072
Sequence: 1 atgaatttcataaagacaa.....cttttaaacagtagtaactgct 3072

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 396772 seqs, 224632407 residues

Word size : 12
Total number of hits satisfying chosen parameters: 84721

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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6: /cgn2_6/ptodata/1/pubpna/FCUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3072	100.0	3072	10 US-09-841-739-3	Sequence 3, Appli
2	3072	100.0	3133	10 US-09-841-739-1	Sequence 1, Appli
3	2868	93.4	3396	9 US-09-864-921-96	Sequence 96, Appli
4	2634	85.7	3612	10 US-09-841-739-6	Sequence 6, Appli
5	2634	85.7	3615	10 US-09-841-739-4	Sequence 4, Appli
6	2634	85.7	3615	10 US-09-841-739-12	Sequence 12, Appli
7	840	27.3	891	9 US-09-864-921-179	Sequence 179, Appl
8	815	26.5	1395	9 US-09-864-921-98	Sequence 98, Appli
9	618	20.1	618	9 US-09-864-921-181	Sequence 181, Appl
10	461	15.0	768	9 US-09-864-921-102	Sequence 102, Appl
11	420	13.7	608	10 US-09-764-864-339	Sequence 339, Appl
12	304	9.9	522	10 US-09-764-864-754	Sequence 754, Appl
13	269	8.8	578	9 US-09-864-921-100	Sequence 100, Appl
14	261	8.5	261	9 US-09-864-921-177	Sequence 177, Appl
15	242	7.9	421	10 US-09-864-761-4236	Sequence 4236, App
16	220	7.2	220	10 US-09-864-761-20988	Sequence 20988, A
17	114	3.7	165	9 US-09-864-921-183	Sequence 183, Appl
18	29	0.9	29	9 US-09-864-921-160	Sequence 160, Appl
19	25	0.8	25	9 US-09-864-921-161	Sequence 161, Appl

c	20	25	0.8	25	9 US-09-864-921-162	Sequence 162, App
	21	25	0.8	25	9 US-09-864-921-165	Sequence 165, App
	22	24	0.8	24	9 US-09-864-921-159	Sequence 159, App
	23	24	0.8	33	9 US-09-864-921-157	Sequence 157, App
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	25	23	0.7	23	9 US-09-864-921-163	Sequence 163, App
	26	21	0.7	21	9 US-09-864-921-156	Sequence 156, App
c	27	21	0.7	30	9 US-09-864-921-158	Sequence 158, App
	28	21	0.7	483	10 US-09-728-445-337	Sequence 337, App
	29	20	0.7	475	10 US-09-974-300-6263	Sequence 6263, Ap
c	30	20	0.7	768	9 US-09-864-921-102	Sequence 102, App
	31	19	0.6	30310	10 US-09-800-631-96	Sequence 96, Appli
c	32	18	0.6	21	9 US-09-864-921-155	Sequence 155, App
	33	18	0.6	216	10 US-09-867-701-9442	Sequence 9442, Ap
	34	18	0.6	273	10 US-09-878-574-9387	Sequence 9387, Ap
c	35	18	0.6	454	10 US-09-864-761-4716	Sequence 4716, Ap
	36	18	0.6	469	10 US-09-998-598-1369	Sequence 1369, Ap
	37	18	0.6	472	10 US-09-864-761-1714	Sequence 1714, Ap
c	38	18	0.6	501	10 US-09-728-446-43	Sequence 43, Appli
	39	18	0.6	960	9 US-09-738-626-2121	Sequence 2121, Ap
	40	18	0.6	1163	10 US-09-764-877-3957	Sequence 3957, Ap
c	41	18	0.6	1721	9 US-09-360-540-2	Sequence 2, Appli
	42	18	0.6	2619	10 US-09-764-864-1654	Sequence 1654, Ap
	43	18	0.6	3000	9 US-09-957-189-1	Sequence 1, Appli
	44	18	0.6	3460	10 US-09-764-864-1656	Sequence 1656, Ap
c	45	18	0.6	4951	10 US-09-070-927A-261	Sequence 261, App
	46	18	0.6	5173	10 US-09-811-045A-2	Sequence 2, Appli
	47	18	0.6	7386	10 US-09-764-855-208	Sequence 208, App
	48	18	0.6	17252	10 US-09-764-860-1102	Sequence 1102, Ap
	49	18	0.6	17509	10 US-09-880-107-2097	Sequence 2097, Ap
	50	18	0.6	202001	10 US-09-734-674-3	Sequence 3, Appli
c	51	18	0.6	684973	10 US-09-263-959-1	Sequence 1, Appli
	52	17	0.6	51	9 US-09-801-371A-10	Sequence 10, Appli
c	53	17	0.6	136	10 US-09-878-574-10039	Sequence 10039, A
	54	17	0.6	149	10 US-09-770-696-500	Sequence 500, App
c	55	17	0.6	160	10 US-09-878-574-14853	Sequence 14853, A
	56	17	0.6	169	10 US-09-878-574-7678	Sequence 7678, Ap
	57	17	0.6	175	10 US-09-983-965-1317	Sequence 1317, Ap
c	58	17	0.6	214	10 US-09-960-352-12982	Sequence 12982, A
	59	17	0.6	247	10 US-09-878-574-15571	Sequence 15571, A
c	60	17	0.6	257	10 US-09-878-574-6585	Sequence 6585, Ap
	61	17	0.6	260	10 US-09-878-574-10137	Sequence 10137, A
c	62	17	0.6	264	10 US-09-923-876-4513	Sequence 4513, Ap
	63	17	0.6	272	10 US-09-878-574-8191	Sequence 8191, Ap
c	64	17	0.6	272	10 US-09-878-574-12627	Sequence 12627, A
	65	17	0.6	276	9 US-10-040-739-1415	Sequence 1415, Ap
c	66	17	0.6	276	10 US-09-878-574-14107	Sequence 14107, A
	67	17	0.6	312	9 US-09-738-626-1862	Sequence 1862, Ap
c	68	17	0.6	316	9 US-09-796-692-5152	Sequence 5152, Ap
	69	17	0.6	341	10 US-09-878-574-1163	Sequence 1163, Ap
c	70	17	0.6	355	10 US-09-867-701-8170	Sequence 8170, Ap
	71	17	0.6	356	10 US-09-867-550-2095	Sequence 2095, Ap
c	72	17	0.6	356	10 US-09-867-550-2125	Sequence 2125, Ap
	73	17	0.6	357	10 US-09-878-574-2059	Sequence 2059, Ap
c	74	17	0.6	367	10 US-09-878-574-3303	Sequence 3303, Ap
	75	17	0.6	371	10 US-09-878-574-2835	Sequence 2835, Ap
c	76	17	0.6	383	9 US-09-924-400-171	Sequence 171, App
	77	17	0.6	383	10 US-09-810-936-171	Sequence 171, App
c	78	17	0.6	383	10 US-09-429-755-171	Sequence 171, App
	79	17	0.6	386	10 US-09-878-574-3140	Sequence 3140, Ap
c	80	17	0.6	399	10 US-09-983-965-1564	Sequence 1564, Ap
	81	17	0.6	415	10 US-09-878-574-3289	Sequence 3289, Ap
c	82	17	0.6	417	10 US-09-960-352-10604	Sequence 10604, A
	83	17	0.6	418	10 US-09-764-847-232	Sequence 232, App
c	84	17	0.6	422	10 US-09-960-352-12761	Sequence 12761, A
	85	17	0.6	432	10 US-09-925-300-772	Sequence 772, App
c	86	17	0.6	435	10 US-09-864-761-4687	Sequence 4687, Ap
	87	17	0.6	500	10 US-09-827-998-57	Sequence 57, Appli
c	88	17	0.6	522	10 US-09-880-107-1314	Sequence 1314, Ap
	89	17	0.6	541	10 US-09-864-761-21427	Sequence 21427, A
c	90	17	0.6	551	10 US-09-917-800A-722	Sequence 722, App
	91	17	0.6	575	10 US-09-864-761-9538	Sequence 9538, Ap
c	92	17	0.6	588	9 US-09-764-868-342	Sequence 342, App

c 93	17	0.6	588	10	US-09-815-242-7972	Sequence 7972, Ap	c 166	16	0.5	141	10	US-09-864-761-20253	Sequence 20253, A
c 94	17	0.6	590	10	US-09-917-800A-975	Sequence 975, App	c 167	16	0.5	145	10	US-09-864-761-28942	Sequence 28942, A
c 95	17	0.6	591	10	US-09-811-284-89	Sequence 89, Appl	c 168	16	0.5	150	9	US-10-079-623-109	Sequence 109, App
c 96	17	0.6	818	10	US-09-770-445-739	Sequence 739, App	c 169	16	0.5	165	9	US-10-025-380-601	Sequence 601, App
c 97	17	0.6	843	9	US-09-984-245-43	Sequence 43, Appl	c 170	16	0.5	165	10	US-09-922-217-601	Sequence 601, App
c 98	17	0.6	950	10	US-09-867-550-1541	Sequence 1541, Ap	c 171	16	0.5	165	10	US-09-833-263-601	Sequence 601, App
c 99	17	0.6	1001	10	US-09-798-029-3	Sequence 3, Appli	c 172	16	0.5	170	10	US-09-783-590-11272	Sequence 11272, A
c 100	17	0.6	1128	9	US-09-938-842A-1107	Sequence 1107, Ap	c 173	16	0.5	175	10	US-09-864-761-25901	Sequence 25901, A
c 101	17	0.6	1332	9	US-10-023-437-8	Sequence 8, Appli	c 174	16	0.5	182	10	US-09-878-574-15700	Sequence 15700, A
c 102	17	0.6	1339	10	US-09-778-844-73	Sequence 73, Appl	c 175	16	0.5	189	10	US-09-864-761-28808	Sequence 28808, A
c 103	17	0.6	1341	9	US-09-938-842A-2465	Sequence 2465, Ap	c 176	16	0.5	193	10	US-09-960-352-3980	Sequence 3980, Ap
c 104	17	0.6	1359	9	US-09-738-626-526	Sequence 526, App	c 177	16	0.5	208	10	US-09-925-299-726	Sequence 726, App
c 105	17	0.6	1369	10	US-09-778-844-58	Sequence 58, Appl	c 178	16	0.5	216	10	US-09-728-446-257	Sequence 257, App
c 106	17	0.6	1409	9	US-09-895-593-1	Sequence 1, Appli	c 179	16	0.5	220	10	US-09-864-761-19964	Sequence 19964, A
c 107	17	0.6	1409	10	US-09-895-943-1	Sequence 1, Appli	c 180	16	0.5	229	10	US-09-923-876-936	Sequence 936, App
c 108	17	0.6	1419	9	US-09-938-842A-2904	Sequence 2904, Ap	c 181	16	0.5	252	10	US-09-864-761-19331	Sequence 19331, A
c 109	17	0.6	1536	10	US-09-755-325-5	Sequence 5, Appli	c 182	16	0.5	253	10	US-09-728-446-896	Sequence 896, App
c 110	17	0.6	1682	10	US-09-755-325-7	Sequence 7, Appli	c 183	16	0.5	254	10	US-09-878-574-15520	Sequence 15520, A
c 111	17	0.6	1700	10	US-09-728-952-26	Sequence 26, Appl	c 184	16	0.5	264	10	US-09-878-574-14820	Sequence 14820, A
c 112	17	0.6	1857	10	US-09-822-930A-338	Sequence 338, App	c 185	16	0.5	270	10	US-09-867-701-8694	Sequence 8694, Ap
c 113	17	0.6	1949	10	US-09-778-844-57	Sequence 57, Appl	c 186	16	0.5	271	10	US-09-864-761-18446	Sequence 18446, A
c 114	17	0.6	1965	10	US-09-826-660-26	Sequence 26, Appl	c 187	16	0.5	284	10	US-09-878-574-7963	Sequence 7963, Ap
c 115	17	0.6	1974	9	US-09-938-842A-248	Sequence 248, App	c 188	16	0.5	289	10	US-09-878-574-5087	Sequence 5087, Ap
c 116	17	0.6	2000	10	US-09-887-576-110	Sequence 110, App	c 189	16	0.5	293	10	US-09-294-093B-1793	Sequence 1793, Ap
c 117	17	0.6	2035	10	US-09-850-351A-10	Sequence 10, Appl	c 190	16	0.5	298	10	US-09-294-093B-3207	Sequence 3207, Ap
c 118	17	0.6	2073	10	US-09-880-107-1601	Sequence 1601, Ap	c 191	16	0.5	311	10	US-09-864-864-32	Sequence 32, Appl
c 119	17	0.6	2136	9	US-09-938-842A-2144	Sequence 2144, Ap	c 192	16	0.5	322	10	US-09-783-590-7028	Sequence 7028, Ap
c 120	17	0.6	2224	9	US-09-922-364A-44	Sequence 44, Appl	c 193	16	0.5	328	10	US-09-960-352-5993	Sequence 5993, Ap
c 121	17	0.6	2224	9	US-09-254-590-44	Sequence 44, Appl	c 194	16	0.5	330	9	US-09-954-531-713	Sequence 713, App
c 122	17	0.6	2224	9	US-10-115-695-44	Sequence 44, Appl	c 195	16	0.5	341	10	US-09-764-860-157	Sequence 157, App
c 123	17	0.6	2451	9	US-09-764-868-19	Sequence 19, Appl	c 196	16	0.5	341	10	US-09-728-445-565	Sequence 565, App
c 124	17	0.6	2462	9	US-09-922-364A-48	Sequence 48, Appl	c 197	16	0.5	345	10	US-09-864-761-29498	Sequence 29498, A
c 125	17	0.6	2462	9	US-09-254-590-48	Sequence 48, Appl	c 198	16	0.5	351	9	US-09-938-842A-614	Sequence 614, App
c 126	17	0.6	2462	9	US-10-115-695-48	Sequence 48, Appl	c 199	16	0.5	355	9	US-09-924-400-78	Sequence 78, Appl
c 127	17	0.6	2521	10	US-09-925-300-521	Sequence 521, App	c 200	16	0.5	355	9	US-09-924-400-248	Sequence 248, App
c 128	17	0.6	2626	12	US-10-002-600-45	Sequence 45, Appl	c 201	16	0.5	355	10	US-09-810-936-78	Sequence 78, Appl
c 129	17	0.6	2670	12	US-10-002-600-44	Sequence 44, Appl	c 202	16	0.5	355	10	US-09-810-936-248	Sequence 248, App
c 130	17	0.6	2805	9	US-09-938-842A-991	Sequence 991, App	c 203	16	0.5	355	10	US-09-429-755-78	Sequence 78, Appl
c 131	17	0.6	2805	10	US-09-887-576-679	Sequence 679, App	c 204	16	0.5	355	10	US-09-429-755-248	Sequence 248, App
c 132	17	0.6	2911	10	US-09-764-864-104	Sequence 104, App	c 205	16	0.5	360	10	US-09-867-701-385	Sequence 385, App
c 133	17	0.6	3183	10	US-09-801-368-409	Sequence 409, App	c 206	16	0.5	362	10	US-09-920-300A-903	Sequence 903, App
c 134	17	0.6	3236	10	US-09-925-297-116	Sequence 116, App	c 207	16	0.5	362	12	US-10-033-528-903	Sequence 903, App
c 135	17	0.6	3378	9	US-09-964-899-48	Sequence 48, Appl	c 208	16	0.5	364	10	US-09-728-445-73	Sequence 73, Appl
c 136	17	0.6	3406	10	US-09-954-456-1789	Sequence 1789, Ap	c 209	16	0.5	370	10	US-09-960-352-7378	Sequence 7378, Ap
c 137	17	0.6	3406	10	US-09-880-107-1628	Sequence 1628, Ap	c 210	16	0.5	375	10	US-09-563-817-869	Sequence 869, App
c 138	17	0.6	3531	9	US-09-918-508-1	Sequence 1, Appli	c 211	16	0.5	387	10	US-09-878-574-487	Sequence 487, App
c 139	17	0.6	3572	10	US-09-925-302-280	Sequence 280, App	c 212	16	0.5	387	10	US-09-983-965-5819	Sequence 5819, Ap
c 140	17	0.6	4407	9	US-10-174-590-351	Sequence 351, App	c 213	16	0.5	390	10	US-09-983-965-2829	Sequence 2829, Ap
c 141	17	0.6	4407	9	US-10-176-758-351	Sequence 351, App	c 214	16	0.5	393	10	US-09-867-701-1787	Sequence 1787, Ap
c 142	17	0.6	4407	9	US-10-175-737-351	Sequence 351, App	c 215	16	0.5	393	10	US-09-983-965-4845	Sequence 4845, Ap
c 143	17	0.6	4437	10	US-10-052-586-351	Sequence 351, App	c 216	16	0.5	395	10	US-09-960-352-8799	Sequence 8799, Ap
c 144	17	0.6	4437	10	US-09-753-143-72	Sequence 72, Appl	c 217	16	0.5	395	10	US-09-983-965-4816	Sequence 4816, Ap
c 145	17	0.6	6242	10	US-09-962-832-112	Sequence 112, App	c 218	16	0.5	400	10	US-09-867-701-6499	Sequence 6499, Ap
c 146	17	0.6	6242	9	US-09-764-868-1436	Sequence 1436, Ap	c 219	16	0.5	401	9	US-09-946-807-756	Sequence 756, App
c 147	17	0.6	6459	9	US-10-029-217A-6	Sequence 6, Appli	c 220	16	0.5	401	9	US-09-946-807-757	Sequence 757, App
c 148	17	0.6	7465	10	US-09-880-107-3357	Sequence 3357, Ap	c 221	16	0.5	401	10	US-09-795-668-756	Sequence 756, App
c 149	17	0.6	10195	10	US-09-764-864-1600	Sequence 1600, Ap	c 222	16	0.5	401	10	US-09-795-668-757	Sequence 757, App
c 150	17	0.6	11221	10	US-09-778-963A-3	Sequence 3, Appli	c 223	16	0.5	401	10	US-09-795-668-756	Sequence 756, App
c 151	17	0.6	13273	10	US-09-764-869-2349	Sequence 2349, Ap	c 224	16	0.5	401	10	US-09-795-668-757	Sequence 757, App
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c 153	17	0.6	24023	9	US-10-094-679-1	Sequence 1, Appli	c 226	16	0.5	403	10	US-09-960-352-8222	Sequence 8222, Ap
c 154	17	0.6	32190	10	US-09-764-877-2844	Sequence 2844, Ap	c 227	16	0.5	404	10	US-09-960-352-11963	Sequence 11963, A
c 155	17	0.6	38374	10	US-09-880-107-3463	Sequence 3463, Ap	c 228	16	0.5	406	9	US-09-933-797-763	Sequence 763, App
c 156	17	0.6	46718	10	US-09-816-093-3	Sequence 3, Appli	c 229	16	0.5	413	10	US-09-962-832-82	Sequence 82, Appl
c 157	17	0.6	106323	10	US-09-803-661-3	Sequence 3, Appli	c 230	16	0.5	413	10	US-09-967-768A-105	Sequence 105, App
c 158	17	0.6	155074	9	US-10-026-188-6	Sequence 6, Appli	c 231	16	0.5	415	10	US-09-864-761-3185	Sequence 3185, Ap
c 159	17	0.6	249487	9	US-10-026-188-3	Sequence 3, Appli	c 232	16	0.5	418	10	US-09-925-299-503	Sequence 503, App
c 160	17	0.6	640681	9	US-09-790-988-1	Sequence 1, Appli	c 233	16	0.5	420	10	US-09-764-860-909	Sequence 909, App
c 161	17	0.5	3309400	9	US-09-738-626-1	Sequence 1, Appli	c 234	16	0.5	420	10	US-09-960-352-3554	Sequence 3554, Ap
c 162	16	0.5	109	10	US-09-864-761-28485	Sequence 28485, A	c 235	16	0.5	422	10	US-09-960-352-2763	Sequence 2763, Ap
c 163	16	0.5	109	10	US-09-783-590-5809	Sequence 5809, Ap	c 236	16	0.5	423	10	US-09-960-352-8117	Sequence 8117, Ap
c 164	16	0.5	112	10	US-09-864-761-30612	Sequence 30612, Ap	c 237	16	0.5	423	10	US-09-983-965-3069	Sequence 3069, Ap
c 165	16	0.5	113	10	US-09-294-093B-3496	Sequence 3496, Ap	c 238	16	0.5	423	10	US-09-983-965-5648	Sequence 5648, Ap

c 239	16	0.5	426	10	US-09-764-860-161	Sequence 161, App	312	16	0.5	545	10	US-09-864-761-32206	Sequence 32206, A
c 240	16	0.5	427	10	US-09-867-701-3928	Sequence 3928, Ap	313	16	0.5	549	10	US-09-974-300-2944	Sequence 2944, Ap
c 241	16	0.5	430	10	US-09-960-352-5031	Sequence 5031, Ap	314	16	0.5	551	10	US-09-864-761-12228	Sequence 12228, A
c 242	16	0.5	432	9	US-09-933-797-440	Sequence 440, App	c 315	16	0.5	555	10	US-09-864-761-9512	Sequence 9512, Ap
c 243	16	0.5	432	10	US-09-867-701-1792	Sequence 1792, Ap	c 316	16	0.5	558	9	US-09-796-692-8615	Sequence 8615, Ap
c 244	16	0.5	434	10	US-09-822-849A-587	Sequence 587, App	c 317	16	0.5	561	10	US-09-560-863-616	Sequence 616, App
c 245	16	0.5	434	10	US-09-960-352-13569	Sequence 13569, A	c 318	16	0.5	563	9	US-09-996-140-64	Sequence 64, Appl
c 246	16	0.5	435	9	US-09-954-531-463	Sequence 463, App	c 319	16	0.5	563	10	US-09-864-761-9542	Sequence 9542, Ap
c 247	16	0.5	435	10	US-09-867-550-65	Sequence 65, Appl	c 320	16	0.5	567	10	US-09-864-761-12387	Sequence 12387, A
c 248	16	0.5	435	10	US-09-867-701-4813	Sequence 4813, Ap	c 321	16	0.5	567	10	US-09-864-761-7531	Sequence 7531, Ap
c 249	16	0.5	437	10	US-09-917-800A-431	Sequence 431, App	c 322	16	0.5	569	10	US-09-864-761-8268	Sequence 8268, Ap
c 250	16	0.5	438	10	US-09-920-300A-283	Sequence 283, App	c 323	16	0.5	569	10	US-09-864-761-9387	Sequence 9387, Ap
c 251	16	0.5	438	12	US-10-033-528-288	Sequence 283, App	c 324	16	0.5	576	10	US-09-920-300A-1018	Sequence 1018, Ap
c 252	16	0.5	440	10	US-09-864-761-10165	Sequence 10165, A	c 325	16	0.5	576	12	US-10-033-528-1018	Sequence 1018, Ap
c 253	16	0.5	444	10	US-09-925-301-696	Sequence 696, App	c 326	16	0.5	576	12	US-10-033-528-1839	Sequence 1839, Ap
c 254	16	0.5	445	10	US-09-864-761-2177	Sequence 2177, Ap	c 327	16	0.5	577	9	US-09-996-140-38	Sequence 38, Appl
c 255	16	0.5	446	10	US-09-770-444-781	Sequence 781, App	c 328	16	0.5	578	10	US-09-998-598-1023	Sequence 1023, Ap
c 256	16	0.5	449	10	US-09-864-761-11513	Sequence 11513, A	c 329	16	0.5	581	10	US-09-864-761-11910	Sequence 11910, A
c 257	16	0.5	451	10	US-09-833-790-330	Sequence 330, App	c 330	16	0.5	587	10	US-09-864-761-9026	Sequence 9026, Ap
c 258	16	0.5	454	10	US-09-864-761-5563	Sequence 5563, Ap	c 331	16	0.5	587	10	US-09-828-302-5	Sequence 5, Appl
c 259	16	0.5	455	10	US-09-880-107-2497	Sequence 2497, Ap	c 332	16	0.5	588	10	US-09-917-800A-999	Sequence 999, App
c 260	16	0.5	457	10	US-09-867-701-10703	Sequence 10703, A	c 333	16	0.5	593	10	US-09-864-761-13697	Sequence 13697, A
c 261	16	0.5	459	10	US-09-960-352-5700	Sequence 5700, Ap	c 334	16	0.5	595	10	US-09-833-381-706	Sequence 706, App
c 262	16	0.5	460	10	US-09-864-761-14052	Sequence 14052, A	c 335	16	0.5	595	10	US-09-867-701-1526	Sequence 1526, Ap
c 263	16	0.5	462	9	US-10-025-380-272	Sequence 272, App	c 336	16	0.5	597	10	US-09-864-761-31718	Sequence 31718, A
c 264	16	0.5	462	10	US-09-922-217-272	Sequence 272, App	c 337	16	0.5	599	10	US-09-864-761-9356	Sequence 9356, Ap
c 265	16	0.5	462	10	US-09-833-263-272	Sequence 272, App	c 338	16	0.5	600	10	US-09-864-761-8623	Sequence 8623, Ap
c 266	16	0.5	463	10	US-09-770-444-378	Sequence 378, App	c 339	16	0.5	600	10	US-09-864-761-13553	Sequence 13553, A
c 267	16	0.5	463	10	US-09-864-761-5550	Sequence 5550, Ap	c 340	16	0.5	604	10	US-09-864-761-17057	Sequence 17057, A
c 268	16	0.5	463	10	US-09-983-965-3664	Sequence 3664, Ap	c 341	16	0.5	607	10	US-09-879-536-205	Sequence 205, App
c 269	16	0.5	465	10	US-09-864-761-649	Sequence 649, App	c 342	16	0.5	610	9	US-10-040-739-475	Sequence 475, App
c 270	16	0.5	465	10	US-09-864-761-10244	Sequence 10244, A	c 343	16	0.5	634	10	US-09-815-343-215	Sequence 215, App
c 271	16	0.5	466	10	US-09-917-800A-263	Sequence 263, App	c 344	16	0.5	640	9	US-10-025-380-630	Sequence 630, App
c 272	16	0.5	467	10	US-09-864-761-3483	Sequence 3483, Ap	c 345	16	0.5	640	10	US-09-922-217-630	Sequence 630, App
c 273	16	0.5	469	10	US-09-864-761-13881	Sequence 13881, A	c 346	16	0.5	640	10	US-09-833-263-630	Sequence 630, App
c 274	16	0.5	471	10	US-09-864-761-2416	Sequence 2416, Ap	c 347	16	0.5	640	10	US-09-833-381-974	Sequence 974, App
c 275	16	0.5	471	10	US-09-864-761-11002	Sequence 11002, A	c 348	16	0.5	694	10	US-09-864-761-26760	Sequence 26760, A
c 276	16	0.5	473	10	US-09-867-701-5013	Sequence 5013, Ap	c 349	16	0.5	694	10	US-09-995-494-57	Sequence 57, Appl
c 277	16	0.5	474	10	US-09-864-761-1690	Sequence 1690, Ap	c 350	16	0.5	695	10	US-09-770-149-286	Sequence 286, App
c 278	16	0.5	475	10	US-09-864-761-2609	Sequence 2609, Ap	c 351	16	0.5	700	10	US-09-910-943-261	Sequence 261, App
c 279	16	0.5	477	9	US-09-981-286A-12	Sequence 12, Appl	c 352	16	0.5	728	9	US-10-066-500-53	Sequence 53, Appl
c 280	16	0.5	477	10	US-09-864-761-146	Sequence 146, App	c 353	16	0.5	730	10	US-09-867-550-677	Sequence 677, App
c 281	16	0.5	479	10	US-09-867-701-2300	Sequence 2300, Ap	c 354	16	0.5	811	9	US-09-938-842A-4121	Sequence 4121, Ap
c 282	16	0.5	482	10	US-09-864-761-27002	Sequence 27002, A	c 355	16	0.5	819	12	US-10-044-090-427	Sequence 427, App
c 283	16	0.5	482	10	US-09-920-300A-1363	Sequence 1363, Ap	c 356	16	0.5	823	9	US-09-842-777-2	Sequence 2, Appl
c 284	16	0.5	482	12	US-10-033-528-1363	Sequence 1363, Ap	c 357	16	0.5	830	9	US-09-842-777-16	Sequence 16, Appl
c 285	16	0.5	483	9	US-09-796-692-4807	Sequence 4807, Ap	c 358	16	0.5	843	10	US-09-974-300-5379	Sequence 5379, Ap
c 286	16	0.5	483	10	US-09-919-580-455	Sequence 455, App	c 359	16	0.5	844	9	US-09-842-777-3	Sequence 3, Appl
c 287	16	0.5	483	10	US-09-974-300-5149	Sequence 5149, Ap	c 360	16	0.5	846	9	US-09-842-777-4	Sequence 4, Appl
c 288	16	0.5	485	10	US-09-864-761-5987	Sequence 5987, Ap	c 361	16	0.5	851	9	US-09-842-777-5	Sequence 5, Appl
c 289	16	0.5	486	10	US-09-920-300A-981	Sequence 981, App	c 362	16	0.5	851	9	US-09-842-777-17	Sequence 17, Appl
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c 291	16	0.5	488	10	US-09-998-598-939	Sequence 939, App	c 364	16	0.5	858	9	US-09-842-777-19	Sequence 19, Appl
c 292	16	0.5	490	10	US-09-783-590-3526	Sequence 3526, Ap	c 365	16	0.5	903	10	US-09-529-063-48	Sequence 48, Appl
c 293	16	0.5	500	10	US-09-998-598-513	Sequence 513, App	c 366	16	0.5	912	9	US-09-938-842A-912	Sequence 912, App
c 294	16	0.5	501	9	US-09-938-842A-4442	Sequence 4442, Ap	c 367	16	0.5	921	10	US-09-801-368-83	Sequence 83, Appl
c 295	16	0.5	502	10	US-09-783-590-452	Sequence 452, App	c 368	16	0.5	965	9	US-09-883-152-9	Sequence 9, Appl
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c 300	16	0.5	512	10	US-09-833-381-1335	Sequence 1335, Ap	c 373	16	0.5	982	10	US-09-770-445-270	Sequence 270, App
c 301	16	0.5	515	10	US-09-998-598-275	Sequence 275, App	c 374	16	0.5	983	10	US-09-780-717-43	Sequence 43, Appl
c 302	16	0.5	523	9	US-10-046-935-2057	Sequence 2057, Ap	c 375	16	0.5	994	10	US-09-887-576-446	Sequence 446, App
c 303	16	0.5	523	9	US-09-878-178-2057	Sequence 2057, Ap	c 376	16	0.5	995	10	US-09-764-853-21	Sequence 21, Appl
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c 307	16	0.5	533	10	US-09-864-761-12363	Sequence 12363, A	c 380	16	0.5	1110	9	US-09-883-152-7	Sequence 7, Appl
c 308	16	0.5	535	10	US-09-864-761-12935	Sequence 12935, A	c 381	16	0.5	1134	9	US-09-938-842A-3556	Sequence 3556, Ap
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c 311	16	0.5	545	10	US-09-864-761-30098	Sequence 30098, A	c 384	16	0.5	1140	10	US-09-764-869-257	Sequence 257, App

385	16	0.5	1151	10	US-09-778-844-164	Sequence 164, App	458	16	0.5	2005	10	US-09-887-576-304	Sequence 304, App
386	16	0.5	1157	10	US-09-778-844-166	Sequence 166, App	c 459	16	0.5	2047	10	US-09-864-761-32004	Sequence 32004, A
387	16	0.5	1158	9	US-09-938-842A-739	Sequence 739, App	c 460	16	0.5	2092	10	US-09-764-869-1930	Sequence 1930, App
388	16	0.5	1159	9	US-09-842-777-1	Sequence 1, Appli	461	16	0.5	2093	10	US-09-880-107-3941	Sequence 3941, App
389	16	0.5	1159	9	US-09-842-777-11	Sequence 11, Appli	c 462	16	0.5	2119	10	US-09-828-310-9	Sequence 9, Appli
390	16	0.5	1172	10	US-09-778-844-163	Sequence 163, App	c 463	16	0.5	2139	9	US-10-095-139-3	Sequence 3, Appli
391	16	0.5	1173	9	US-09-842-777-15	Sequence 15, Appli	c 464	16	0.5	2139	9	US-10-095-139-24	Sequence 24, Appli
392	16	0.5	1178	10	US-09-840-787-88	Sequence 88, Appli	c 465	16	0.5	2160	9	US-09-938-842A-628	Sequence 628, App
393	16	0.5	1200	10	US-09-925-300-488	Sequence 488, App	c 466	16	0.5	2184	10	US-09-880-192-31	Sequence 31, Appli
394	16	0.5	1261	10	US-09-964-824A-579	Sequence 579, App	c 467	16	0.5	2209	10	US-09-925-301-494	Sequence 494, App
395	16	0.5	1263	9	US-09-864-761-19678	Sequence 19678, A	c 468	16	0.5	2224	10	US-09-873-637-1	Sequence 1, Appli
396	16	0.5	1317	9	US-10-011-588-16	Sequence 16, Appli	c 469	16	0.5	2232	9	US-09-774-639-26	Sequence 26, Appli
397	16	0.5	1320	12	US-10-044-090-82	Sequence 82, App	c 470	16	0.5	2295	10	US-09-815-242-7459	Sequence 7459, App
398	16	0.5	1362	9	US-09-938-842A-1584	Sequence 1584, App	c 471	16	0.5	2388	10	US-09-925-302-112	Sequence 112, App
399	16	0.5	1378	10	US-09-809-545A-44	Sequence 44, Appli	c 472	16	0.5	2413	10	US-09-931-087A-2	Sequence 2, Appli
400	16	0.5	1386	9	US-09-910-664-38	Sequence 38, Appli	c 473	16	0.5	2418	9	US-09-989-919-19	Sequence 19, Appli
401	16	0.5	1404	10	US-09-765-272-9	Sequence 9, Appli	c 474	16	0.5	2429	9	US-10-041-007-27	Sequence 27, Appli
402	16	0.5	1464	9	US-09-738-626-216	Sequence 216, App	c 475	16	0.5	2438	9	US-09-895-913A-327	Sequence 327, App
403	16	0.5	1468	10	US-09-967-768A-185	Sequence 185, App	c 476	16	0.5	2488	10	US-09-822-849A-358	Sequence 358, App
404	16	0.5	1470	10	US-09-974-300-6209	Sequence 6209, App	c 477	16	0.5	2526	10	US-09-864-761-21763	Sequence 21763, A
405	16	0.5	1491	10	US-09-892-325-3	Sequence 3, Appli	c 478	16	0.5	2531	9	US-09-070-927A-96	Sequence 96, Appli
406	16	0.5	1494	9	US-09-938-842A-569	Sequence 569, App	c 479	16	0.5	2540	9	US-09-966-955A-5	Sequence 5, Appli
407	16	0.5	1495	12	US-10-044-090-798	Sequence 798, App	c 480	16	0.5	2554	9	US-10-108-605-338	Sequence 338, App
408	16	0.5	1502	10	US-09-883-797-11	Sequence 11, Appli	c 481	16	0.5	2577	10	US-09-822-849A-335	Sequence 335, App
409	16	0.5	1514	10	US-09-939-980-219	Sequence 897, App	c 482	16	0.5	2608	10	US-09-884-441-386	Sequence 386, App
410	16	0.5	1529	10	US-09-764-860-897	Sequence 897, App	c 483	16	0.5	2617	9	US-10-016-157A-121	Sequence 121, App
411	16	0.5	1529	10	US-09-764-860-898	Sequence 898, App	c 484	16	0.5	2656	9	US-09-798-889-33	Sequence 33, Appli
412	16	0.5	1529	10	US-09-764-860-899	Sequence 899, App	c 485	16	0.5	2681	10	US-09-917-800A-1619	Sequence 1619, App
413	16	0.5	1529	10	US-09-764-860-900	Sequence 900, App	c 486	16	0.5	2798	10	US-09-954-456-1145	Sequence 1145, App
414	16	0.5	1533	9	US-09-938-842A-2430	Sequence 2430, App	c 487	16	0.5	2808	10	US-09-954-456-2205	Sequence 2205, App
c 415	16	0.5	1542	9	US-09-938-842A-2222	Sequence 2222, App	c 488	16	0.5	2916	10	US-09-956-004-22	Sequence 22, Appli
416	16	0.5	1542	10	US-09-962-832-4	Sequence 4, Appli	c 489	16	0.5	2943	10	US-09-884-441-385	Sequence 385, App
417	16	0.5	1554	9	US-09-938-842A-1059	Sequence 1059, App	c 490	16	0.5	2960	9	US-10-098-841-16	Sequence 16, Appli
418	16	0.5	1557	10	US-09-815-242-8181	Sequence 8181, App	c 491	16	0.5	2996	10	US-09-778-320-205	Sequence 205, App
419	16	0.5	1569	10	US-09-822-830A-467	Sequence 467, App	c 492	16	0.5	2996	10	US-09-910-689-205	Sequence 205, App
c 420	16	0.5	1582	10	US-09-764-877-2303	Sequence 2303, App	c 493	16	0.5	2996	10	US-09-884-441-311	Sequence 311, App
c 421	16	0.5	1582	9	US-09-938-842A-4378	Sequence 2304, App	c 494	16	0.5	2996	12	US-09-884-441-452	Sequence 462, App
c 422	16	0.5	1583	9	US-09-938-842A-4378	Sequence 4378, App	c 495	16	0.5	3024	10	US-10-010-742-205	Sequence 205, App
423	16	0.5	1584	10	US-09-815-242-4211	Sequence 4211, App	c 496	16	0.5	3030	10	US-09-833-381-889	Sequence 889, App
424	16	0.5	1587	10	US-09-867-550-1879	Sequence 1879, App	c 497	16	0.5	3090	10	US-09-768-436-1	Sequence 1, Appli
425	16	0.5	1597	10	US-09-954-456-734	Sequence 734, App	c 498	16	0.5	3091	10	US-09-764-860-1001	Sequence 1001, App
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c 428	16	0.5	1636	10	US-09-911-513-3	Sequence 7, Appli	c 501	16	0.5	3112	8	US-08-927-939-34	Sequence 34, Appli
c 429	16	0.5	1636	10	US-09-884-441-467	Sequence 467, App	c 502	16	0.5	3147	10	US-09-741-669-216	Sequence 216, App
c 430	16	0.5	1642	10	US-09-911-513-5	Sequence 5, Appli	c 503	16	0.5	3147	10	US-09-815-242-5965	Sequence 5965, App
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c 432	16	0.5	1643	10	US-09-911-513-3	Sequence 3, Appli	c 505	16	0.5	3227	9	US-10-095-139-22	Sequence 22, Appli
c 433	16	0.5	1668	10	US-09-822-830A-87	Sequence 87, Appli	c 506	16	0.5	3437	10	US-09-919-497-34	Sequence 34, Appli
c 434	16	0.5	1711	10	US-09-867-550-1379	Sequence 1379, App	c 507	16	0.5	3437	10	US-09-954-456-1170	Sequence 1170, App
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c 437	16	0.5	1761	10	US-09-884-441-387	Sequence 387, App	c 510	16	0.5	3557	10	US-09-884-441-463	Sequence 463, App
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c 439	16	0.5	1807	10	US-09-892-325-2	Sequence 2, Appli	c 512	16	0.5	3609	10	US-09-799-875-6	Sequence 6, Appli
c 440	16	0.5	1824	10	US-09-814-786-1	Sequence 1, Appli	c 513	16	0.5	3649	10	US-09-801-574-15	Sequence 15, Appli
441	16	0.5	1840	10	US-09-954-456-723	Sequence 723, App	c 514	16	0.5	3649	10	US-09-801-574-15	Sequence 15, Appli
c 442	16	0.5	1917	10	US-09-864-761-27095	Sequence 27095, A	c 515	16	0.5	3705	12	US-10-044-090-307	Sequence 307, App
c 443	16	0.5	1931	9	US-10-098-841-102	Sequence 102, App	c 516	16	0.5	3722	10	US-09-892-325-1	Sequence 1, Appli
c 444	16	0.5	1960	10	US-09-731-872-179	Sequence 179, App	c 517	16	0.5	3740	9	US-09-925-300-345	Sequence 345, App
c 445	16	0.5	1963	10	US-09-864-761-2897	Sequence 2897, App	c 518	16	0.5	3795	9	US-10-002-344A-25	Sequence 25, Appli
c 446	16	0.5	1964	10	US-09-911-513-1	Sequence 1, Appli	c 519	16	0.5	3795	9	US-10-002-344A-25	Sequence 25, Appli
c 447	16	0.5	1969	10	US-09-864-761-15490	Sequence 15490, A	c 520	16	0.5	3833	9	US-09-954-531-1390	Sequence 1390, App
c 448	16	0.5	1971	9	US-09-938-842A-3410	Sequence 3410, App	c 521	16	0.5	3833	10	US-09-969-708-391	Sequence 391, App
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450	16	0.5	1989	10	US-09-974-300-2023	Sequence 2023, App	c 523	16	0.5	4006	10	US-09-768-436-3	Sequence 3, Appli
451	16	0.5	1991	10	US-09-864-761-5037	Sequence 5037, App	c 524	16	0.5	4313	9	US-09-978-295A-424	Sequence 424, App
452	16	0.5	2000	9	US-09-938-842A-2949	Sequence 2949, App	c 525	16	0.5	4313	9	US-09-978-697-424	Sequence 424, App
453	16	0.5	2000	9	US-09-938-842A-3916	Sequence 3916, App	c 526	16	0.5	4313	9	US-09-978-192A-424	Sequence 424, App
454	16	0.5	2000	9	US-09-938-842A-4550	Sequence 4550, App	c 527	16	0.5	4313	9	US-09-999-832A-424	Sequence 424, App
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457	16	0.5	2004	10	US-09-887-576-252	Sequence 252, App	c 530	16	0.5	4344	10	US-09-880-107-1754	Sequence 1754, App

c 531	16	0.5	4359	9	US-10-042-431-10	Sequence 10, Appl	604	16	0.5	43058	10	US-09-880-107-3950	Sequence 3350, Ap
c 532	16	0.5	4369	10	US-09-764-877-2824	Sequence 2824, Ap	605	16	0.5	51552	10	US-09-733-294A-30	Sequence 30, Appl
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c 536	16	0.5	4754	10	US-09-982-091A-1	Sequence 1, Appl1	c 609	16	0.5	75270	9	US-09-790-852-1	Sequence 1, Appl1
c 537	16	0.5	4758	9	US-09-842-777-9	Sequence 9, Appl1	c 610	16	0.5	75899	10	US-09-854-883-243	Sequence 243, App
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c 544	16	0.5	5591	10	US-09-764-846-309	Sequence 309, App	c 617	16	0.5	202061	10	US-09-734-674-3	Sequence 3, Appl1
c 545	16	0.5	5983	10	US-09-799-875-4	Sequence 4, Appl1	c 618	16	0.5	203654	10	US-09-820-905-3	Sequence 3, Appl1
c 546	16	0.5	6147	9	US-09-938-842A-2441	Sequence 2441, Ap	c 619	16	0.5	326014	10	US-09-731-231A-3	Sequence 3, Appl1
c 547	16	0.5	6319	10	US-09-995-454-581	Sequence 58, Appl1	c 620	16	0.5	397658	10	US-09-813-320-3	Sequence 3, Appl1
c 548	16	0.5	6381	10	US-09-969-347-216	Sequence 216, App	c 621	16	0.5	465237	10	US-09-933-287A-1	Sequence 1, Appl1
c 549	16	0.5	6457	10	US-09-880-107-3389	Sequence 3389, Ap	c 622	16	0.5	640681	10	US-09-790-988-1	Sequence 1, Appl1
c 550	16	0.5	6501	9	US-10-029-413A-3	Sequence 3, Appl1	c 623	16	0.5	659158	9	US-09-771-208-20	Sequence 20, Appl1
c 551	16	0.5	6915	10	US-09-983-531A-1	Sequence 1, Appl1	c 624	16	0.5	1503841	9	US-09-946-807-1	Sequence 1, Appl1
c 552	16	0.5	7193	9	US-10-029-413A-17	Sequence 17, Appl1	c 625	16	0.5	1503841	10	US-09-795-668-1	Sequence 1, Appl1
c 553	16	0.5	7193	9	US-10-029-413A-19	Sequence 19, Appl1	c 626	16	0.5	1503841	10	US-09-795-686-1	Sequence 1, Appl1
c 554	16	0.5	7237	10	US-09-070-927A-239	Sequence 239, App	c 627	15	0.5	20	9	US-09-946-807-103	Sequence 103, App
c 555	16	0.5	7362	9	US-10-029-413A-15	Sequence 15, Appl1	c 628	15	0.5	20	10	US-09-795-668-103	Sequence 103, App
c 556	16	0.5	7414	10	US-09-764-853-876	Sequence 876, App	c 629	15	0.5	20	10	US-09-795-686-103	Sequence 103, App
c 557	16	0.5	7509	10	US-09-772-316-4	Sequence 4, Appl1	c 630	15	0.5	22	9	US-09-978-295A-312	Sequence 312, App
c 558	16	0.5	7537	10	US-09-764-869-1735	Sequence 1735, Ap	c 631	15	0.5	22	9	US-09-978-697-312	Sequence 312, App
c 559	16	0.5	7736	10	US-09-764-846-333	Sequence 333, App	c 632	15	0.5	22	9	US-09-978-192A-312	Sequence 312, App
c 560	16	0.5	8001	10	US-09-070-927A-622	Sequence 622, App	c 633	15	0.5	22	9	US-09-999-832A-312	Sequence 312, App
c 561	16	0.5	8253	9	US-09-790-852-9	Sequence 9, Appl1	c 634	15	0.5	22	9	US-09-978-189-312	Sequence 312, App
c 562	16	0.5	8761	9	US-10-098-841-11	Sequence 11, Appl1	c 635	15	0.5	30	9	US-10-004-551-63	Sequence 63, Appl1
c 563	16	0.5	9664	10	US-09-764-869-2126	Sequence 2126, Ap	c 636	15	0.5	50	10	US-09-738-847-32	Sequence 32, Appl1
c 564	16	0.5	10758	12	US-10-044-090-61	Sequence 61, Appl1	c 637	15	0.5	57	10	US-09-756-250B-4	Sequence 4, Appl1
c 565	16	0.5	11071	10	US-09-764-877-2793	Sequence 2793, Ap	c 638	15	0.5	60	10	US-09-756-250B-8	Sequence 8, Appl1
c 566	16	0.5	11176	10	US-09-738-968-43	Sequence 43, Appl1	c 639	15	0.5	86	10	US-09-864-761-29742	Sequence 29742, A
c 567	16	0.5	11469	10	US-09-764-877-2791	Sequence 2791, Ap	c 640	15	0.5	89	10	US-09-878-574-6486	Sequence 6486, Ap
c 568	16	0.5	11764	10	US-09-070-927A-48	Sequence 48, Appl1	c 641	15	0.5	93	10	US-09-864-761-20218	Sequence 20218, A
c 569	16	0.5	12001	10	US-09-955-807-13	Sequence 13, Appl1	c 642	15	0.5	108	10	US-09-969-373-121	Sequence 121, App
c 570	16	0.5	12104	10	US-09-764-877-2761	Sequence 2761, Ap	c 643	15	0.5	113	10	US-09-864-761-23072	Sequence 23072, A
c 571	16	0.5	12327	10	US-09-764-869-2424	Sequence 2424, Ap	c 644	15	0.5	114	10	US-09-864-761-23381	Sequence 23381, A
c 572	16	0.5	14175	9	US-09-764-868-1474	Sequence 1474, Ap	c 645	15	0.5	116	10	US-09-878-574-7211	Sequence 7211, Ap
c 573	16	0.5	15418	10	US-09-783-203-1	Sequence 1, Appl1	c 646	15	0.5	118	9	US-09-796-692-7556	Sequence 7556, Ap
c 574	16	0.5	15418	10	US-09-994-427A-1	Sequence 1, Appl1	c 647	15	0.5	121	9	US-09-728-444-883	Sequence 883, App
c 575	16	0.5	15819	10	US-09-764-877-2765	Sequence 2765, Ap	c 648	15	0.5	121	10	US-09-815-242-2575	Sequence 2575, Ap
c 576	16	0.5	16150	10	US-09-764-869-2316	Sequence 2316, Ap	c 649	15	0.5	123	10	US-09-864-761-19617	Sequence 19617, A
c 577	16	0.5	16489	9	US-09-764-868-1483	Sequence 1483, Ap	c 650	15	0.5	129	10	US-09-864-761-25002	Sequence 25002, A
c 578	16	0.5	16511	10	US-09-764-869-2064	Sequence 2064, Ap	c 651	15	0.5	134	10	US-09-969-373-415	Sequence 415, App
c 579	16	0.5	16596	10	US-09-764-867-504	Sequence 504, App	c 652	15	0.5	136	10	US-09-864-761-28718	Sequence 28718, A
c 580	16	0.5	17946	10	US-09-764-869-2312	Sequence 2312, Ap	c 653	15	0.5	136	10	US-09-920-300A-511	Sequence 511, App
c 581	16	0.5	18501	10	US-09-764-847-1916	Sequence 1916, Ap	c 654	15	0.5	136	12	US-10-033-528-511	Sequence 511, App
c 582	16	0.5	20268	10	US-09-764-855-173	Sequence 173, App	c 655	15	0.5	140	10	US-09-864-761-17413	Sequence 17413, A
c 583	16	0.5	20860	10	US-09-070-927A-355	Sequence 355, App	c 656	15	0.5	141	10	US-09-783-550-12243	Sequence 12243, A
c 584	16	0.5	21636	10	US-09-416-384A-3	Sequence 3, Appl1	c 657	15	0.5	142	10	US-09-833-381-1409	Sequence 1409, Ap
c 585	16	0.5	22452	9	US-09-764-868-1487	Sequence 1487, Ap	c 658	15	0.5	142	10	US-09-960-352-13462	Sequence 13462, A
c 586	16	0.5	22452	9	US-09-764-868-1489	Sequence 1489, Ap	c 659	15	0.5	148	10	US-09-864-761-20604	Sequence 20604, A
c 587	16	0.5	22494	10	US-09-768-436-5	Sequence 5, Appl1	c 660	15	0.5	151	10	US-09-864-761-26359	Sequence 26359, A
c 588	16	0.5	26006	10	US-09-764-869-1963	Sequence 1963, Ap	c 661	15	0.5	151	10	US-09-960-352-123	Sequence 123, App
c 589	16	0.5	26006	10	US-09-764-864-1638	Sequence 1638, Ap	c 662	15	0.5	151	10	US-09-770-696-408	Sequence 408, App
c 590	16	0.5	26013	10	US-09-764-869-1961	Sequence 1961, Ap	c 663	15	0.5	160	10	US-09-864-761-31886	Sequence 31886, A
c 591	16	0.5	26013	10	US-09-764-864-1636	Sequence 1636, Ap	c 664	15	0.5	160	10	US-09-864-761-32962	Sequence 32962, A
c 592	16	0.5	26018	10	US-09-764-869-1962	Sequence 1962, Ap	c 665	15	0.5	163	9	US-09-796-692-7707	Sequence 7707, Ap
c 593	16	0.5	26018	10	US-09-764-864-1637	Sequence 1637, Ap	c 666	15	0.5	165	10	US-09-864-761-17210	Sequence 17210, A
c 594	16	0.5	27377	10	US-09-816-248-18	Sequence 18, Appl1	c 667	15	0.5	171	10	US-09-864-761-18068	Sequence 18068, A
c 595	16	0.5	31132	10	US-09-764-864-1690	Sequence 1690, Ap	c 668	15	0.5	173	9	US-09-232-880-147	Sequence 147, App
c 596	16	0.5	31132	10	US-09-764-877-3062	Sequence 3062, Ap	c 669	15	0.5	173	9	US-10-012-896-147	Sequence 147, App
c 597	16	0.5	31885	10	US-09-764-860-775	Sequence 775, App	c 670	15	0.5	173	9	US-09-895-793-147	Sequence 147, App
c 598	16	0.5	31885	10	US-09-764-877-2530	Sequence 2530, Ap	c 671	15	0.5	173	9	US-09-895-814-147	Sequence 147, App
c 599	16	0.5	31885	10	US-09-764-877-2541	Sequence 2541, Ap	c 672	15	0.5	173	10	US-09-759-143-147	Sequence 147, App
c 600	16	0.5	32132	10	US-09-764-877-2308	Sequence 2308, Ap	c 673	15	0.5	173	10	US-09-864-761-31312	Sequence 31312, A
c 601	16	0.5	41907	10	US-09-967-013-5	Sequence 5, Appl1	c 674	15	0.5	173	10	US-09-780-669-147	Sequence 147, App
c 602	16	0.5	43058	10	US-09-934-456-292	Sequence 292, App	c 675	15	0.5	173	10	US-09-030-606-147	Sequence 147, App
c 603	16	0.5	43058	10	US-09-954-456-529	Sequence 529, App	c 676	15	0.5	173	10	US-09-822-827-147	Sequence 147, App

c 677	15	0.5	173	10	US-09-115-453-147	Sequence 147, App	c 750	15	0.5	263	10	US-09-783-590-8506	Sequence 8506, Ap
c 678	15	0.5	179	10	US-09-864-761-18380	Sequence 18380, A	c 751	15	0.5	263	10	US-09-960-352-5188	Sequence 5188, Ap
c 679	15	0.5	181	10	US-09-770-696-280	Sequence 280, App	c 752	15	0.5	264	9	US-09-232-880-211	Sequence 211, App
c 680	15	0.5	184	10	US-09-864-761-22332	Sequence 22332, A	c 753	15	0.5	264	9	US-10-012-896-211	Sequence 211, App
c 681	15	0.5	185	10	US-09-815-242-2036	Sequence 2036, Ap	c 754	15	0.5	264	9	US-09-895-793-211	Sequence 211, App
c 682	15	0.5	186	10	US-09-864-761-17986	Sequence 17986, A	c 755	15	0.5	264	9	US-09-895-814-211	Sequence 211, App
c 683	15	0.5	186	10	US-09-864-761-19162	Sequence 19162, A	c 756	15	0.5	264	10	US-09-294-093B-4047	Sequence 4047, Ap
c 684	15	0.5	187	9	US-09-796-692-2912	Sequence 2912, Ap	c 757	15	0.5	264	10	US-09-759-143-211	Sequence 211, App
c 685	15	0.5	187	10	US-09-960-352-5772	Sequence 5772, Ap	c 758	15	0.5	264	10	US-09-780-669-211	Sequence 211, App
c 686	15	0.5	191	10	US-09-878-574-8273	Sequence 8273, Ap	c 759	15	0.5	264	10	US-09-030-606-211	Sequence 211, App
c 687	15	0.5	191	10	US-09-783-590-7728	Sequence 7728, Ap	c 760	15	0.5	264	10	US-09-822-827-211	Sequence 211, App
c 688	15	0.5	192	9	US-09-736-457-243	Sequence 243, App	c 761	15	0.5	264	10	US-09-115-453-211	Sequence 211, App
c 689	15	0.5	192	9	US-09-902-941-243	Sequence 243, App	c 762	15	0.5	264	10	US-09-115-453-211	Sequence 211, App
c 690	15	0.5	192	9	US-09-849-626-243	Sequence 243, App	c 763	15	0.5	265	10	US-09-878-574-15020	Sequence 15020, A
c 691	15	0.5	193	10	US-09-998-598-2473	Sequence 2473, Ap	c 764	15	0.5	265	10	US-09-864-761-30086	Sequence 30086, A
c 692	15	0.5	194	9	US-09-736-457-1241	Sequence 1241, Ap	c 765	15	0.5	265	10	US-09-878-574-6402	Sequence 6402, Ap
c 693	15	0.5	194	9	US-09-902-941-1241	Sequence 1241, Ap	c 766	15	0.5	265	10	US-09-878-574-9323	Sequence 9323, Ap
c 694	15	0.5	194	9	US-09-849-626-1241	Sequence 1241, Ap	c 767	15	0.5	266	9	US-09-796-692-8945	Sequence 8945, Ap
c 695	15	0.5	196	10	US-09-864-761-20007	Sequence 20007, A	c 768	15	0.5	266	10	US-09-878-574-12431	Sequence 12431, A
c 696	15	0.5	197	10	US-09-864-761-32734	Sequence 32734, A	c 769	15	0.5	267	10	US-09-867-701-8481	Sequence 8481, Ap
c 697	15	0.5	197	10	US-09-960-352-10024	Sequence 10024, A	c 770	15	0.5	267	10	US-09-563-817-582	Sequence 582, App
c 698	15	0.5	199	10	US-09-783-590-8362	Sequence 8362, Ap	c 771	15	0.5	267	10	US-09-983-965-1984	Sequence 1984, Ap
c 699	15	0.5	200	10	US-09-770-696-167	Sequence 167, App	c 772	15	0.5	268	9	US-09-796-692-3102	Sequence 3102, Ap
c 700	15	0.5	200	10	US-09-903-377-3	Sequence 3, App11	c 773	15	0.5	270	9	US-09-796-692-8985	Sequence 8985, Ap
c 701	15	0.5	205	10	US-09-864-761-21903	Sequence 21903, A	c 774	15	0.5	271	9	US-09-796-692-9532	Sequence 9532, Ap
c 702	15	0.5	205	10	US-09-960-352-192	Sequence 192, App	c 775	15	0.5	271	10	US-09-923-876-164	Sequence 164, App
c 703	15	0.5	207	10	US-09-864-761-17446	Sequence 17446, A	c 776	15	0.5	271	10	US-09-867-701-7578	Sequence 7578, Ap
c 704	15	0.5	208	10	US-09-770-696-106	Sequence 106, App	c 777	15	0.5	272	9	US-10-046-935-1523	Sequence 1523, Ap
c 705	15	0.5	212	10	US-09-798-598-2047	Sequence 2047, App	c 778	15	0.5	272	9	US-09-878-178-1523	Sequence 1523, Ap
c 706	15	0.5	215	10	US-09-770-696-69	Sequence 69, App1	c 779	15	0.5	272	10	US-09-815-242-3335	Sequence 3335, Ap
c 707	15	0.5	215	10	US-09-815-242-3593	Sequence 3593, Ap	c 780	15	0.5	272	10	US-09-878-574-6734	Sequence 6734, Ap
c 708	15	0.5	215	10	US-09-815-242-3601	Sequence 3601, Ap	c 781	15	0.5	272	10	US-09-878-574-15648	Sequence 15648, A
c 709	15	0.5	215	10	US-09-833-381-459	Sequence 459, App	c 782	15	0.5	273	10	US-09-878-574-12834	Sequence 12834, A
c 710	15	0.5	216	10	US-09-864-761-23766	Sequence 23766, A	c 783	15	0.5	274	10	US-09-878-574-11827	Sequence 11827, A
c 711	15	0.5	218	10	US-09-864-761-23412	Sequence 23412, A	c 784	15	0.5	276	10	US-09-923-876-4134	Sequence 4134, Ap
c 712	15	0.5	221	9	US-09-736-968A-94	Sequence 94, App1	c 785	15	0.5	276	10	US-09-815-242-4859	Sequence 4859, Ap
c 713	15	0.5	221	9	US-09-796-692-7336	Sequence 7336, Ap	c 786	15	0.5	276	10	US-09-815-242-8566	Sequence 8566, Ap
c 714	15	0.5	224	10	US-09-783-590-3206	Sequence 3206, Ap	c 787	15	0.5	276	10	US-09-815-242-8866	Sequence 8866, Ap
c 715	15	0.5	224	10	US-09-983-965-4934	Sequence 4934, Ap	c 788	15	0.5	276	10	US-09-815-242-9062	Sequence 9062, Ap
c 716	15	0.5	227	9	US-09-924-400-183	Sequence 183, App	c 789	15	0.5	277	10	US-09-878-574-11254	Sequence 11254, A
c 717	15	0.5	227	10	US-09-810-936-183	Sequence 183, App	c 790	15	0.5	278	9	US-09-796-692-3869	Sequence 3869, Ap
c 718	15	0.5	227	10	US-09-429-755-183	Sequence 183, App	c 791	15	0.5	279	10	US-09-864-761-19127	Sequence 19127, A
c 719	15	0.5	228	10	US-09-833-381-301	Sequence 301, App	c 792	15	0.5	280	10	US-09-004-068-5	Sequence 5, Appl1
c 720	15	0.5	229	10	US-09-294-093B-759	Sequence 759, App	c 793	15	0.5	280	10	US-09-004-068-8	Sequence 8, Appl1
c 721	15	0.5	229	10	US-09-864-761-27663	Sequence 27663, A	c 794	15	0.5	281	10	US-09-294-093B-880	Sequence 880, App
c 722	15	0.5	230	9	US-09-796-692-9407	Sequence 9407, Ap	c 795	15	0.5	282	9	US-09-954-531-392	Sequence 392, App
c 723	15	0.5	230	10	US-09-783-590-3884	Sequence 3884, Ap	c 796	15	0.5	282	9	US-09-796-692-4907	Sequence 4907, App
c 724	15	0.5	230	10	US-09-960-352-3875	Sequence 3875, Ap	c 797	15	0.5	282	10	US-09-004-068-11	Sequence 11, Appl1
c 725	15	0.5	234	10	US-09-923-876-3260	Sequence 3260, Ap	c 798	15	0.5	282	10	US-09-969-708-21	Sequence 21, Appl1
c 726	15	0.5	240	10	US-09-878-574-10335	Sequence 10335, A	c 799	15	0.5	283	10	US-09-294-093B-557	Sequence 557, App
c 727	15	0.5	241	10	US-09-878-574-5190	Sequence 5190, App	c 800	15	0.5	284	9	US-09-954-531-83	Sequence 83, Appl1
c 728	15	0.5	241	10	US-09-867-701-4336	Sequence 4336, Ap	c 801	15	0.5	284	10	US-09-923-876-5170	Sequence 5170, Ap
c 729	15	0.5	242	10	US-09-923-876-1173	Sequence 1173, Ap	c 802	15	0.5	284	10	US-09-864-761-20944	Sequence 20944, A
c 730	15	0.5	244	10	US-09-923-876-3255	Sequence 3255, Ap	c 803	15	0.5	286	10	US-09-834-975-682	Sequence 682, App
c 731	15	0.5	244	10	US-09-894-882-279	Sequence 279, App	c 804	15	0.5	290	9	US-10-079-623-94	Sequence 94, Appl1
c 732	15	0.5	244	10	US-09-894-882-276	Sequence 276, App	c 805	15	0.5	292	10	US-09-878-574-8225	Sequence 8225, Ap
c 733	15	0.5	244	10	US-09-894-882-282	Sequence 282, App	c 806	15	0.5	293	10	US-09-563-817-897	Sequence 897, App
c 734	15	0.5	244	10	US-09-878-574-6193	Sequence 6193, Ap	c 807	15	0.5	296	10	US-09-867-701-6616	Sequence 6616, Ap
c 735	15	0.5	245	10	US-09-878-574-8820	Sequence 8820, Ap	c 808	15	0.5	297	9	US-09-796-692-3405	Sequence 3405, Ap
c 736	15	0.5	249	10	US-09-878-574-10269	Sequence 10269, A	c 809	15	0.5	299	10	US-09-969-347-75	Sequence 75, Appl1
c 737	15	0.5	252	9	US-09-796-692-7617	Sequence 7617, Ap	c 810	15	0.5	299	10	US-09-880-107-3086	Sequence 3086, Ap
c 738	15	0.5	252	10	US-09-878-574-10645	Sequence 10645, A	c 811	15	0.5	300	10	US-09-294-093B-3190	Sequence 3190, Ap
c 739	15	0.5	252	10	US-09-834-975-205	Sequence 205, App	c 812	15	0.5	306	9	US-10-015-219-1221	Sequence 1221, Ap
c 740	15	0.5	253	9	US-09-796-692-3423	Sequence 3423, Ap	c 813	15	0.5	306	10	US-09-777-564-1221	Sequence 1221, Ap
c 741	15	0.5	253	10	US-09-728-445-673	Sequence 673, App	c 814	15	0.5	306	10	US-09-864-761-22841	Sequence 22841, A
c 742	15	0.5	256	10	US-09-923-876-1966	Sequence 1966, App	c 815	15	0.5	309	9	US-09-796-692-7881	Sequence 7881, Ap
c 743	15	0.5	256	10	US-09-878-574-5849	Sequence 5849, Ap	c 816	15	0.5	309	10	US-09-960-352-4106	Sequence 4106, Ap
c 744	15	0.5	258	10	US-09-878-574-5599	Sequence 5599, Ap	c 817	15	0.5	310	10	US-09-884-441-81	Sequence 81, Appl1
c 745	15	0.5	258	10	US-09-878-574-9277	Sequence 9277, Ap	c 818	15	0.5	310	10	US-09-884-441-308	Sequence 308, App
c 746	15	0.5	259	10	US-09-783-590-1358	Sequence 1358, Ap	c 819	15	0.5	310	10	US-09-983-965-5359	Sequence 5359, Ap
c 747	15	0.5	260	10	US-09-878-574-7966	Sequence 7966, Ap	c 820	15	0.5	310	10	US-09-880-107-746	Sequence 746, App
c 748	15	0.5	261	10	US-09-878-574-11953	Sequence 11953, A	c 821	15	0.5	311	10	US-09-783-590-2167	Sequence 2167, Ap
c 749	15	0.5	263	10	US-09-878-574-9334	Sequence 9334, Ap	c 822	15	0.5	312	10	US-09-880-107-662	Sequence 662, App


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c 969      15      0.5      425      10      US-09-864-761-19815
c 970      15      0.5      425      10      US-09-960-352-15002
c 971      15      0.5      426      9      US-09-954-531-700
c 972      15      0.5      426      9      US-09-954-531-1119
c 973      15      0.5      426      10      US-09-878-574-3516
c 974      15      0.5      428      10      US-09-867-761-4183
c 975      15      0.5      428      10      US-09-867-761-5901
c 976      15      0.5      428      10      US-09-764-847-1230
c 977      15      0.5      428      10      US-09-764-847-1231
c 978      15      0.5      429      10      US-09-764-847-1232
c 979      15      0.5      430      10      US-09-960-352-9343
c 980      15      0.5      431      10      US-09-815-343-1483
c 981      15      0.5      433      10      US-09-864-761-5081
c 982      15      0.5      433      10      US-09-867-761-2701
c 983      15      0.5      435      10      US-09-764-869-2106
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c 985      15      0.5      437      10      US-09-770-444-5998
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c 996      15      0.5      442      10      US-09-867-761-7674
c 997      15      0.5      443      10      US-09-912-020-431
c 998      15      0.5      444      10      US-09-764-860-1044
c 999      15      0.5      446      10      US-09-770-444-772
c 1000     15      0.5      447      10      US-09-864-761-1636
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ALIGNMENTS

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RESULT 1
US-09-841-739-3
; Sequence 3, Application US/09841739
; Patent No. US200200347841
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-3
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Best Local Similarity 100.08; Pred. No. 0;
Matches 3072; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGAATTTTCATAAAGGACAAATAGCGAGCCCTTATTCAAAGAAATGGGAATGACTCTTATA 60

QY 61 AAGCAATACACAGATGACCTATTCTGATGGAATGTTCTGAATCGCGAAGAAAGTAACATC 120
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Db 61 AAGCAATACACAGATGACCTATTCTGATGGAATGTTCTGAATCGCGAAGAAAGTAACATC 120

QY 121 ATTTGCTGGAGAGGTGGAGCAGATGCTGCTAGAGGATCATTCACATGATTTTGA 180
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Db 181 AAGGTTTCAGAGTCTCTGTAACCTCTTTCTTAATCCCTTTAAGAGTGGAACTATCCTCTA 240
QY 241 TTTTCAGGACTTCAATGGACAAAAGTCTTTTTCATCAGACATCAGAGGACATTTGGACGAT 300
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Db 241 TTTTCAGGACTTCAATGGACAAAAGTCTTTTTCATCAGACATCAGAGGACATTTGGACGAT 300
QY 301 TTGGCTCAGGATTTAAAGGACTTTGTACCATACCCCTCTTTTCTGAACCTTTTATCCCTTT 360
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Db 301 TTGGCTCAGGATTTAAAGGACTTTGTACCATACCCCTCTTTTCTGAACCTTTTATCCCTTT 360
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Db 361 GGTGAAGATATTGACATATTATTTTAACTTGAAGACACCTTCACAGAACCTGCTCTGTGG 420
QY 421 AGGAAGGACCAACACCATCACCCTGTTGGAGCAGCTGACCTGAATGGCTCTCTGCAGGCT 480
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Db 421 AGGAAGGACCAACACCATCACCCTGTTGGAGCAGCTGACCTGAATGGCTCTCTGCAGGCT 480
QY 481 CTTTCAGAGCCCTGTCATCATTTGAAGGGGAATCTGGCAAAGCAAGTCCACTCTGCTGCAG 540
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Db 481 CTTTCAGAGCCCTGTCATCATTTGAAGGGGAATCTGGCAAAGCAAGTCCACTCTGCTGCAG 540
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Db 601 TTTCTTCTCCGCTCAGCAGAGGCCCCAGGGTGGACCTTTTGAACCTCTGTCATCAACATC 660
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Db 661 CTGGATATACCTTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGTGGCG 720
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Db 721 CAGAGGGTCTTTTCTTCTTCTGATGGCTACAATGAATTCAGCCCAAGCAACTGCCAGAA 780
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Db 781 ATCGAAGCCCTCATAAAGAAAACACCGCTTCAAGAACATGCTCATCTGCTACCCTACC 840
QY 841 ACTGAGTGCCTGAGGCACATACGGCAGTTTGTGTCCTGACTGCTGAGGTGGGGATATG 900
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Db 841 ACTGAGTGCCTGAGGCACATACGGCAGTTTGTGTCCTGACTGCTGAGGTGGGGATATG 900
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Db 901 ACAGAAGACAGCGCCCGAGCTCTCATCCGAGAAGTGCCTGATCAAGAGCTTCTGCTGAGGC 960
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Qy	1361	CTGCTGACAACTGGGCTCCTCTGTAAATATACAGCTCAAAGGTTCAAAGCCAAAGTATATAA	1320
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Qy	1321	TTCTTTTACAAAGTCATTCCAGGAGTACACAGCAGACGACAAACACTCAGCAGTTATTTCAGC	1380
Db	1321	TTCTTTTACAAAGTCATTCCAGGAGTACACAGCAGACGACAAACACTCAGCAGTTATTTCAGC	1380
Qy	1381	TCTCATGAGCCAGAGGAGTGACCAAGGGAAATGGTTACTTTGCAGAAAAATGGTTTCCATT	1440
Db	1381	TCTCATGAGCCAGAGGAGTGACCAAGGGAAATGGTTACTTTGCAGAAAAATGGTTTCCATT	1440
Qy	1441	TCGGACATTACATCCACTTTATAGCAGCCTGCTCCGGTACACCTGTGGGTCACTGTGTGGAA	1500
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Qy	1501	GCCACCAAGGCTCTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGA	1560
Db	1501	GCCACCAAGGCTCTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGA	1560
Qy	1561	CTTTTCCATCGCCAAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACC	1620
Db	1561	CTTTTCCATCGCCAAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACC	1620
Qy	1621	ACTGAGCAAGAAATTCGAAAGCCATAACATCAATTCCTTTGTAGAGTGTGGCATCCAT	1680
Db	1621	ACTGAGCAAGAAATTCGAAAGCCATAACATCAATTCCTTTGTAGAGTGTGGCATCCAT	1680
Qy	1681	TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTCTTTTCAA	1740
Db	1681	TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTCTTTTCAA	1740
Qy	1741	GGTAAAGCTTTATATCAACTCAGGGAACATCCCCGATTACTTATTGTACTTCTTTTCAA	1800
Db	1741	GGTAAAGCTTTATATCAACTCAGGGAACATCCCCGATTACTTATTGTACTTCTTTTCAA	1800
Qy	1801	CATTTCGCCAAATTCGCAAGTCTCTCGACATTCATTAAACTTGGACTTTTATGGGGAGCT	1860
Db	1801	CATTTCGCCAAATTCGCAAGTCTCTCGACATTCATTAAACTTGGACTTTTATGGGGAGCT	1860
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Qy	1921	GAACCTTACATTCAGCCTCGCCACAGCCTCAGCCTGCAATTAAGAGATGTGCTGTGTG	1980
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Qy	1981	ACTCTGGAGTGCACCTCCGGATTTTCAGCAGTTGTAATAGCAAGATATACACATATCTG	2040
Db	1981	ACTCTGGAGTGCACCTCCGGATTTTCAGCAGTTGTAATAGCAAGATATACACATATCTG	2040
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Qy	2101	GCTGGAAAGCCTCAGTTTGGTCTCAGACCTGTAAAGACATTTATCTCTCATGGTGGAA	2160
Db	2101	GCTGGAAAGCCTCAGTTTGGTCTCAGACCTGTAAAGACATTTATCTCTCATGGTGGAA	2160
Qy	2161	GCCAGTCCCTCACCATAAGATGAGGACATCACATCTGTAACAAACCTGAAAACC	2220
Db	2161	GCCAGTCCCTCACCATAAGATGAGGACATCACATCTGTAACAAACCTGAAAACC	2220
Qy	2221	TTGAGTATTATGACCTACAGAAATCAACGGCTTCCCGGTTGCTGTACTGACAGCTTGGGT	2280
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Qy	2281	AACTTGAAAGAACCTTCAAAAGCTCATATGGATATACATAAAGATGAATGAAGAAGATGCT	2340
Db	2281	AACTTGAAAGAACCTTCAAAAGCTCATATGGATATACATAAAGATGAATGAAGAAGATGCT	2340

RESULT 2

US-09-841-739-1

US-09-841-739-1
: Sequence 1, Application US/09841739

; Patent No. US20020034784A1

; FACILE NO. 032002003
; GENERAL INFORMATION:

APPLICANT: Bertin, John

; TITLE OF INVENTION: NOVEL MO

FILE REFERENCE: 07334-329001

; CURRENT APPLICATION NUMBER: US/09/841,739

; CURRENT FILING DATE: 2001-08-29

; PRIORITY APPLICATION NUMBER: US 09/697,089

;
PRIOR FILING DATE: 2000-10-2

; PRIOR APPLICATION NUMBER: US 60/161,822

;
PRIOR FILING DATE: 1999-10-27

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 3133

TYPE: DNA

; ORGANISM: Homo sapiens

FEATURE:									
NAME/KEY: CDS									
LOCATION: (36)...(3107)									
us-09-841-739-1									
Query Match 100.0%; Score 3072; DB 10; Length 3133;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 3072; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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QY	61	AAGCAATACACATGACCTATTGTTGATGAATGTTCTGAATCGCGAAGAAGTAACATC	120						
Db	96	AAGCAATACACATGACCTATTGTTGATGAATGTTCTGAATCGCGAAGAAGTAACATC	155						
QY	121	ATTGCTGCGAGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAA	180						
Db	156	ATTGCTGCGAGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAA	215						
QY	181	AAGGTTACAGAGTCCTGTAACTCTTTCTTAAATCCCTTAAGAGTGGAACTATCCTCTA	240						
Db	216	AAGGTTACAGAGTCCTGTAACTCTTTCTTAAATCCCTTAAGAGTGGAACTATCCTCTA	275						
QY	241	TTTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAGGAGCTTGGAGAT	300						
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QY	301	TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTT	360						
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QY	361	GGTGAAGATATTGACATATTATTTAACTTGAAGCAACCTTCACAGAACCTGTCTGTGG	420						
Db	396	GGTGAAGATATTGACATATTATTTAACTTGAAGCAACCTTCACAGAACCTGTCTGTGG	455						
QY	421	AGGAAGACCAACACCATCACCGGTGGAGCAGCTACCCCTGATGGCCCTCTGAGGCT	480						
Db	456	AGGAAGACCAACACCATCACCGGTGGAGCAGCTACCCCTGATGGCCCTCTGAGGCT	515						
QY	481	CTTCAGAGCCCTGTCATATTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGTGCGAG	540						
Db	516	CTTCAGAGCCCTGTCATATTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGTGCGAG	575						
QY	541	CGCATTTGCCATGCTCTGGGGCTCCGGAAGTGCAGGCTCTGACCAAGTTCAAAATTCGTC	600						
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QY	601	TTCTTCCCTCCGCTCAGCAGGGCCAGGGTGGACTTTTGTGAACCCCTCTGTATCAACTC	660						
Db	636	TTCTTCCCTCCGCTCAGCAGGGCCAGGGTGGACTTTTGTGAACCCCTCTGTATCAACTC	695						
QY	661	CTGGATATACCTGGCACAATCAGGAAGCAGACATTATGCGCCATGCTGTGAAGCTGGGG	720						
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QY	721	CAGAGGGTCTTTTCTCTTCTGATGGCTACAAATGAATTCAGCCCGCAAGCTGCCAGAA	780						
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QY	781	ATCGAAGCCCTGATAAAGAAACCAACCGCTTCAAGAACATGGTCTATCGTCAACTACC	840						
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QY	901	ACAGAAGACAGCCCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGAGCTTGTCTGAAGGC	960						
Db	936	ACAGAAGACAGCCCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGAGCTTGTCTGAAGGC	995						
QY	961	TTGTTGCTCCAAATTCAGAAATCCAGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT	1020						
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QY	1021	GTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCACATCTCTCACACAAACA	1080						
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QY	1081	ACGCTGTTCATACCTCTTATGATCTGTGATACAGAAAACAAACAAACATAAAGGT	1140						
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QY	1201	GTGTTCTCCCAACAAGTTTGATTTGCAACTGTCAGAGTGTGCCAGCGTGAATGAGGATGTC	1260						
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QY	1261	CTGCTGACAACTGGGCTCCTCTGTAATAATACAGCTCAAAGGTTCAGGCCAAAAGTATAA	1320						
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QY	1381	TCATGATGCCAGAGGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAATGGTTTCCAT	1440						
Db	1416	TCATGATGCCAGAGGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAATGGTTTCCAT	1475						
QY	1441	TCGGACATTACATPCCACTTATAGCAGCTGCTCCCGGTACACCTGTGGGTGCTCTGTGGAA	1500						
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QY	1681	TTATATCAAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAA	1740						
Db	1716	TTATATCAAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAA	1775						
QY	1741	GGTAAAGCTTATATCAACTCAGGGAACATCCCGGATTTACTTTTACACTTCTTTGAA	1800						
Db	1776	GGTAAAGCTTATATCAACTCAGGGAACATCCCGGATTTACTTTTACACTTCTTTGAA	1835						
QY	1801	CATTTGCCCAATTTGTGCAAGTCTCTGGACTTCAATTAACCTGGAGCTTTTATGGGGAGCT	1860						
Db	1836	CATTTGCCCAATTTGTGCAAGTCTCTGGACTTCAATTAACCTGGAGCTTTTATGGGGAGCT	1895						
QY	1861	ATGGCTTTCATGGGAAAGGCTGCGAAGACAGAGTGGAAATCCCATGGAAGAGGCCCA	1920						
Db	1896	ATGGCTTTCATGGGAAAGGCTGCGAAGACAGAGTGGAAATCCCATGGAAGAGGCCCA	1955						
QY	1921	GAACTCATTCTCCAGCAGGCTGTATCTTGTGTTCTTCACTGGAAGCAGGAATTCAGG	1980						
Db	1956	GAACTCATTCTCCAGCAGGCTGTATCTTGTGTTCTTCACTGGAAGCAGGAATTCAGG	2015						
QY	1981	ACTCTGGAGGTCACACTCCGGGATTTACAGCAAGTTGAATAAGCAAGATATCACATCTG	2040						
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QY 2161 GCAGTCCCTCCACATAGAGATGAGAGGCACATCACAATCTGTAAACAACCTGAAACCC 2220
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QY 3061 CTAGTAACCTGCT 3072
Db 3096 CTAGTAACCTGCT 3107
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RESULT 3

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US-09-864-921-96
; Sequence 96, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Plo, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; CURRENT APPLICATION NUMBER: US/09/864,921
; PRIORITY FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(3348)
US-09-864-921-96

Query Match 93.4%; Score 2868; DB 9; Length 3396;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3068; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 61 AAGCAAAATCACAGATGACCTATTGTTGTAATGTAATGTTCTGAATCGCGAAGAAGTAAACATC 120
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QY 121 ATTTGCTGCGAGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 180
Db 397 ATTTGCTGCGAGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 456
QY 181 AAGGGTTCAGAGTCTCTGTAACCTCTTTCTTAATCCCTTAAAGAGTGGAACTATCCTCTA 240
Db 457 AAGGGTTCAGAGTCTCTGTAACCTCTTTCTTAATCCCTTAAAGAGTGGAACTATCCTCTA 516
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QY 301 TTGGCTCAGGATTTAAAGGACTTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTTT 360
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QY 421 AGGAAGGACCAACACCATCACCGGTGGAGCAGCTGACCCCTGAATGGCCCTCTCGAGGCT 480
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Db 877 TTTCTTCCCTGCTCTCAGCAGGGCCAGGGTGCATTTTGAAGCCCTCTCTGTCATCAACT 936
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Db 2354 CAGAAGACACAGTGGAAATCCATGGAAGAGGCCCCAGAAACCTACATTTCCAGAGG 2413
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Db 3134 GGGCTGTGAGCTGCAAGGAGGCTGAGCAGCTGTTGAAACATTTGGAGAGGTTCCAC 3193
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Db 3194 AACTCTCAAGCTTGGTTTGAAGAACTGGAGACTCACAGATACAGAGATTAGAAATTTTAG 3253
QY 2783 GTGCATTTTGTGAAAGAACCCCTCTGAAAGAACTTCCAGCAGTTGAAATTTGGGGGAAATC 2842
Db 3254 GTGCATTTTGTGAAAGAACCCCTCTGAAAGAACTTCCAGCAGTTGAAATTTGGGGGAAATC 3313
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QY 2903 TGTGTTTTCACCTTAGTACTAAGAACTTCTACCTGATCCAGCATTTAGTCAGAAACTTA 2962
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QY 2963 GCCAAGCTGTATCCAAAGTTAACTTTCTCCAGAAAGCTAGGCTTGTGGTGGCAATTG 3022
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QY 3023 ATGATGATGATCTCAGTGTATTACAG 3049
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RESULT 6

US-09-841-739-12/c
; Sequence 12, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-12

Query Match 85.7%; Score 2634; DB 10; Length 3615;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 2102 AGAT 3GGTGAAGTGTGCTCACTCTCACACAAACACGCTGTTCATACCTTCTCTATG 2043
QY 1103 ATCT 3TTGATACAGAAACAAACAAACAACTAAAGTGTGGCTCAAGTGAATTCATTC 1162
Db 2042 ATCT 3TTGATACAGAAACAAACAAACAACTAAAGTGTGGCTCAAGTGAATTCATTC 1983
QY 1163 GGAG 3TGGACCACTGTGGAGACCTAGCTGTGGAGGTGTGTCTCCACAGTTGAT 1222
Db 1982 GGAG 3TGGACCACTGTGGAGACCTAGCTGTGGAGGTGTGTCTCCACAGTTGAT 1923
QY 1223 TCGAA 3TGCAGGATGTCTCCAGCGTGAATGAGGATGTCTGCTGACACTGGGCTCTCT 1282
Db 1922 TCGAA 3TGCAGGATGTCTCCAGCGTGAATGAGGATGTCTGCTGACACTGGGCTCTCT 1863
QY 1283 GTAA 3ATACAGCTCAAGGTTCAAGCCAAAGTATAAATCTTTTCAAGTCAATTCACAG 1342
Db 1862 GTAA 3ATACAGCTCAAGGTTCAAGCCAAAGTATAAATCTTTTCAAGTCAATTCACAG 1803
QY 1343 AGTA 3CAGAGGAGCAAGACTCAGCACTTATTGACCTCTCATGAGCCAGAGGAGTGA 1402
Db 1802 AGTA 3CAGAGGAGCAAGACTCAGCACTTATTGACCTCTCATGAGCCAGAGGAGTGA 1743
QY 1403 CCAAG 3GGAATGGTTACTTGCAGAAATGGTTTCCATTTCCGACATTTACATCCACTTATA 1462
Db 1742 CCAAG 3GGAATGGTTACTTGCAGAAATGGTTTCCATTTCCGACATTTACATCCACTTATA 1683
QY 1463 GCAG 3TGCCTCGGTACACCTGTGGGTCTATCTGTGAAAGCCACAGGCTGTATGAAAG 1522
Db 1682 GCAG 3TGCCTCGGTACACCTGTGGGTCTATCTGTGAAAGCCACAGGCTGTATGAAAG 1623
QY 1523 ACCT 3CAGCAGTGTATCAACACGCTGCTTCTCGGACTTTTCCATCCCAAGAGGCTC 1582
Db 1622 ACCT 3CAGCAGTGTATCAACACGCTGCTTCTCGGACTTTTCCATCCCAAGAGGCTC 1563
QY 1583 TCTG 3GACAGGAATCTTTGCAAGTGTGAAACACCACTGAGCAAGAAATTCGAAAG 1642
Db 1562 TCTG 3GACAGGAATCTTTGCAAGTGTGAAACACCACTGAGCAAGAAATTCGAAAG 1503
QY 1643 CATA 3ACATCAATCTTTGTAGAGTGTGGCATCCATTTTATATCAAGAGAGTACATCCA 1702
Db 1502 CATA 3ACATCAATCTTTGTAGAGTGTGGCATCCATTTTATATCAAGAGAGTACATCCA 1443

QY 1703 AATCAGCCTGAGCCGAAGAAATTTGAAGCTTTCTTTCAAGSTAAAAGCTTATATATCAACT 1762
Db 1442 AATCAGCCTGAGCCGAAGAAATTTGAAGCTTTCTTTCAAGSTAAAAGCTTATATATCAACT 1383
QY 1763 CAGGGAACATCCCGAATTAATTTGACTTCTTTGAACATTTGCCAATTTGTGCAAGTG 1822
Db 1382 CAGGGAACATCCCGAATTAATTTGACTTCTTTGAACATTTGCCAATTTGTGCAAGTG 1323
QY 1823 CTCTGACATTCATTAACCTGGAGCTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1882
Db 1322 CCTGGACTTCATTAACCTGGAGCTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1263
QY 1883 CAGAAGACAGGTGGAATCCACATCGAAGAGGCCCCAGAAACCTACATTCACAGAGGG 1942
Db 1262 CAGAAGACAGGTGGAATCCACATCGAAGAGGCCCCAGAAACCTACATTCACAGAGGG 1203
QY 1943 CTGTATCTTTGTTCTTCAACTGGAACGAGAAATTCAGGACTCTGGAGGTCACACTCCGG 2002
Db 1202 CTGTATCTTTGTTCTTCAACTGGAACGAGAAATTCAGGACTCTGGAGGTCACACTCCGG 1143
QY 2003 ATTTACAGAGTTGAATAAGCAAGATATCACATATCTGGGAAAATATTTCAGCTCTGCCA 2062
Db 1142 ATTTACAGAGTTGAATAGCAAGATATCAGATATCTGGGAAAATATTTCAGCTCTGCCA 1083
QY 2063 CAAGCCTCAGGCTGCAAAATAAGAGATGTCTGGTGTGGCTGGAAGCCCTCAGTTTGGTCC 2122
Db 1082 CAAGCCTCAGGCTGCAAAATAAGAGATGTCTGGTGTGGCTGGAAGCCCTCAGTTTGGTCC 1023
QY 2123 TCAGCACCCTGTAGACATTTATTTCTCATGTGTGAAGCCAGTCCCTCACCATAGAG 2182
Db 1022 TCAGCACCCTGTAGACATTTATTTCTCTCATGTGTGAAGCCAGTCCCTCACCATAGAG 963
QY 2183 ATCAGAGGCACATCACATCTGTAAACAACTTGAAACCTTGAGTATTCATGACCTACAGA 2242
Db 962 ATCAGAGGCACATCACATCTGTAAACAACTTGAAACCTTGAGTATTCATGACCTACAGA 903
QY 2243 ATCAAGGCTCGCGGTGGTCTGACTGACAGCTTGGGTAACTTGAAGAACCCTTACAAAGC 2302
Db 902 ATCAAGGCTCGCGGTGGTCTGACTGACAGCTTGGGTAACTTGAAGAACCCTTACAAAGC 843
QY 2303 TCATAATGATACATATAAGATGAATGAAGAAGATGCTATAAATCTAGCTGAAGGCTGA 2362
Db 842 TCATAATGATACATATAAGATGAATGAAGAAGATGCTATAAATCTAGCTGAAGGCTGA 783
QY 2363 AAAACCTGAAGAAGATGTGTTATTTTCATTTGACCCACTTGTCTGACATTTGGAGAGGAA 2422
Db 782 AAAACCTGAAGAAGATGTGTTATTTTCATTTGACCCACTTGTCTGACATTTGGAGAGGAA 723
QY 2423 TGGATTACATAGTCAAGTCTCTGCAAGTGAACCCCTGTGACCTTGAAGAAATTCAAATTAG 2482
Db 722 TGGATTACATAGTCAAGTCTCTGCAAGTGAACCCCTGTGACCTTGAAGAAATTCAAATTAG 663
QY 2483 TCTCCTGCTGCTGTCTGCAATGCAAGTGAATAATCTAGCTCAGATCTTCACAATTTGG 2542
Db 662 TCTCCTGCTGCTGTCTGCAATGCAAGTGAATAATCTAGCTCAGATCTTCACAATTTGG 603
QY 2543 TCAAACTGAGCATCTTGTATTATCAGAAAATTTACCTGTAAGAAAGATGGAATGAAGCTC 2602
Db 602 TCAAACTGAGCATCTTGTATTATCAGAAAATTTACCTGTAAGAAAGATGGAATGAAGCTC 543
QY 2603 TTTATGAACCTGATCGACAGATGAACGTGTGTAAGACAGCTTCACCGACATGATGCTGCCCT 2662
Db 542 TTTATGAACCTGATCGACAGATGAACGTGTGTAAGACAGCTTCACCGACATGATGCTGCCCT 483
QY 2663 GGGGCTGTGACGTTGCAAGGACGCTGAGCAGCCTGTTTGAACATTTTGGAGGAGTCCAC 2722
Db 482 GGGGCTGTGACGTTGCAAGGACGCTGAGCAGCCTGTTTGAACATTTTGGAGGAGTCCAC 423
QY 2723 AACTGCTCAAGCTTGGGTTGAAAACCTGGAGACTCAGATACAGAGATTTAGATTTTAG 2782
Db 422 AACTGCTCAAGCTTGGGTTGAAAACCTGGAGACTCAGATACAGAGATTTAGATTTTAG 363
QY 2783 GTGCATTTTTTGGAAAAGAACCTCTGAAAACCTTCCAGCAGTTGAATTTGGCGGGAATC 2842

Db 362 GTGCATTTTTTGGAAAAGAACCTCTGAAAACCTTCCAGCAGTTGAATTTGGCGGGAATC 303
QY 2843 GTGTGAGCAGTATGATGCTTGCCTTCATGGGTGATTTGAGAATCTTAAGCAATTAG 2902
Db 302 GTGTGAGCAGTATGATGCTTGCCTTCATGGGTGATTTGAGAATCTTAAGCAATTAG 243
QY 2903 TGTGTTTTTGTACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTA 2962
Db 242 TGTGTTTTTGTACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTA 183
QY 2963 GCCAAGTGTATCCAAAGTTAACTTTTTCGAGAAGCTAGGCTTGTGGTGCAATTG 3022
Db 182 GCCAAGTGTATCCAAAGTTAACTTTTTCGAGAAGCTAGGCTTGTGGTGCAATTG 123
QY 3023 ATGATGATGATCTCAGTGTATTACAG 3049
Db 122 ATGATGATGATCTCAGTGTATTACAG 96

RESULT 7
US-09-864-921-179
; Sequence 179, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(891)
US-09-864-921-179

Query Match 27.3%; Score 840; DB 9; Length 891;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 890; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 481 CTTTCAGAGCCCTTCATCATTTGAAGGGGAATCTGCAAGGCAAGTCCCACTCTGCTGCAG 540
Db 1 CTTTCAGAGCCCTTCATCATTTGAAGGGGAATCTGCAAGGCAAGTCCCACTCTGCTGCAG 60
QY 541 CGCATTTGCCATGCTCTGGGCTCCGGAAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTC 600
Db 61 CGCATTTGCCATGCTCTGGGCTCCGGAAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTC 120
QY 601 TTTCTTCTCCGCTCAGCAGGCGCCAGGGTGAGACTTTTGAACCCCTCTGTGTATCAACTC 660
Db 121 TTTCTTCTCCGCTCAGCAGGCGCCAGGGTGAGACTTTTGAACCCCTCTGTGTATCAACTC 180
QY 661 CTGGATATACCTGGCAATCATCAGGAAGCAGACATTTCATGGCCATTCATGCTGAAGCTGCG 720

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; NUMBER OF SIQ ID NOS: 195
; SOFTWARE: PstSEQ for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: (DS
; LOCATION: (277) ... (1353)
US-09-864-921-98

Query Match      26.5%; Score 815; DB 9; Length 1395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 815; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2258 GTGGTCTGACGTGACAGCTTGGGTAACTTGAAGACCTTACAAAGCTCATATGGAATAACA 2317
Db 539 GTGGTCTGACGTGACAGCTTGGGTAACTTGAAGACCTTACAAAGCTCATATGGAATAACA 598
Qy 2318 TAAAGATGAATGAAGAGATGCTATATAAAGCTAGCTGAAGGCTGAAAACCTGGAAGAAGA 2377
Db 599 TAAAGATGAATGAAGAGATGCTATATAAAGCTAGCTGAAGGCTGAAAACCTGGAAGAAGA 658
Qy 2378 TGTGTATATTTCAATTTGACCCACTTGTCTGACATTTGGAGAGGGAATGGAATACATAGTCA 2437
Db 659 TGTGTATATTTCAATTTGACCCACTTGTCTGACATTTGGAGAGGGAATGGAATACATAGTCA 718
Qy 2438 AGTCTTGTCAAGTGAACCCCTGTGACCTTGAAGAAATTCATATTAGTCTCCTGCTGCTTGT 2497
Db 719 AGTCTTGTCAAGTGAACCCCTGTGACCTTGAAGAAATTCATATTAGTCTCCTGCTGCTTGT 778
Qy 2498 CTGCAATGTCAGTGAATAATCTAGCTCAGAAATCTTCAACAATTTGGTCAAACTGAGCATTC 2557
Db 779 CTGCAATGTCAGTGAATAATCTAGCTCAGAAATCTTCAACAATTTGGTCAAACTGAGCATTC 838
Qy 2558 TTGATATATCAGAAATTTACCTGGAAAAGATGGAATGAAAGCTTCTTCATCAACTGATCG 2617
Db 839 TTGATATATCAGAAATTTACCTGGAAAAGATGGAATGAAAGCTTCTTCATCAACTGATCG 898
Qy 2618 ACAGCTGACAGCTGCTAGACAGCTCACCGCACTGATCTGCCCTGGGGCTGTGACGTGC 2677
Db 899 ACAGCTGACAGCTGCTAGACAGCTCACCGCACTGATCTGCCCTGGGGCTGTGACGTGC 958
Qy 2678 AAGGCTGCTGACAGCTGCTGAAACATTTGGAGGAGTCCCAACTCTGCAAGCTTG 2737
Db 959 AAGGCTGCTGACAGCTGCTGAAACATTTGGAGGAGTCCCAACTCTGCAAGCTTG 1018
Qy 2738 GGTGT/AAAAGTGGAGACTACAGATACAGAGATTTAGTAATTTTGGTGCATTTTGGAA 2797
Db 1019 GGTGT/AAAAGTGGAGACTACAGATACAGAGATTTAGTAATTTTGGTGCATTTTGGAA 1078
Qy 2798 AGAAGCTCTCGAAAAGCTTCCAGCAGTTGAATTTGGCGGGAATCGTGTGACGATGATG 2857
Db 1079 AGAAGCTCTCGAAAAGCTTCCAGCAGTTGAATTTGGCGGGAATCGTGTGACGATGATG 1138
Qy 2858 GATGCTTTGCTTTCATGGGTGATTTTGAAGATCTTAAGCAATTTAGTGTGTTTGGACTTTA 2917
Db 1139 GATGCTTTGCTTTCATGGGTGATTTTGAAGATCTTAAGCAATTTAGTGTGTTTGGACTTTA 1198
Qy 2918 GTACTAAGAATTTCTACTGATCCAGCATTAGTCAGAAAACCTTAGCCAAAGTGTATATCA 2977
Db 1199 GTACTAAGAATTTCTACTGATCCAGCATTAGTCAGAAAACCTTAGCCAAAGTGTATATCA 1258
Qy 2978 AGTTAAATTTTCTCAGAAAGCTAGGCTGTGGTGGCAATTTTCATCATGATGATCA 3037
Db 1259 AGTTAAATTTTCTCAGAAAGCTAGGCTGTGGTGGCAATTTTCATCATGATGATCA 1318
Qy 3038 GTGTTAATACAGGTCTTTTAAACTAGTAAGTGT 3072
Db 1319 GTGTTAATACAGGTCTTTTAAACTAGTAAGTGT 1353

RESULT 9
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Db 181 CTGGATATACCTGGACAAATCAGGAAGCAGACATTCATGGCCATGCTCTGAAGCTGCGG 240
Qy 721 CAGAGGGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 780
Db 241 CAGAGGGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 300
Qy 781 ATCGAAGCCCTGATAAAGAAAACCCAGCGCTTCAAGAACATGCTCATGCTCACCCTACC 840
Db 301 ATCGAAGCCCTGATAAAGAAAACCCAGCGCTTCAAGAACATGCTCATGCTCACCCTACC 360
Qy 841 ACTGAGTCTGAGGCACATACGGCAGTTTGGTGGCCCTGACTGCTGAGTGGGGGATATG 900
Db 361 ACTGAGTCTGAGGCACATACGGCAGTTTGGTGGCCCTGACTGCTGAGTGGGGGATATG 420
Qy 901 ACAGAGACAGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGGAGCTTGTCTGAAGGC 960
Db 421 ACAGAGACAGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGGAGCTTGTCTGAAGGC 480
Qy 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGATCTCATGAAGACCCCTCTCTTT 1020
Db 481 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGATCTCATGAAGACCCCTCTCTTT 540
Qy 1021 GTGGTCATCATCTTGCAATCCAGATGGGTGAAAGTGAAGTGTCCACTCTCACACAAACA 1080
Db 541 GTGGTCATCATCTTGCAATCCAGATGGGTGAAAGTGAAGTGTCCACTCTCACACAAACA 600
Qy 1081 AGCGTGTCCATACCTTCTATGATCTGTGTATACAGAAAACAAACACAAACATAAAGGT 1140
Db 601 AGCGTGTCCATACCTTCTATGATCTGTGTATACAGAAAACAAACACAAACATAAAGGT 660
Qy 1141 GTGGTCAAGTGAAGTCTTCAATCGGAGCTGGACCACTGTGGAGACTGAGCTCTGGAGGCT 1200
Db 661 GTGGTCAAGTGAAGTCTTCAATCGGAGCTGGACCACTGTGGAGACTGAGCTCTGGAGGCT 720
Qy 1201 GTGTTCTCCCAAGTGTGATTTCGAATGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTG 1260
Db 721 GTGTTCTCCCAAGTGTGATTTCGAATGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTG 780
Qy 1261 CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGTGTCAAGCTCAAGTGTCAAG 1320
Db 781 CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGTGTCAAGCTCAAGTGTCAAG 840
Qy 1321 TTTCTTTCACAGTCAATCCAGAGTACACAGCAGGACCAAGCACTCAGCAGT 1371
Db 841 TTTCTTTCACAGTCAATCCAGAGTACACAGCAGGACCAAGCACTCAGCAGT 891

RESULT 8
US-09-864-921-98
; Sequence 98, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4753
; CURRENT APPLICATION NUMBER: US/09/864,921
; PRIOR FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-05-24 US/579,240
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
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[illegible][illegible]

Db 577 TTGGCTCAGGATTTAAAGGACTTGACCATACCCACCTTTTCTGAACATTTTATCCCCCTT 636
Qy 361 GGTGAAGATATGACATTTATTTTAACTTGAAGACACCTTCACAGAACCTGTCTCTGTGG 420
Db 637 GGTGAAGATATGACATTTATTTTAACTTGAAGACACCTTCACAGAACCTGTCTCTGTGG 696
Qy 421 AGGAAGGACCAACACCATCATCCGGCTGGAGGAGCTGACCCCT 461
Db 697 AGGAAGGACCAACACCATCATCCGGCTGGAGGAGCTGACCCCT 737

RESULT 11
US-09-764-864-339
; Sequence 339, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 339
; LENGTH: 608
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (23)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (26)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (86)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-339

Query Match 13.7%; Score 420; DB 10; Length 608;
Best Local Similarity 99.6%; Pred. No. 9.3e-212;
Matches 520; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1494 TGTGAAGCCACCGGCTGTATGAAGCAGCTCGCAGCATGTATCAACACGGCTGCCT 1553
Db 87 TGTGAAGCCACCGGCTGTATGAAGCAGCTCGCAGCATGTATCAACACGGCTGCCT 146
Qy 1554 TCTGGAGCTTCCATCGCCAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAA 1613
Db 147 TCTGGAGCTTCCATCGCCAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAA 206
Qy 1614 AAACACCAGTGAAGAGATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGG 1673
Db 207 AAACACCAGTGAAGAGATCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGG 266
Qy 1674 CATCATTTATATCAAGAGATGATATCAAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTT 1733
Db 267 CATCATTTATATCAAGAGATGATATCAAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTT 326
Qy 1734 CTTTCAAGTAAAGCTTTATATCAACTCAGGGAACATCCCGATATCTTATTTGACTT 1793
Db 327 CTTTCAAGTAAAGCTTTATATCAACTCAGGGAACATCCCGATATCTTATTTGACTT 386
Qy 1794 CTTTGAACATTTGCCAATTTGCAAGTGTGAGTCTGAGCTTCATTAACHTGGACTTTATGG 1853
Db 387 CTTTGAACATTTGCCAATTTGCAAGTGTGAGTCTGAGCTTCATTAACHTGGACTTTATGG 446
Qy 1854 GGGAGCTATGGCTTCATGGGAAAGGCTGCGAGAGACACAGGCTGAATCCACATGGGAAGA 1913
|||||

Db 447 GGGATCTATGGCTTCATGGGAAAGGCTGCAGAGACACAGGCGAATCCACATCGAAGA 506
Qy 1914 GGCC CAGAAACCTACATTTCCAGCAGGCGTGTATCTTTGTTCTTCAACTGGAACAGGA 1973
Db 507 GGCC CAGAAACCTACATTTCCAGCAGGCGTGTATCTTTGTTCTTCAACTGGAACAGGA 566
Qy 1974 ATTCAGGACTCTGGAGGTCACACTCCGGGATTTTCAGCAAGTT 2015
Db 567 ATTCAGGACTCTGGAGGTCACACTCCGGGATTTTCAGCAAGTT 608

RESULT 12
US-09-764-864-754
; Sequence 754, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 754
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (160)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (468)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (499)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (505)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-754

Query Match 9.9%; Score 304; DB 10; Length 522;
Best Local Similarity 99.7%; Pred. No. 2.2e-150;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 236 CTCAT TCAAGACTTGAATGGACAAAGCTTTTTCATCAGACATCAGAGGAGACTTGG 295
Db 1 CTCAT TCAAGACTTGAATGGACAAAGCTTTTTCATCAGACATCAGAGGAGACTTGG 60
Qy 296 ACGATT TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACCTTTATC 355
Db 61 ACGATT TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACCTTTATC 120
Qy 356 CCCTTG TGAAGATATTGACATTTATTTTAACTTGAAGGAGCCCTTCACAGAACCTGTCC 415
Db 121 CCCTTG TGAAGATATTGACATTTATTTTAACTTGAAGGAGCCCTTCACAGAACCTGTCC 180
Qy 416 TGTGAG GAAGGACCAACACCATCACCGCTGGAGCAGCTGACCTGAATGCGCTCTGC 475
Db 181 TGTGAG GAAGGACCAACACCATCACCGCTGGAGCAGCTGACCTGAATGCGCTCTGC 240
Qy 476 AGGCTCT CAGAGCCCTGATCATTTGAAGGAGATCTGCAAGGAGTCCACTCTGC 535
Db 241 AGGCTCT CAGAGCCCTGATCATTTGAAGGAGATCTGCAAGGAGTCCACTCTGC 300
Qy 536 TGCAGCG ATTGGCATGCTGTGGGGCTCCGGAAAGTGCAGGCTCTGACCAAGTT 590
Db 301 TGCAGCG ATTGGCATGCTGTGGGGCTCCGGAAAGTGCAGGCTCTGACCAAGTT 355

RESULT 13

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US-09-864-921-100
; Sequence 100, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Plo, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(552)
US-09-864-921-100

Query Match      8.8%; Score 269; DB 9; Length 578;
Best Local Similarity 100.0%; Pred. No. 7,2e-132;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGAATTTCATAAGACACAATAGCCGAGGCCCTTATTCAAAGAATGGGAATGACTCTTATA 60
Db      277  ATGAATTTCATAAGACACAATAGCCGAGGCCCTTATTCAAAGAATGGGAATGACTCTTATA 336

QY      61  AAGCAATACAGATGACCTATTGTGTGAATGTTCTGAATCGCGAAGAAAGTAAACATC 120
Db      337  AAGCAATACAGATGACCTATTGTGTGAATGTTCTGAATCGCGAAGAAAGTAAACATC 396

QY      121  ATTGTGCGGAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGGAA 180
Db      397  ATTGTGCGGAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGGAA 456

QY      181  AAGGGTTCAGAGTCCTGTAACTCTTCTTAATCCCTTAAGSAGTGAACATATCCTCTA 240
Db      457  AAGGGTTCAGAGTCCTGTAACTCTTCTTAATCCCTTAAGSAGTGAACATATCCTCTA 516

QY      241  TTTTCAGSACTTGAATGGACAAAGTCCTTT 269
Db      517  TTTTCAGSACTTGAATGGACAAAGTCCTTT 545

RESULT 14
US-09-864-921-177
; Sequence 177, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Plo, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4236
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011232.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BT47A, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: NT HIT: U75273.1, EVALUATE 8.20e+00
; OTHER INFORMATION: EST HUMAN HIT: AT264294.1, EVALUATE 1.00e-121
; OTHER INFORMATION: SWISSPROT HIT: P24583, EVALUATE 1.60e+00
US-09-864-761-4236
```

```
Query Match 7.9%; Score 242; DB 10; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.3e-117;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2781 AGTGCATTTTGGAAAGAACCTCTGAAAACTCCAGCAGTTGAATTTGGCGGAAA 2840
Db 180 AGTGCATTTTGGAAAGAACCTCTGAAAACTCCAGCAGTTGAATTTGGCGGAAA 239

Qy 2841 TCGGTGAGCAGTGATGGCTTGCCTTCATGGGTGATTTGAGAACTCTTAAGCAATT 2900
Db 240 TCGGTGAGCAGTGATGGCTTGCCTTCATGGGTGATTTGAGAACTCTTAAGCAATT 299

Qy 2901 AGTGTGTTTGGACCTTACTAAGAAATTTCTACCTGATCCAGCAATAGTCAGAAAAT 2960
Db 300 AGTGTGTTTGGACCTTACTAAGAAATTTCTACCTGATCCAGCAATAGTCAGAAAAT 359

Qy 2961 TAGCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTCTGGTGGCAATT 3020
Db 360 TAGCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAAGCTAGGCTTCTGGTGGCAATT 419

Qy 3021 TG 3022
Db 420 TG 421
```

```
RESULT 16
US-09-864-761-20988
; Sequence 20988, Application US/09864761
```

```
; Patent NO. US 20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Fenn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aequica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20983
; LENGTH: 220
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011232.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BT47A, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: NT HIT: U75273.1, EVALUATE 8.20e+00
; OTHER INFORMATION: EST HUMAN HIT: AT264294.1, EVALUATE 1.00e-121
; OTHER INFORMATION: SWISSPROT HIT: P24583, EVALUATE 1.60e+00
US-09-864-761-20988
```

```
Query Match 7.2%; Score 220; DB 10; Length 220;
Best Local Similarity 100.0%; Pred. No. 5.5e-106;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 2830 TTGGCGGGAATCGTGTGAGCAGTGATGGCTTGCCTTCATGGGTATTTGAGAAAT 2889
|||||
Db 1 TTGGCGGGAATCGTGTGAGCAGTGATGGCTTGCCTTCATGGGTATTTGAGAAAT 60
QY 2890 CTTAAGCAATAGTGTGTTTTGACTTTAGTACTAAGAATTTCTACCTGATCCAGCATTA 2949
|||||
Db 61 CTTAAGCAATAGTGTGTTTTGACTTTAGTACTAAGAATTTCTACCTGATCCAGCATTA 120
QY 2950 GTCAGAAACTTAGCCAGTGTATCCAGTTAACTTTCTCGAAGACCTAGGCTGTT 3009
|||||
Db 121 GTCAGAAACTTAGCCAGTGTATCCAGTTAACTTTCTCGAAGACCTAGGCTGTT 180
QY 3010 GGGTGGCAATTTGATGATGATCATCTCAGTGTATTATACAG 3049
|||||
Db 181 GGGTGGCAATTTGATGATGATCATCTCAGTGTATTATACAG 220

RESULT 17
US-09-864-921-183
; Sequence 183, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(165)
US-09-864-921-183

Query Match 3.7%; Score 114; DB 9; Length 165;
Best Local Similarity 99.4%; Pred. No. 6.4e-50;
Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1924 ACCTACATCCAGCAGGCGTGTATCTTTGTTCTCACTGGAAGCAGGAATTCAGGACT 1983
|||||
Db 1 ACCTACATCCAGCAGGCGTGTATCTTTGTTCTCACTGGAAGCAGGAATTCAGGACT 60
QY 1984 CTGGAGGTCACACTCCGGGATTCAGCAAGTTGAATAAGCAGAGATATCATATATCTGGG 2043
|||||
Db 61 CTGGAGGTCACACTCCGGGATTCAGCAAGTTGAATAAGCAGAGATATCATATATCTGGG 120
QY 2044 AAAATATTTCAGCTGCCCAAGCCTCAGGCTGCAAAATAAGAGA 2088
|||||
Db 121 AAAATATTTCAGCTGCCCAAGCCTCAGGCTGCAAAATAAGAGA 165

RESULT 18
US-09-864-921-160/c

; Sequence 160, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-160

Query Match 0.9%; Score 29; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1152 TGACCTTCATTCGGAGCCTGGACCACCTGTG 1180
|||||
Db 29 TGACCTTCATTCGGAGCCTGGACCACCTGTG 1

RESULT 19
US-09-864-921-161
; Sequence 161, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence

```
;
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-161

Query Match      0.8%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 CATCATTTGCTGCCGAGAGTGGAG 141
Db 1 CATCATTTGCTGCCGAGAGTGGAG 25

RESULT 20
US-09-864-921-162/c
; Sequence 162, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864, 921
; PRIOR FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-05-24
; PRIOR FILING DATE: 2000-10-10
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-162

Query Match      0.8%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2959 CTTAGCCCAAGTGTATCCAAAGTTAA 2983
Db 25 CTTAGCCCAAGTGTATCCAAAGTTAA 1

RESULT 21
US-09-864-921-165
; Sequence 165, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864, 921
; PRIOR FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-05-24
; PRIOR FILING DATE: 2000-10-10
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-162

Query Match      0.8%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2959 CTTAGCCCAAGTGTATCCAAAGTTAA 2983
Db 25 CTTAGCCCAAGTGTATCCAAAGTTAA 1
```

```
;
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864, 921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-115

Query Match      0.8%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AATTTCATAAAGGACAATAGCCGAG 28
Db 1 AATTTCATAAAGGACAATAGCCGAG 25

RESULT 22
US-09-864-921-119
; Sequence 159, Application US/09864921
; Patent No. US:0020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864, 921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-151

Query Match      0.8%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 GGTGGAACAGGATGCTCTAGAGG 158
Db 1 GGTGGAACAGGATGCTCTAGAGG 24

RESULT 23
```

```
US-09-864-921-157
; Sequence 157, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1 Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-157

Query Match      0.8%; Score 24; DB 9; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTCATAAAGGCAATAGC 24
   |||||
Db 10 ATGAATTCATAAAGGCAATAGC 33

RESULT 24
US-09-864-921-153/c
; Sequence 153, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1 Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-163
; Sequence 163, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1 Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-163

Query Match      0.7%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 GTAAACATCATTTGCTGCGAGAA 134
   |||||
Db 1 GTAAACATCATTTGCTGCGAGAA 23

RESULT 26
US-09-864-921-156
; Sequence 156, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1 Card Domain Containing
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-153

Query Match      0.7%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 CTGCTAGAGGATCATTCACATG 171
   |||||
Db 23 CTGCTAGAGGATCATTCACATG 1

RESULT 25
US-09-864-921-163
; Sequence 163, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1 Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-163

Query Match      0.7%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 GTAAACATCATTTGCTGCGAGAA 134
   |||||
Db 1 GTAAACATCATTTGCTGCGAGAA 23

RESULT 26
US-09-864-921-156
; Sequence 156, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1 Card Domain Containing
```

```
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-156

Query Match          0.7%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GTATGGAATGTTCTGAATGCG 105
      |||||
DB 1  GTATGGAATGTTCTGAATGCG 21

RESULT 27
US-09-864-921-158/c
; Sequence 158, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-158

Query Match          0.7%; Score 21; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 TATCCTCTATTTCAGACTTG 252
      |||||
DB 30 TATCCTCTATTTCAGACTTG 10
```

```
RESULT 28
US-09-728-445-37
; Sequence 337, Application US/09728445
; Patent No. US20020102543A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020102543A1el Mutated Mammalian Cells and
; TITLE OF INVENTION: Animals
; FILE REFERENCE: LEX-0102-USA
; CURRENT APPLICATION NUMBER: US/09/728,445
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 337
; LENGTH: 483
; TYPE: DNA
; ORGANISM: M1s musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(483)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-445-37

Query Match          0.7%; Score 21; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2965 CAAGTATTATCCAAAGTTAACT 2985
      |||||
DB 167 CAAGTATTATCCAAAGTTAACT 187

RESULT 29
US-09-974-300-63
; Sequence 6263, Application US/09974300
; Patent No. US 0020146721A1
; GENERAL INFORMATION:
; APPLICANT: Borka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6263
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-6263

Query Match          0.7%; Score 20; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1881 TGCAGACACACAGGTGGAA 1900
      |||||
DB 378 TGCAGACACACAGGTGGAA 397

RESULT 30
US-09-864-921-10/c
; Sequence 102, Application US/09864921
; Patent No. US20020176853A1
```



```
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(744)
US-09-864-921-102

Query Match 0.7%; Score 20; DB 9; Length 768;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2331 AGAAGATGCTATAAACTAG 2350
      |||||||
Db 755 AGAAGATGCTATAAACTAG 736

RESULT 31
US-09-800-631-96/c
; Sequence 96, Application US/09800631
; Patent No. US20020082228A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXPR
; FILE REFERENCE: ISPH-0544
; CURRENT APPLICATION NUMBER: US/09/800,631
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US/09/657,346
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 96
; LENGTH: 30310
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19791)...(19802)
; NAME/KEY: CDS
; LOCATION: (21160)...(21370)
; NAME/KEY: CDS
; LOCATION: (24168)...(24307)
; NAME/KEY: CDS
; LOCATION: (25696)...(25908)
; NAME/KEY: CDS
; LOCATION: (27235)...(27246)
US-09-800-631-96

Query Match 0.6%; Score 19; DB 10; Length 30310;
```

```
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1265 TGACAACCTGGGCTCCTCTG 1283
      |||||||
Db 13062 TGACAACCTGGGCTCCTCTG 13044

RESULT 32
US-09-864-921-155
; Sequence 155, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-864-921-155

Query Match 0.6%; Score 18; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ATAGCCGAGCCCTTATTC 37
      |||||||
Db 4 ATAGCCGAGCCCTTATTC 21

RESULT 33
US-09-867-701-9442/c
; Sequence 9442, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9442
; LENGTH: 216
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-9442
```

```
Query Match
Best Local Similarity 0.6%; Score 18; DB 10; Length 216;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 CTGTAACCTCTTCTTAA 212
Db 128 CTGTAACCTCTTCTTAA 111

RESULT 34
US-09-878-574-9387/c
; Sequence 9387, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-08-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 9387
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701102423H1
US-09-878-574-9387

Query Match
Best Local Similarity 0.6%; Score 18; DB 10; Length 273;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 468 CCTCTGCAGGCTCTTCA 485
Db 263 CCTCTGCAGGCTCTTCA 246

RESULT 35
US-09-864-761-4716/c
; Sequence 4716, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
```

```
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4715
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL109823.11
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
US-09-864-761-4716

Query Match
Best Local Similarity 0.6%; Score 18; DB 10; Length 454;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 505 GGGGAATCTGCGCAAGGC 522
Db 29 GGGGAATCTGCGCAAGGC 12

RESULT 36
US-09-998-598-1359
; Sequence 1359, Application US/09998598
; Patent No. US200150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xie, Jiangchun
; APPLICANT: Cienault, Ruth A.
; APPLICANT: Magher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Cor.xa Invention Disclosure Database
; SEQ ID NO 1369
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-1359

Query Match
Best Local Similarity 0.6%; Score 18; DB 10; Length 469;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATTTCATAAAGGAC 18
```

```
|||||
Db 88 ATGAATTCATAAGGAC 105

RESULT 37
US-09-864-761-1714
; Sequence 1714, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1714
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010087.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
US-09-864-761-1714

Query Match 0.6%; Score 18; DB 10; Length 472;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 AGAAGTGGAGCAGGATG 148
|||||
Db 143 AGAAGTGGAGCAGGATG 160

RESULT 38
US-09-728-446-43/c
; Sequence 43, Application US/09728446
; Patent No. US20020081668A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NO. US20020081668A1 Murine Polynucleotide Sequences
; TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
; FILE REFERENCE: LEX-0101-USA
; CURRENT APPLICATION NUMBER: US/09/728,446
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,270
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 1461
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(501)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-446-43

Query Match 0.6%; Score 18; DB 10; Length 501;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1958 TCAACTGGAAGCAGGAAT 1975
|||||
Db 18 TCAACTGGAAGCAGGAAT 1

RESULT 39
US-09-738-626-2121
; Sequence 2121, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOUCUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
```

```
; SEQ ID NO 2121
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2121

Query Match          0.6%; Score 18; DB 9; Length 960;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3005 TTGTTGGTGGCAATTG 3022
|||||
Db 394 TTGTTGGTGGCAATTG 411

RESULT 40
US-09-764-877-3957
; Sequence 3957, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764.877
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3957
; LENGTH: 1163
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3957

Query Match          0.6%; Score 18; DB 10; Length 1163;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2047 ATATTGAGCTGCGACA 2064
|||||
Db 379 ATATTGAGCTGCGACA 396

RESULT 41
US-09-540-540-2/c
; Sequence 2, Application US/09360540
; Patent No. US2002015553A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Murty, Lynn E.
; TITLE OF INVENTION: HUMAN VESICLE BINDING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/360,540
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/857,213
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
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; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: EP-0297 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: FIBRNGT01
; CLONE: 148415
US-09-360-540-2

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Qy 1 ATGAA'TTCATAAAGGAC 18
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Db 1538 ATGAA'TTCATAAAGGAC 1521

RESULT 42
US-09-764-864-1654/c
; Sequence 1654, Application US/09764864
; Patent No. US:0020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764.864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1654
; LENGTH: 2619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1654

Query Match          0.6%; Score 18; DB 10; Length 2619;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2980 TTAAC'TTCTGCAAGAA 2997
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Db 2432 TTAAC'TTCTGCAAGAA 2415

RESULT 43
US-09-957-189-1
; Sequence 1, Application US/09957189
; Patent No. US200177210A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Blinkovsky
; APPLICANT: Tony Byun
; APPLICANT: Alan V. Klotz
; APPLICANT: Alan Sloma
; APPLICANT: Maria Tang
; APPLICANT: Mikio Fujii
; APPLICANT: Chigusa Marumoto
; APPLICANT: Lene Venke Kofod
; TITLE OF INVENTION: Polypeptides Having Aminoamidase
; TITLE OF INVENTION: Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5379.200-US
; CURRENT APPLICATION NUMBER: US/09/957,189
; CURRENT FILING DATE: 2001-09-19
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/192,104
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1465/97
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 00670
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3000
; TYPE: DNA
; ORGANISM: Spingomonas
; US-09-957-189-1

Query Match      0.6%; Score 18; DB 9; Length 3000;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2092 GCTGGTGTGCTGGAAGC 2109
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Db 1911 GCTGGTGTGCTGGAAGC 1928

RESULT 44
US-09-764-864-1656
; Sequence 1656, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1656
; LENGTH: 3460
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-864-1656

Query Match      0.6%; Score 18; DB 10; Length 3460;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2980 TTAACTTTCTGCAAGAA 2997
|||||
Db 1026 TTAACTTTCTGCAAGAA 1043

RESULT 45
US-09-070-927A-261/c
; Sequence 261, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
;              Patrick J. Dillon
;              Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
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; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 261:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 261:
US-09-070-927A-261

Query Match      0.6%; Score 18; DB 10; Length 4951;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2492 GCTGTCTGCAAAATGCAG 2509
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Db 1288 GCTGTCTGCAAAATGCAG 1271

RESULT 46
US-09-811-045A-2
; Sequence 2, Application US/09811045A
; Patent No. US20020035080A1
; GENERAL INFORMATION:
; APPLICANT: Scott, Robert E.
; TITLE OF INVENTION: cDNA encoding P2P proteins and use of P2P cDNA-
; TITLE OF INVENTION: derived antibodies and antisense reagents
; TITLE OF INVENTION: in determining the proliferative potential of
; TITLE OF INVENTION: normal, abnormal and cancer cells in animals
; TITLE OF INVENTION: and humans
; FILE REFERENCE: D6386D
; CURRENT APPLICATION NUMBER: US/09/811,045A
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 08/801,308
; PRIOR FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 5173
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: cDNA
; OTHER INFORMATION: P2P cDNA
US-09-811-045A-2

Query Match      0.6%; Score 18; DB 10; Length 5173;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2796 AAAGAACCCTCTGAAAAA 2813
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Db 3187 AAAGAACCCTCTGAAAAA 3204

RESULT 47
US-09-764-855-208
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; Sequence 208, Application US/09764855
; Patent No. US20020119919A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA110
; CURRENT APPLICATION NUMBER: US/09/764,855
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
; LENGTH: 7386
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-855-208

Query Match 0.6%; Score 18; DB 10; Length 7386;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 131 AGAAGGTGGAGCAGGATG 148
|||||
Db 3282 AGAAGGTGGAGCAGGATG 3299

RESULT 48
US-09-764-860-1102
; Sequence 1102, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1102
; LENGTH: 17252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-1102

Query Match 0.6%; Score 18; DB 10; Length 17252;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2796 AAAGAACCCCTCTGAAAAA 2813
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Db 14764 AAAGAACCCCTCTGAAAAA 14781

RESULT 49
US-09-880-107-2097
; Sequence 2097, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20:7
; LENGTH: 17:09
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 J03764
US-09-880-107-2097

Query Match 0.6%; Score 18; DB 10; Length 17509;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2051 TCAGCTCTGCCACAAGCC 2068
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Db 15793 TCAGCTCTGCCACAAGCC 15810

RESULT 50
US-09-734-674-3
; Sequence 3, Application US/09734674
; Patent No. US20020081648A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001018
; CURRENT APPLICATION NUMBER: US/09/734,674
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 20201
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)-(202001)
; OTHER INFORMATION: n = A,T,C or G
US-09-734-674-3

Query Match 0.6%; Score 18; DB 10; Length 202001;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 TTTTC'GAAC'TTTTATCC 356
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Db 39930 TTTTC'GAAC'TTTTATCC 39947

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OM nucleic - nucleic search, using sw model

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6	3072	100.0	3133	32	US-09-841-739-1	Sequence 1, Appli
7	2919	95.0	3075	41	US-10-156-733-1	Sequence 1, Appli
8	2919	95.0	3219	41	US-10-156-733-14	Sequence 14, Appli
9	2919	95.0	3545	18	US-09-491-404-1319	Sequence 1319, Ap
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13	2918	95.0	3213	42	US-10-221-097-23	Sequence 96, Appli
14	2868	93.4	3396	33	US-09-864-921-96	Sequence 96, Appli
15	2849	92.7	3396	27	US-09-686-347-96	Sequence 66, Appli
16	2765	90.0	3260	1	PCT-US01-14826-66	Sequence 66, Appli
17	2765	90.0	3260	26	US-09-667-298-66	Sequence 66, Appli
18	2634	85.7	3612	27	US-09-697-089-6	Sequence 6, Appli
19	2634	85.7	3612	32	US-09-841-739-6	Sequence 6, Appli
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22	2634	85.7	3615	27	US-09-697-089-4	Sequence 4, Appl1	95	412	13.4	480	17	US-09-332-782-15784	Sequence 15784, A
23	2634	85.7	3615	27	US-09-697-089-12	Sequence 12, Appl1	96	412	13.4	480	29	US-09-737-223-15784	Sequence 15784, A
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28	2208	71.9	6012	38	US-10-043-938-911	Sequence 911, App	101	384	12.5	407	17	US-09-359-067-46762	Sequence 46762, A
29	2208	71.9	6012	38	US-10-043-938-917	Sequence 917, App	102	369	12.0	443	19	US-09-528-409-24681	Sequence 24681, A
30	2207	71.8	2343	22	US-09-578-789-15	Sequence 15, Appl	103	369	12.0	443	35	US-09-933-524-24681	Sequence 24681, A
31	2207	71.8	2343	22	US-09-578-789-15	Sequence 15, Appl	104	369	12.0	443	35	US-09-933-524A-24681	Sequence 24681, A
32	2205	71.8	2415	22	US-09-578-789-17	Sequence 17, Appl	105	360	11.7	443	19	US-09-431-517-20384	Sequence 20384, A
33	2205	71.8	2415	22	US-09-578-789-17	Sequence 17, Appl	106	360	11.7	443	19	US-09-528-409-72666	Sequence 72666, A
34	2205	71.8	3018	22	US-09-577-408-3077	Sequence 3077, Ap	107	358	11.7	404	19	US-09-528-409-72666	Sequence 72666, A
35	2062	67.1	2215	1	PCT-US01-07143-22	Sequence 22, Appl	108	358	11.7	404	35	US-09-933-524A-72666	Sequence 72666, A
36	2062	67.1	2215	42	US-10-221-097-22	Sequence 22, Appl	109	335	10.9	457	18	US-09-431-517-23615	Sequence 23615, A
37	1946	63.3	6900	22	US-09-578-789-73	Sequence 73, Appl	110	334	10.5	426	18	US-09-404-284-65	Sequence 65, Appl
38	1946	63.3	6900	27	US-09-579-240-73	Sequence 73, Appl	111	324	10.5	436	19	US-09-524-038-65	Sequence 65, Appl
39	1946	63.3	6900	27	US-09-686-347-73	Sequence 73, Appl	112	324	10.5	436	38	US-10-011-154-65	Sequence 70, Appl
40	1945	63.3	4098	22	US-09-557-676-906	Sequence 906, App	113	323	10.5	425	19	US-09-404-284-70	Sequence 70, Appl
41	1945	63.3	4098	22	US-09-557-676-912	Sequence 912, App	114	323	10.5	425	19	US-09-524-038-70	Sequence 70, Appl
42	1945	63.3	4098	38	US-10-043-938-906	Sequence 906, App	115	323	10.5	435	38	US-10-011-154-70	Sequence 70, Appl
43	1945	63.3	4098	38	US-10-043-938-912	Sequence 912, App	116	319	10.4	535	13	US-08-971-050-2500	Sequence 2500, Ap
44	1844	60.0	2002	38	US-10-029-386-22135	Sequence 25135, A	117	319	10.4	535	13	US-08-971-050C-2500	Sequence 2500, Ap
45	1823	59.3	1976	38	US-10-029-386-22860	Sequence 22860, A	118	319	10.4	535	13	US-08-971-050C-2500	Sequence 2500, Ap
46	1781	58.0	2950	1	PCT-US00-35017A-416	Sequence 416, App	119	319	10.4	535	34	US-09-912-292-72724	Sequence 72724, A
47	1781	58.0	3152	18	US-09-471-215-7095	Sequence 7095, Ap	120	317	10.3	409	19	US-09-528-409-72714	Sequence 72714, A
48	1267	41.2	4826	1	PCT-US02-09921-438	Sequence 429, App	121	317	10.3	409	35	US-09-933-524A-72714	Sequence 72714, A
49	880	27.3	1891	23	US-09-864-921-179	Sequence 98, App	122	317	10.3	409	35	US-09-933-524A-72714	Sequence 72714, A
50	815	26.5	1395	27	US-09-864-921-98	Sequence 98, Appl	123	317	10.3	548	18	US-09-489-036-30762	Sequence 30762, A
51	815	26.5	1395	33	US-09-864-921-98	Sequence 98, Appl	124	317	10.3	548	35	US-09-943-143-30762	Sequence 30762, A
52	766	24.3	885	33	US-09-489-036-31530	Sequence 31530, A	125	316	10.3	380	17	US-09-332-782-1560	Sequence 1560, Ap
53	766	24.3	885	33	US-09-943-143-31530	Sequence 31530, A	126	316	10.3	380	19	US-09-515-694-1560	Sequence 1560, Ap
54	700	22.8	791	1	PCT-US01-14826-498	Sequence 498, App	127	305	9.9	411	19	US-09-528-409-22294	Sequence 22294, A
55	700	22.8	791	18	US-09-489-036-31154	Sequence 31154, A	128	305	9.9	411	35	US-09-933-524A-22294	Sequence 22294, A
56	700	22.8	791	22	US-09-577-408-3075	Sequence 3075, Ap	129	304	9.9	522	30	PCT-US01-01341-754	Sequence 754, App
57	700	22.8	791	35	US-09-943-143-31154	Sequence 31154, A	130	304	9.9	522	30	US-09-764-864-754	Sequence 754, App
58	660	21.5	703	63	US-60-192-739-1413	Sequence 1413, Ap	131	304	9.9	522	39	US-10-080-129-754	Sequence 754, App
59	660	21.5	703	63	US-60-194-243-1022	Sequence 1022, Ap	132	298	9.7	471	17	US-09-396-970-764	Sequence 764, App
60	636	20.7	636	56	US-60-126-246-119	Sequence 119, App	133	298	9.7	471	24	US-09-637-886-7386	Sequence 7386, Ap
61	626	20.4	641	19	US-09-404-284-4029	Sequence 4029, Ap	134	295	9.6	462	18	US-09-404-284-4507	Sequence 4507, Ap
62	626	20.4	641	19	US-09-524-038-4029	Sequence 4029, Ap	135	295	9.6	462	19	US-09-524-038-4507	Sequence 4507, Ap
63	626	20.4	641	38	US-10-011-154-4029	Sequence 4029, Ap	136	295	9.6	462	38	US-10-011-154-4507	Sequence 4507, Ap
64	620	20.2	677	18	US-09-489-036-6709	Sequence 6709, Ap	137	295	9.6	462	38	US-10-011-154-4507	Sequence 4507, Ap
65	620	20.2	677	32	US-09-943-143-6709	Sequence 6709, Ap	138	292	9.5	707	24	US-09-634-306B-258047	Sequence 258047, A
66	618	20.1	618	33	US-09-864-921-181	Sequence 181, App	139	292	9.5	457	16	US-10-027-632-258047	Sequence 258047, A
67	591	19.2	3890	22	US-09-577-408-3078	Sequence 3078, Ap	140	283	9.2	457	16	US-09-205-070-29417	Sequence 29417, A
68	586	19.1	637	63	US-60-196-718-2279	Sequence 2279, Ap	141	283	9.2	457	19	US-09-340-623-29417	Sequence 29417, A
69	575	18.7	638	62	US-60-181-996-702	Sequence 702, App	142	283	9.2	457	19	US-09-515-128-135	Sequence 125, App
70	569	18.5	715	61	US-60-177-571-855	Sequence 855, App	143	283	9.2	457	29	US-09-721-544-135	Sequence 125, App
71	553	18.0	4275	76	US-60-324-185-22577	Sequence 12877, A	144	283	9.2	457	33	US-09-898-888A-29417	Sequence 29417, A
72	530	17.3	3112	61	US-60-172-360-12877	Sequence 12877, A	145	283	9.2	457	33	US-09-898-888A-29417	Sequence 29417, A
73	527	17.2	677	35	US-09-489-036-7693	Sequence 7693, Ap	146	278	9.0	429	17	US-09-399-720-6025	Sequence 6025, Ap
74	527	17.2	677	35	US-09-943-143-7693	Sequence 7693, Ap	147	278	9.0	429	34	US-09-921-378-6025	Sequence 6025, Ap
75	519	16.9	567	18	US-09-457-877-63	Sequence 63, Appl	148	269	8.8	578	33	US-09-864-921-100	Sequence 100, App
76	519	16.9	567	36	US-09-953-981-63	Sequence 63, Appl	149	261	8.5	578	33	US-09-864-921-177	Sequence 177, App
77	514	16.7	575	63	US-60-196-718-3717	Sequence 3717, Ap	150	257	8.4	296	13	US-08-951-197-4320	Sequence 4320, Ap
78	503	16.4	627	61	US-60-171-481-722	Sequence 722, App	151	257	8.4	296	20	US-09-539-806-14441	Sequence 12441, A
79	489	15.9	2735	1	PCT-US00-36534B-1253	Sequence 1253, Ap	152	257	8.4	296	46	US-60-027-243-250	Sequence 250, App
80	489	15.9	2735	40	US-10-106-668-102	Sequence 1263, Ap	153	253	8.2	427	18	US-09-404-284-100	Sequence 100, App
81	461	15.0	768	33	US-09-864-921-102	Sequence 102, App	154	253	8.2	427	19	US-09-524-038-100	Sequence 100, App
82	442	14.4	768	27	US-09-686-347-102	Sequence 102, App	155	253	8.2	427	38	US-10-011-154-100	Sequence 100, App
83	435	14.2	2037	22	US-09-577-408-3076	Sequence 3076, Ap	156	250	8.1	578	27	US-09-686-347-100	Sequence 100, App
84	420	13.7	608	1	PCT-US01-01341-339	Sequence 339, App	157	243	7.9	548	13	US-08-976-343B-6715	Sequence 6715, Ap
85	420	13.7	608	30	US-09-764-864-339	Sequence 339, App	158	243	7.9	548	13	US-08-976-343B-6715	Sequence 6715, Ap
86	420	13.7	608	39	US-10-080-129-339	Sequence 339, App	159	242	7.9	548	13	PCT-US01-00663-4450	Sequence 4450, Ap
87	420	13.7	608	39	US-10-080-129-339	Sequence 4030, Ap	160	242	7.9	421	1	US-09-864-761-4236	Sequence 4236, Ap
88	419	13.6	642	19	US-09-404-284-4030	Sequence 4030, Ap	161	242	7.9	421	33	US-10-183-993-4236	Sequence 4236, Ap
89	419	13.6	642	38	US-10-011-154-4030	Sequence 4030, Ap	162	242	7.9	421	41	US-10-183-993-4236	Sequence 4236, Ap
90	412	13.4	465	39	US-09-528-409-66142	Sequence 66142, A	163	242	7.9	421	41	US-10-183-997-4322	Sequence 4322, Ap
91	412	13.4	465	35	US-09-933-524-66142	Sequence 66142, A	164	242	7.9	421	41	US-10-183-997-4322	Sequence 4322, Ap
92	412	13.4	465	35	US-09-933-524-66142	Sequence 66142, A	165	242	7.9	421	41	US-10-183-998-4204	Sequence 4204, Ap
93	412	13.4	480	16	US-09-235-076-15784	Sequence 15784, A	166	242	7.9	421	42	US-10-203-134-4358	Sequence 4358, Ap
94	412	13.4	480	16	US-09-248-797-36563	Sequence 36563, A	167	242	7.9	421	42	US-10-203-135-4353	Sequence 4353, Ap

168	242	7.9	421	42	US-10-203-136-4438	Sequence 4438, Ap	241	76	2.5	275	21	US-09-540-764-21846	Sequence 21846, A
169	242	7.9	421	42	US-10-203-137-4450	Sequence 4450, Ap	242	60	2.0	60	34	US-09-908-975-13195	Sequence 13195, A
170	242	7.9	421	42	US-10-203-138-4307	Sequence 4307, Ap	243	60	2.0	34	US-09-908-975A-13195	Sequence 13195, A	
171	242	7.9	421	42	US-10-203-139-4424	Sequence 4424, Ap	244	60	2.0	60	72	US-60-287-724-13195	Sequence 13195, A
172	242	7.9	421	67	US-60-236-359-5178	Sequence 5178, Ap	245	50	1.6	200	8	US-08-401-791A-10292	Sequence 10292, A
173	236	7.7	236	14	US-09-010-638-1010	Sequence 1010, Ap	246	50	1.6	200	8	US-08-401-791B-10292	Sequence 10292, A
174	236	7.7	236	20	US-09-534-846B-3440	Sequence 3440, Ap	247	39	1.3	3435	80	US-60-360-207-4654	Sequence 4654, Ap
175	228	7.4	229	7	US-08-373-361A-5375	Sequence 5375, Ap	c 248	29	0.9	29	33	US-09-864-921-160	Sequence 160, App
176	220	7.2	220	1	PCR-US01-00663-17598	Sequence 17590, A	c 249	26	0.8	312	12	US-08-803-610C-7881	Sequence 7881, Ap
177	220	7.2	220	33	US-09-864-761-20988	Sequence 20988, A	c 250	26	0.8	312	12	US-08-803-610D-7881	Sequence 7881, Ap
178	220	7.2	220	41	US-10-182-993-17035	Sequence 17035, A	c 251	26	0.8	312	12	US-08-803-610E-7881	Sequence 7881, Ap
179	220	7.2	220	41	US-10-182-995-14134	Sequence 14134, A	c 252	26	0.8	521	69	US-60-253-652-10892	Sequence 10892, A
180	220	7.2	220	41	US-10-182-997-13523	Sequence 13523, A	253	25	0.8	25	33	US-09-864-921-161	Sequence 161, App
181	220	7.2	220	41	US-10-182-998-9197	Sequence 9197, Ap	c 254	25	0.8	25	33	US-09-864-921-162	Sequence 162, App
182	220	7.2	220	42	US-10-203-134-17385	Sequence 17385, A	255	25	0.8	25	33	US-09-864-921-165	Sequence 165, App
183	220	7.2	220	42	US-10-203-135-16875	Sequence 16875, A	256	24	0.8	24	33	US-09-864-921-159	Sequence 159, App
184	220	7.2	220	42	US-10-203-136-17449	Sequence 17449, A	257	24	0.8	33	33	US-09-864-921-157	Sequence 157, App
185	220	7.2	220	42	US-10-203-137-17590	Sequence 17590, A	c 258	24	0.8	508	25	US-09-652-355-6270	Sequence 6270, Ap
186	220	7.2	220	42	US-10-203-138-9429	Sequence 9429, Ap	c 259	24	0.8	1523	17	US-09-396-970-7819	Sequence 7819, Ap
187	220	7.2	220	42	US-10-203-139-17009	Sequence 17009, Ap	c 260	24	0.8	1523	18	US-09-404-549-4709	Sequence 4709, Ap
188	220	7.2	220	67	US-60-236-359-12476	Sequence 12476, A	c 261	24	0.8	1523	18	US-09-404-549A-4709	Sequence 4709, Ap
189	206	6.7	255	22	US-09-578-789-19	Sequence 19, Appl	262	24	0.8	2583	29	US-09-749-247-13	Sequence 13, Appl
190	206	6.7	255	22	US-09-579-240-19	Sequence 19, Appl	263	24	0.8	2583	43	US-10-268-842-13	Sequence 13, Appl
191	188	6.1	366	18	US-09-489-036-9164	Sequence 9164, Ap	c 264	23	0.7	23	33	US-09-864-921-153	Sequence 153, App
192	188	6.1	366	35	US-09-943-143-9164	Sequence 9164, Ap	265	23	0.7	23	33	US-09-864-921-163	Sequence 163, App
193	186	6.1	488	16	US-09-235-076-33935	Sequence 33935, A	c 266	23	0.7	512	6	US-08-220-691-1757	Sequence 1757, Ap
194	186	6.1	488	16	US-09-277-227-3011	Sequence 3011, Ap	c 267	23	0.7	512	6	US-08-220-691B-1757	Sequence 1757, Ap
195	186	6.1	488	17	US-09-332-782-33935	Sequence 33935, A	c 268	23	0.7	512	31	US-09-813-155-1757	Sequence 1757, Ap
196	186	6.1	488	29	US-09-337-223-33935	Sequence 33935, A	c 269	23	0.7	554	18	US-09-404-549-486	Sequence 486, App
197	186	6.1	488	34	US-09-909-627-3011	Sequence 3011, Ap	c 270	23	0.7	554	18	US-09-404-549A-486	Sequence 486, App
198	186	6.1	488	34	US-09-918-995-33935	Sequence 33935, A	c 271	23	0.7	554	23	US-09-617-182-933	Sequence 933, App
199	183	6.0	192	12	US-08-878-669-2131	Sequence 2131, Ap	c 272	23	0.7	709	25	US-09-652-355-9992	Sequence 9992, Ap
200	176	5.7	417	17	US-09-359-067-47749	Sequence 47749, A	c 273	23	0.7	1046	62	US-60-185-215-4488	Sequence 4488, Ap
201	171	5.6	548	38	US-10-029-386-9153	Sequence 9153, Ap	c 274	23	0.7	1047	22	US-09-585-944-1071	Sequence 1071, Ap
202	149	4.9	251	12	US-08-810-325-2748	Sequence 2748, Ap	c 275	23	0.7	1047	61	US-60-172-360-10437	Sequence 10437, A
203	149	4.9	251	20	US-09-534-846B-3439	Sequence 3439, Ap	c 276	23	0.7	1350	27	US-09-698-012-8420	Sequence 8420, Ap
204	149	4.9	251	45	US-60-012-458-225	Sequence 225, App	c 277	23	0.7	2762	30	US-09-770-174-3223	Sequence 3223, Ap
205	140	4.6	205	12	US-08-823-271-2555	Sequence 2555, Ap	c 278	22	0.7	215	22	US-09-572-409-78440	Sequence 78440, A
206	140	4.6	205	21	US-09-540-764-22408	Sequence 22408, A	c 279	22	0.7	606	18	US-09-428-151A-3571	Sequence 3571, A
207	140	4.6	205	45	US-60-015-513-2555	Sequence 2555, Ap	280	22	0.7	606	23	US-09-614-387-3333	Sequence 3333, Ap
208	135	4.4	458	18	US-09-404-284-142	Sequence 142, App	281	21	0.7	21	33	US-09-864-921-156	Sequence 156, App
209	135	4.4	458	19	US-09-524-038-142	Sequence 142, App	c 282	21	0.7	30	33	US-09-864-921-158	Sequence 158, App
210	135	4.4	458	38	US-10-011-154-142	Sequence 142, App	c 283	21	0.7	121	18	US-09-404-520-17539	Sequence 17539, A
211	114	3.7	165	33	US-09-864-921-183	Sequence 183, App	c 284	21	0.7	264	14	US-09-041-894-2673	Sequence 2673, A
212	110	3.6	500	38	US-10-029-386-11426	Sequence 11426, A	c 285	21	0.7	264	21	US-09-540-210B-1187	Sequence 1187, Ap
213	109	3.5	160	7	US-08-373-361A-818	Sequence 818, App	c 286	21	0.7	264	48	US-60-040-199-2673	Sequence 2673, Ap
214	102	3.3	386	19	US-09-528-409-38106	Sequence 38106, A	c 287	21	0.7	300	23	US-09-605-698-16749	Sequence 16749, A
215	102	3.3	386	35	US-09-933-524-38106	Sequence 38106, A	c 288	21	0.7	300	23	US-09-611-520-5688	Sequence 5688, Ap
216	102	3.3	386	35	US-09-933-524A-38106	Sequence 38106, A	c 289	21	0.7	300	39	US-10-075-564-5688	Sequence 5688, Ap
217	98	3.2	2595	25	US-09-644-869-8962	Sequence 8962, Ap	290	21	0.7	337	16	US-09-289-768-31863	Sequence 31863, A
218	98	3.2	2595	25	US-09-652-122-4263	Sequence 4263, Ap	291	21	0.7	337	35	US-09-939-397-31863	Sequence 31863, A
219	98	3.2	2595	25	US-09-652-123-9442	Sequence 9442, Ap	292	21	0.7	365	22	US-09-565-240-26389	Sequence 26389, A
220	98	3.2	2595	25	US-09-652-913-10693	Sequence 10693, A	293	21	0.7	365	58	US-60-141-136-1316	Sequence 1316, Ap
221	98	3.2	2595	25	US-09-652-914-9400	Sequence 9400, Ap	c 294	21	0.7	426	16	US-09-213-604B-5419	Sequence 5419, Ap
222	98	3.2	2595	25	US-09-652-918-8327	Sequence 8327, Ap	c 295	21	0.7	426	23	US-09-605-698-9026	Sequence 9026, Ap
223	98	3.2	2595	26	US-09-667-617-1970	Sequence 1970, Ap	c 296	21	0.7	426	23	US-09-611-520-2814	Sequence 2814, Ap
224	98	3.2	2595	27	US-09-699-998-10530	Sequence 10530, A	c 297	21	0.7	426	39	US-10-075-564-2814	Sequence 2814, Ap
225	98	3.2	2595	28	US-09-700-000-5800	Sequence 5800, Ap	298	21	0.7	449	19	US-09-521-640-111312	Sequence 111312
226	98	3.2	2595	28	US-09-710-286-4037	Sequence 4037, Ap	299	21	0.7	450	31	US-09-804-730-2425	Sequence 2425, Ap
227	98	3.2	2595	28	US-09-716-953-2586	Sequence 2586, Ap	300	21	0.7	450	62	US-60-189-657-2425	Sequence 2425, Ap
228	98	3.2	2595	29	US-09-721-589-6951	Sequence 6951, Ap	301	21	0.7	471	19	US-09-521-640-231002	Sequence 231002
229	98	3.2	2595	29	US-09-726-802-2827	Sequence 2827, Ap	302	21	0.7	471	58	US-60-140-769-30093	Sequence 30093, A
230	93	3.0	507	22	US-09-557-676-909	Sequence 909, App	303	21	0.7	483	29	US-09-728-445-337	Sequence 337, App
231	93	3.0	507	22	US-09-557-676-915	Sequence 915, App	c 304	21	0.7	497	16	US-09-750-456-337	Sequence 337, App
232	93	3.0	507	38	US-10-042-938-909	Sequence 909, App	c 305	21	0.7	497	16	US-09-213-604B-1365	Sequence 1365, Ap
233	93	3.0	507	38	US-10-042-938-915	Sequence 915, App	c 306	21	0.7	497	23	US-09-698-9362	Sequence 9362, Ap
234	92	3.0	414	18	US-09-404-284-109	Sequence 109, App	c 307	21	0.7	497	23	US-09-611-520-2772	Sequence 2772, Ap
235	92	3.0	414	19	US-09-524-038-109	Sequence 109, App	c 308	21	0.7	497	39	US-10-075-564-2772	Sequence 2772, Ap
236	92	3.0	414	38	US-10-011-154-109	Sequence 109, App	309	21	0.7	531	57	US-60-132-861-13489	Sequence 13489, A
237	90	2.9	412	18	US-09-489-036-30982	Sequence 30982, A	310	21	0.7	531	57	US-60-138-103-13273	Sequence 13273, A
238	90	2.9	412	35	US-09-943-143-30982	Sequence 30982, A	311	21	0.7	538	62	US-60-184-771-765	Sequence 765, App
239	76	2.5	275	11	US-08-792-739-868	Sequence 868, App	312	21	0.7	580	19	US-09-505-532-41223	Sequence 41223, A
240	76	2.5	275	13	US-08-951-195-868	Sequence 868, App	313	21	0.7	580	31	US-09-819-091A-41223	Sequence 41223, A

c 314	21	0.7	1222	18	US-09-404-520-7149	Sequence 7149, Ap	c 387	19	0.6	221	23	US-09-605-702-13997	Sequence 13997, A
c 315	21	0.7	1622	38	US-10-015-127-2687	Sequence 2687, Ap	c 388	19	0.6	229	25	US-09-539-806-5282	Sequence 5282, Ap
c 316	21	0.7	2961	16	US-09-248-796-1267	Sequence 1255, Ap	c 389	19	0.6	230	25	US-09-654-617-49153	Sequence 49153, A
c 317	21	0.7	2961	53	US-60-096-409-1255	Sequence 1255, Ap	c 390	19	0.6	230	25	US-09-684-016-49153	Sequence 49153, A
c 318	21	0.7	5097	41	US-10-179-131-1688	Sequence 1688, Ap	c 391	19	0.6	233	26	US-09-244-000A-98929	Sequence 98929, A
c 319	21	0.7	80346	21	US-09-534-859-669	Sequence 669, App	c 392	19	0.6	233	26	US-09-678-703-98929	Sequence 98929, A
c 320	21	0.7	80346	21	US-09-534-859-669	Sequence 669, App	c 393	19	0.6	236	17	US-09-304-517A-121002	Sequence 121002, A
c 321	21	0.7	84499	20	US-09-534-859-670	Sequence 670, App	c 394	19	0.6	236	17	US-09-371-146A-121002	Sequence 121002, A
c 322	21	0.7	84499	31	US-09-534-859-670	Sequence 670, App	c 395	19	0.6	256	37	US-09-985-678-121002	Sequence 121002, A
c 323	21	0.7	86710	31	US-09-534-859-671	Sequence 671, App	c 396	19	0.6	256	37	US-09-985-678-121002	Sequence 121002, A
c 324	21	0.7	86710	31	US-09-534-859-671	Sequence 671, App	c 397	19	0.6	289	20	US-09-535-896-32146	Sequence 32146, A
c 325	21	0.7	351576	19	US-09-528-237A-1489	Sequence 1489, Ap	c 398	19	0.6	305	63	US-08-197-872-56992	Sequence 56992, A
c 326	20	0.7	240	64	US-60-207-458-6596	Sequence 6596, Ap	c 399	19	0.6	309	11	US-08-761-066-236	Sequence 236, App
c 327	20	0.7	302	14	US-09-070-694-897	Sequence 897, Ap	c 400	19	0.6	321	13	US-08-993-002A-1573	Sequence 1573, App
c 328	20	0.7	302	14	US-09-070-694-897	Sequence 897, Ap	c 401	19	0.6	321	13	US-08-993-002A-1573	Sequence 1573, App
c 329	20	0.7	321	25	US-09-654-617-180545	Sequence 180545, A	c 402	19	0.6	329	17	US-09-534-840-695	Sequence 60870, A
c 330	20	0.7	321	25	US-09-654-617-180545	Sequence 180545, A	c 403	19	0.6	329	17	US-09-534-840-695	Sequence 60870, A
c 331	20	0.7	333	64	US-60-207-458-18913	Sequence 18913, A	c 404	19	0.6	345	29	US-09-388-906A-20870	Sequence 4224, Ap
c 332	20	0.7	333	64	US-60-207-458-18913	Sequence 18913, A	c 405	19	0.6	345	29	US-09-514-000-4224	Sequence 4224, Ap
c 333	20	0.7	370	18	US-09-440-687-1492	Sequence 1492, Ap	c 406	19	0.6	345	29	US-09-739-449-5752	Sequence 5752, Ap
c 334	20	0.7	370	18	US-09-440-687-1492	Sequence 1492, Ap	c 407	19	0.6	351	31	US-09-803-110-5752	Sequence 5752, Ap
c 335	20	0.7	405	62	US-60-144-084-30387	Sequence 30387, A	c 408	19	0.6	351	25	US-09-654-617-40356	Sequence 40356, A
c 336	20	0.7	423	16	US-09-185-215-4134	Sequence 4124, Ap	c 409	19	0.6	351	25	US-09-654-617-40356	Sequence 40356, A
c 337	20	0.7	423	16	US-09-229-413B-1907	Sequence 1907, Ap	c 410	19	0.6	351	25	US-09-654-617-40356	Sequence 40356, A
c 338	20	0.7	430	22	US-09-922-293-1907	Sequence 1907, Ap	c 411	19	0.6	351	25	US-09-654-617-40356	Sequence 40356, A
c 339	20	0.7	431	30	US-09-572-409-56345	Sequence 56345, A	c 412	19	0.6	351	25	US-09-654-617-40356	Sequence 40356, A
c 340	20	0.7	439	17	US-09-785-276A-46682	Sequence 46682, A	c 413	19	0.6	372	13	US-08-993-002A-1573	Sequence 1573, App
c 341	20	0.7	439	17	US-09-304-517A-100977	Sequence 100977, A	c 414	19	0.6	392	22	US-09-565-240-38119	Sequence 38119, A
c 342	20	0.7	439	17	US-09-304-517A-100977	Sequence 100977, A	c 415	19	0.6	395	17	US-09-362-510-35891	Sequence 35891, A
c 343	20	0.7	439	22	US-09-365-306-69634	Sequence 69634, A	c 416	19	0.6	395	17	US-09-362-510-35891	Sequence 35891, A
c 344	20	0.7	439	37	US-09-585-678-100977	Sequence 100977, A	c 417	19	0.6	395	34	US-09-904-013-35891	Sequence 35891, A
c 345	20	0.7	460	23	US-09-605-701-985	Sequence 985, App	c 418	19	0.6	397	1	PCT-US03-25766-10041	Sequence 10041, A
c 346	20	0.7	492	36	US-09-974-300-6263	Sequence 6263, Ap	c 419	19	0.6	406	26	US-09-666-355A-22423	Sequence 22423, A
c 347	20	0.7	492	6	US-08-276-163B-6495	Sequence 6495, Ap	c 420	19	0.6	406	26	US-09-666-355A-22423	Sequence 22423, A
c 348	20	0.7	492	6	US-08-276-163B-6495	Sequence 6495, Ap	c 421	19	0.6	407	25	US-09-654-617-199629	Sequence 199629, A
c 349	20	0.7	492	32	US-09-840-145-6495	Sequence 6495, Ap	c 422	19	0.6	407	25	US-09-654-617-199629	Sequence 199629, A
c 350	20	0.7	496	23	US-09-605-701-798	Sequence 798, App	c 423	19	0.6	408	22	US-09-572-409-71409	Sequence 71409, A
c 351	20	0.7	583	24	US-09-504-576A-9938	Sequence 9938, Ap	c 424	19	0.6	408	24	US-09-637-086A-1396	Sequence 1396, Ap
c 352	20	0.7	715	19	US-09-686-347-102	Sequence 102, App	c 425	19	0.6	408	24	US-09-637-086A-1396	Sequence 1396, Ap
c 353	20	0.7	768	27	US-09-864-921-102	Sequence 102, App	c 426	19	0.6	408	27	US-09-654-617-203912	Sequence 203912, A
c 354	20	0.7	1036	33	US-09-614-150-36103	Sequence 36103, A	c 427	19	0.6	409	16	US-09-293-972-4061	Sequence 4061, Ap
c 355	20	0.7	1036	33	US-09-614-150-36103	Sequence 36103, A	c 428	19	0.6	409	16	US-09-293-972-4061	Sequence 4061, Ap
c 356	20	0.7	3946	63	US-60-173-464-22228	Sequence 22228, A	c 429	19	0.6	409	34	US-09-904-939-4061	Sequence 13274, A
c 357	20	0.7	3946	63	US-60-191-681-28901	Sequence 28901, A	c 430	19	0.6	410	16	US-09-287-618-13274	Sequence 13274, A
c 358	20	0.7	4309	60	US-60-167-217-3594	Sequence 3594, Ap	c 431	19	0.6	421	42	US-10-206-272-98	Sequence 98, Appl
c 359	20	0.7	4309	60	US-60-167-217-3594	Sequence 3594, Ap	c 432	19	0.6	421	42	US-10-206-272-98	Sequence 98, Appl
c 360	20	0.7	4737	23	US-09-614-150-3532	Sequence 3532, Ap	c 433	19	0.6	424	16	US-09-234-611-644	Sequence 644, App
c 361	20	0.7	4737	23	US-09-614-150-3532	Sequence 3532, Ap	c 434	19	0.6	424	16	US-09-234-611-644	Sequence 644, App
c 362	20	0.7	4737	61	US-60-171-625-70	Sequence 70, Appl	c 435	19	0.6	424	16	US-09-248-797-23880	Sequence 23880, A
c 363	20	0.7	4737	61	US-60-171-625-70	Sequence 70, Appl	c 436	19	0.6	424	17	US-09-332-782-7049	Sequence 7049, Ap
c 364	20	0.7	4737	61	US-60-171-625-70	Sequence 70, Appl	c 437	19	0.6	424	29	US-09-737-223-7049	Sequence 7049, Ap
c 365	20	0.7	4737	61	US-60-171-625-70	Sequence 70, Appl	c 438	19	0.6	424	34	US-09-904-809-644	Sequence 644, App
c 366	20	0.7	4737	63	US-60-191-681-2839	Sequence 2839, Ap	c 439	19	0.6	424	34	US-09-918-995-7049	Sequence 7049, Ap
c 367	20	0.7	16704	24	US-09-620-392-42788	Sequence 42788, A	c 440	19	0.6	424	34	US-09-925-564-23880	Sequence 23880, A
c 368	20	0.7	16704	24	US-09-620-392-42788	Sequence 42788, A	c 441	19	0.6	424	34	US-09-925-564-23880	Sequence 23880, A
c 369	20	0.7	17469	31	US-09-815-264-65020	Sequence 65020, A	c 442	19	0.6	429	66	US-60-169-403-135	Sequence 135, App
c 370	20	0.7	17469	31	US-09-815-264-65020	Sequence 65020, A	c 443	19	0.6	431	1	PCT-US01-01334-1908	Sequence 1908, Ap
c 371	20	0.7	19321	28	US-09-702-134-5751	Sequence 5751, Ap	c 444	19	0.6	431	30	US-09-764-874-1908	Sequence 1908, Ap
c 372	20	0.7	19321	28	US-09-702-134-5751	Sequence 5751, Ap	c 445	19	0.6	431	30	US-09-764-874-1908	Sequence 1908, Ap
c 373	20	0.7	69509	34	US-09-620-392-68308	Sequence 68308, A	c 446	19	0.6	433	16	US-10-092-400-1908	Sequence 1908, Ap
c 374	20	0.7	69509	34	US-09-620-392-68308	Sequence 68308, A	c 447	19	0.6	433	16	US-10-092-400-1908	Sequence 1908, Ap
c 375	20	0.7	69911	28	US-09-702-134-6576	Sequence 6576, Ap	c 448	19	0.6	441	22	US-09-939-397-4341	Sequence 4341, Ap
c 376	20	0.7	69911	28	US-09-702-134-6576	Sequence 6576, Ap	c 449	19	0.6	441	22	US-09-939-397-4341	Sequence 4341, Ap
c 377	20	0.7	21832	68	US-60-243-468-81650	Sequence 81650, Ap	c 450	19	0.6	451	25	US-09-572-409-50093	Sequence 50093, A
c 378	20	0.7	243630	19	US-09-528-237A-1180	Sequence 349, App	c 451	19	0.6	451	25	US-09-572-409-50093	Sequence 50093, A
c 379	20	0.7	2840917	24	US-09-634-306B-174763	Sequence 174763, A	c 452	19	0.6	455	25	US-09-684-016-387758	Sequence 387758, A
c 380	19	0.6	71	23	US-10-021-632-174763	Sequence 174763, A	c 453	19	0.6	455	25	US-09-684-016-387758	Sequence 387758, A
c 381	19	0.6	80	58	US-60-146-905-2262	Sequence 2262, Ap	c 454	19	0.6	455	25	US-09-684-016-387758	Sequence 387758, A
c 382	19	0.6	185	12	US-08-823-271-1965	Sequence 1965, Ap	c 455	19	0.6	460	6	US-09-605-700-500	Sequence 5000, App
c 383	19	0.6	185	21	US-09-540-764-370	Sequence 370, App	c 456	19	0.6	460	31	US-08-220-691B-10000	Sequence 10000, A
c 384	19	0.6	185	45	US-60-015-513-1965	Sequence 1965, Ap	c 457	19	0.6	464	22	US-09-813-155-10000	Sequence 10000, A
c 385	19	0.6	188	63	US-09-197-872-4346	Sequence 4346, Ap	c 458	19	0.6	464	22	US-09-399-720-16058	Sequence 16058, A
c 386	19	0.6	188	27	US-09-685-045-429	Sequence 429, App	c 459	19	0.6	464	34	US-09-921-378-16058	Sequence 16058, A
										468	17	US-09-362-510-4985	Sequence 4985, Ap

460	19	0.6	468	17	US-09-362-510A-4985	Sequence 4985, Ap	533	19	0.6	1044	18	US-09-428-944-905	Sequence 905, App
461	19	0.6	468	34	US-09-904-013-4985	Sequence 4985, Ap	534	19	0.6	1099	24	US-09-634-306B-118099	Sequence 118099,
462	19	0.6	470	32	US-09-843-620-708	Sequence 708, App	535	19	0.6	1099	38	US-10-027-632-118099	Sequence 118099,
463	19	0.6	477	23	US-09-607-200-455	Sequence 455, App	536	19	0.6	1416	18	US-09-428-944-1395	Sequence 1395, Ap
464	19	0.6	478	19	US-09-521-640-168795	Sequence 168795,	c 537	19	0.6	1425	1	PCT-US02-10522-63	Sequence 63, Appl
465	19	0.6	480	24	US-09-634-306B-4089	Sequence 4089, Ap	c 538	19	0.6	1435	58	US-10-115-482-63	Sequence 63, Appl
466	19	0.6	480	24	US-09-634-306B-4090	Sequence 4090, Ap	539	19	0.6	1430	58	US-60-144-351-541	Sequence 541, App
467	19	0.6	480	38	US-10-027-632-4089	Sequence 4089, Ap	540	19	0.6	1501	31	US-09-815-264-8837	Sequence 8837, Ap
468	19	0.6	480	38	US-10-027-632-4090	Sequence 4090, Ap	541	19	0.6	1501	31	US-09-815-264-47717	Sequence 47717, A
469	19	0.6	480	69	US-60-253-654-21143	Sequence 21143, A	542	19	0.6	1574	24	US-09-620-392-54056	Sequence 54056, A
470	19	0.6	480	69	US-60-255-592-21143	Sequence 21143, A	543	19	0.6	1619	27	US-09-699-997-10297	Sequence 10297, A
471	19	0.6	483	23	US-09-605-700-609	Sequence 609, App	544	19	0.6	1780	1	PCT-US01-04942A-469	Sequence 469, App
472	19	0.6	503	17	US-09-304-517A-216097	Sequence 216097,	545	19	0.6	1780	19	US-09-519-705-5525	Sequence 5525, Ap
473	19	0.6	503	22	US-09-552-086-13036	Sequence 13036, A	546	19	0.6	1780	22	US-09-574-454-5525	Sequence 5525, Ap
474	19	0.6	503	22	US-09-552-086-13036	Sequence 13036, A	547	19	0.6	1780	42	US-10-221-278-469	Sequence 469, App
475	19	0.6	511	20	US-09-539-802A-2357	Sequence 2357, Ap	c 548	19	0.6	1863	16	US-09-248-796-6543	Sequence 6543, Ap
476	19	0.6	511	20	US-09-539-802A-2357	Sequence 2357, Ap	c 549	19	0.6	1863	41	US-10-179-131-3052	Sequence 3052, Ap
477	19	0.6	514	25	US-09-654-617-187439	Sequence 187439,	c 550	19	0.6	1863	53	US-60-096-409-6543	Sequence 6543, Ap
478	19	0.6	514	27	US-09-684-016-187439	Sequence 187439,	551	19	0.6	1908	20	US-09-533-559-5621	Sequence 5621, Ap
479	19	0.6	516	69	US-60-253-654-2899	Sequence 2899, Ap	552	19	0.6	2005	58	US-60-140-803-227	Sequence 227, App
480	19	0.6	516	69	US-60-255-592-2899	Sequence 2899, Ap	553	19	0.6	2132	24	US-09-620-392-9532	Sequence 9532, Ap
481	19	0.6	516	24	US-09-629-469A-8287	Sequence 8287, Ap	554	19	0.6	2221	71	US-60-278-258-12415	Sequence 12415, A
482	19	0.6	556	17	US-09-397-424-2185	Sequence 2185, Ap	c 555	19	0.6	2438	25	US-09-644-868-8042	Sequence 8042, Ap
483	19	0.6	556	17	US-09-397-424A-2185	Sequence 2185, Ap	c 556	19	0.6	2438	25	US-09-652-913-8436	Sequence 8436, Ap
484	19	0.6	556	31	US-09-824-518-5688	Sequence 5688, Ap	c 557	19	0.6	2475	17	US-09-399-932-5172	Sequence 5172, Ap
485	19	0.6	563	69	US-60-253-654-12310	Sequence 12310, A	c 558	19	0.6	2539	23	US-09-607-200-6644	Sequence 6644, Ap
486	19	0.6	563	69	US-60-253-654-12310	Sequence 12310, A	559	19	0.6	2591	25	US-09-644-868-9637	Sequence 9637, Ap
487	19	0.6	565	22	US-09-592-12310	Sequence 12310, A	560	19	0.6	2603	22	US-09-572-411-6747	Sequence 6747, Ap
488	19	0.6	565	22	US-09-605-700-608	Sequence 608, App	c 561	19	0.6	2825	24	US-09-629-469A-15005	Sequence 15005, A
489	19	0.6	567	21	US-09-572-411-3585	Sequence 3585, Ap	562	19	0.6	3217	23	US-09-614-150-11341	Sequence 11341, A
490	19	0.6	567	21	US-09-540-229-126232	Sequence 126232,	563	19	0.6	3217	61	US-60-173-464-9197	Sequence 9197, A
491	19	0.6	571	24	US-09-634-306B-321654	Sequence 321654,	564	19	0.6	3217	63	US-60-191-637-11373	Sequence 11373, A
492	19	0.6	571	24	US-09-634-306B-321655	Sequence 321655,	565	19	0.6	3217	63	US-60-191-681-8907	Sequence 8907, Ap
493	19	0.6	571	38	US-10-027-632-321654	Sequence 321654,	566	19	0.6	3235	60	US-60-167-217-11369	Sequence 11369, A
494	19	0.6	579	1	US-10-027-632-321655	Sequence 321655,	567	19	0.6	3307	58	US-60-144-351-2304	Sequence 2304, Ap
495	19	0.6	579	1	PCT-US97-22104-83	Sequence 83, Appl	c 568	19	0.6	3861	18	US-09-428-944-892	Sequence 892, App
496	19	0.6	579	12	US-08-823-745-1590	Sequence 1590, App	569	19	0.6	4042	65	US-60-213-847-282	Sequence 282, App
497	19	0.6	585	13	US-08-993-002A-1575	Sequence 1575, Ap	c 570	19	0.6	4275	58	US-60-145-138-37	Sequence 37, Appl
498	19	0.6	585	24	US-09-634-306B-212537	Sequence 212537,	c 571	19	0.6	4275	58	US-60-146-394-47	Sequence 47, Appl
499	19	0.6	590	38	US-10-027-632-212537	Sequence 212537,	572	19	0.6	4710	16	US-09-205-070-9150	Sequence 9150, Ap
500	19	0.6	590	69	US-60-253-654-2841	Sequence 2841, Ap	573	19	0.6	4710	17	US-09-340-623-9150	Sequence 9150, Ap
501	19	0.6	590	69	US-60-255-592-2841	Sequence 2841, Ap	574	19	0.6	4710	33	US-09-898-888-9150	Sequence 9150, Ap
502	19	0.6	593	29	US-09-758-473-482	Sequence 482, App	575	19	0.6	4710	33	US-09-898-888A-9150	Sequence 9150, Ap
503	19	0.6	593	42	US-10-222-939-482	Sequence 482, App	576	19	0.6	4717	18	US-09-428-944-1384	Sequence 1384, Ap
504	19	0.6	601	25	US-09-654-617-187282	Sequence 187282,	c 577	19	0.6	5189	1	PCT-US99-22855-2241	Sequence 2241, Ap
505	19	0.6	601	27	US-09-684-016-187282	Sequence 187282,	578	19	0.6	5557	65	US-60-213-847-391	Sequence 391, App
506	19	0.6	601	35	US-09-948-933-5069	Sequence 5069, Ap	579	19	0.6	5557	65	US-60-213-847-392	Sequence 392, App
507	19	0.6	601	61	US-60-172-376-2815	Sequence 2815, Ap	c 580	19	0.6	5581	28	US-09-702-134-15506	Sequence 15506, A
508	19	0.6	620	24	US-09-634-306B-189751	Sequence 189751,	c 581	19	0.6	5581	31	US-09-815-264-78176	Sequence 78176, A
509	19	0.6	620	38	US-10-027-632-189751	Sequence 189751,	c 582	19	0.6	6316	18	US-09-496-914A-4587	Sequence 4587, Ap
510	19	0.6	625	24	US-09-634-306B-226909	Sequence 226909,	c 583	19	0.6	6316	22	US-09-560-875A-4587	Sequence 4587, Ap
511	19	0.6	625	24	US-09-634-306B-226910	Sequence 226910,	c 584	19	0.6	6408	24	US-09-620-392-54052	Sequence 54052, A
512	19	0.6	625	38	US-10-027-632-226909	Sequence 226909,	585	19	0.6	6445	24	US-09-620-392-20633	Sequence 20633, A
513	19	0.6	625	38	US-10-027-632-226910	Sequence 226910,	586	19	0.6	6445	28	US-09-702-134-10631	Sequence 10631, A
514	19	0.6	634	22	US-09-572-411-3589	Sequence 3589, Ap	587	19	0.6	6445	31	US-09-815-264-86815	Sequence 86815, A
515	19	0.6	634	60	US-60-162-247-1637	Sequence 1637, Ap	588	19	0.6	7031	24	US-09-620-392-20621	Sequence 20621, A
516	19	0.6	649	1	PCT-US98-06371-1051	Sequence 1051, Ap	589	19	0.6	7031	31	US-09-702-134-10649	Sequence 10649, A
517	19	0.6	649	13	US-08-902-615A-317	Sequence 317, App	590	19	0.6	7031	31	US-09-815-264-68427	Sequence 68427, A
518	19	0.6	649	33	US-09-882-227-317	Sequence 317, App	591	19	0.6	7163	17	US-09-359-922-257	Sequence 257, App
519	19	0.6	666	28	US-09-708-427-24169	Sequence 24169, A	592	19	0.6	7163	17	US-09-359-922-257	Sequence 257, App
520	19	0.6	677	63	US-60-196-718-2252	Sequence 2252, Ap	593	19	0.6	7163	34	US-09-919-003-257	Sequence 257, App
521	19	0.6	677	63	US-60-196-718-2253	Sequence 2253, Ap	c 594	19	0.6	8095	24	US-09-620-392-42020	Sequence 42020, A
522	19	0.6	677	63	US-60-196-718-2254	Sequence 2254, Ap	c 595	19	0.6	8095	28	US-09-702-134-8727	Sequence 8727, Ap
523	19	0.6	677	63	US-60-196-718-2255	Sequence 2255, Ap	c 596	19	0.6	8095	31	US-09-815-264-86543	Sequence 86543, A
524	19	0.6	677	63	US-60-196-718-3126	Sequence 3126, Ap	597	19	0.6	10204	24	US-09-620-392-42152	Sequence 42152, A
525	19	0.6	734	60	US-60-162-247-573	Sequence 573, App	598	19	0.6	10204	28	US-09-702-134-1874	Sequence 1874, Ap
526	19	0.6	744	63	US-60-197-872-46936	Sequence 46936, A	599	19	0.6	10204	31	US-09-815-264-69896	Sequence 69896, A
527	19	0.6	759	18	US-09-406-292A-1947	Sequence 1947, Ap	600	19	0.6	10757	19	US-09-514-000-235	Sequence 235, App
528	19	0.6	868	33	US-09-861-478-7055	Sequence 7055, Ap	601	19	0.6	10917	33	US-09-871-107-1	Sequence 1, Appl1
529	19	0.6	876	21	US-09-540-209B-1452	Sequence 1452, Ap	602	19	0.6	10917	41	US-10-195-963-1	Sequence 1, Appl1
530	19	0.6	912	10	US-08-621-425-23	Sequence 23, Appl	603	19	0.6	10917	64	US-60-209-394-1	Sequence 1, Appl1
531	19	0.6	1034	1	PCT-US01-08631-6388	Sequence 6388, Ap	604	19	0.6	11195	24	US-09-620-392-48482	Sequence 48482, A
532	19	0.6	1035	28	US-09-708-427-28012	Sequence 28012, A	c 605	19	0.6	11486	28	US-09-702-134-13129	Sequence 13129, A

c 606	19	0.6	11486	31	US-09-815-264-61067	Sequence 61067, A	18	0.6	96	28	US-09-704-424-20514	Sequence 20514, A
c 607	19	0.6	11518	24	US-09-620-392-20209	Sequence 20209, A	18	0.6	107	13	US-08-918-972-1242	Sequence 1242, Ap
c 608	19	0.6	13020	24	US-09-620-392-13955	Sequence 13955, A	18	0.6	107	21	US-09-540-766-39613	Sequence 39613, A
c 609	19	0.6	13020	28	US-09-702-134-28825	Sequence 28825, A	18	0.6	107	46	US-60-025-133-1242	Sequence 1242, Ap
c 610	19	0.6	13020	31	US-09-815-264-77553	Sequence 77553, A	18	0.6	115	12	US-08-885-2208-3447	Sequence 3447, Ap
c 611	19	0.6	13633	59	US-60-150-584-106	Sequence 101, App	18	0.6	115	21	US-09-540-229-41541	Sequence 41541, A
c 612	19	0.6	13633	59	US-60-150-584-306	Sequence 306, App	18	0.6	115	46	US-60-020-591-3447	Sequence 3447, Ap
c 613	19	0.6	14306	65	US-60-213-177-392	Sequence 392, App	18	0.6	124	26	US-09-677-367-502	Sequence 502, App
c 614	19	0.6	14346	1	PCT-US01-01335-505	Sequence 505, App	18	0.6	135	14	US-09-093-822-1361	Sequence 1361, Ap
c 615	19	0.6	14346	39	US-10-074-024-505	Sequence 505, App	18	0.6	135	21	US-08-540-499-28675	Sequence 28675, A
c 616	19	0.6	15109	67	US-60-230-445-306	Sequence 306, App	18	0.6	135	21	US-08-540-499-28675	Sequence 28675, A
c 617	19	0.6	16250	19	US-09-528-2378-1854	Sequence 1854, App	18	0.6	135	21	US-08-540-499-28675	Sequence 28675, A
c 618	19	0.6	18963	68	US-60-348-498-6	Sequence 6, Appl	18	0.6	135	21	US-08-540-499-28675	Sequence 28675, A
c 619	19	0.6	23928	69	US-60-258-275-157	Sequence 157, App	18	0.6	135	21	US-08-540-499-28675	Sequence 28675, A
c 620	19	0.6	23943	28	US-09-620-392-23760	Sequence 23760, A	18	0.6	137	20	US-09-539-3310-22882	Sequence 22882, A
c 621	19	0.6	23943	28	US-09-702-134-24858	Sequence 24858, A	18	0.6	137	20	US-09-539-3310-22882	Sequence 22882, A
c 622	19	0.6	23943	31	US-09-815-264-76955	Sequence 76955, A	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 623	19	0.6	25570	64	US-60-207-583-4	Sequence 4, Appl	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 624	19	0.6	25620	67	US-60-230-445-787	Sequence 787, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 625	19	0.6	28665	85	US-60-413-583-40	Sequence 40, Appl	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 626	19	0.6	29064	65	US-60-212-358-70	Sequence 70, Appl	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 627	19	0.6	29814	65	US-60-212-655-325	Sequence 325, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 628	19	0.6	30310	1	PCT-US01-27316-96	Sequence 96, Appl	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 629	19	0.6	30310	25	US-09-657-346A-96	Sequence 96, Appl	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 630	19	0.6	30310	31	US-09-800-631-96	Sequence 96, Appl	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 631	19	0.6	32768	65	US-60-212-655-326	Sequence 326, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 632	19	0.6	32768	65	US-60-213-177-245	Sequence 245, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 633	19	0.6	32768	66	US-60-229-515-168	Sequence 168, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 634	19	0.6	32768	67	US-60-230-435-535	Sequence 535, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 635	19	0.6	32768	67	US-60-230-445-731	Sequence 731, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 636	19	0.6	32768	67	US-60-230-445-783	Sequence 783, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 637	19	0.6	32768	67	US-60-233-644-1	Sequence 1, Appl	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 638	19	0.6	35806	24	US-09-620-392-43786	Sequence 43786, A	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 639	19	0.6	35806	28	US-09-702-134-21781	Sequence 21781, A	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 640	19	0.6	35806	31	US-08-915-264-63788	Sequence 63788, A	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 641	19	0.6	38593	28	US-09-702-134-7480	Sequence 7480, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 642	19	0.6	38593	31	US-09-815-264-64552	Sequence 64552, A	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 643	19	0.6	38658	28	US-60-144-351-296	Sequence 296, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 644	19	0.6	42303	68	US-60-248-498-75	Sequence 75, Appl	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 645	19	0.6	42303	68	US-60-248-498-75	Sequence 75, Appl	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 646	19	0.6	42303	68	US-60-248-498-75	Sequence 75, Appl	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 647	19	0.6	79684	38	US-10-034-650-40	Sequence 40, Appl	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 648	19	0.6	83698	38	US-10-035-832-1592	Sequence 1592, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 649	19	0.6	83698	38	US-09-534-859-806	Sequence 806, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 650	19	0.6	83698	31	US-09-803-736-806	Sequence 806, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 651	19	0.6	90902	20	US-09-534-859-653	Sequence 653, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 652	19	0.6	90902	31	US-09-803-736-653	Sequence 653, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 653	19	0.6	96589	37	US-09-597-722-220	Sequence 220, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 654	19	0.6	96589	38	US-10-035-832-1472	Sequence 1472, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 655	19	0.6	100626	68	US-60-243-468-664	Sequence 664, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 656	19	0.6	104364	20	US-09-534-859-337	Sequence 337, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 657	19	0.6	104364	31	US-09-803-736-337	Sequence 337, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 658	19	0.6	125497	35	US-09-534-859-583	Sequence 583, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 659	19	0.6	162850	65	US-60-212-664-52	Sequence 52, Appl	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 660	19	0.6	176787	65	US-60-212-664-184	Sequence 184, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 661	19	0.6	199261	33	US-09-881-797-712	Sequence 712, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 662	19	0.6	199261	33	US-10-021-698-712	Sequence 712, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 663	19	0.6	219490	33	US-09-881-797-714	Sequence 714, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 664	19	0.6	219490	33	US-10-021-698-714	Sequence 714, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 665	19	0.6	21245	66	US-60-226-176-125	Sequence 125, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 666	19	0.6	21245	66	US-60-233-468-125	Sequence 125, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 667	19	0.6	21245	66	US-60-313-371-125	Sequence 125, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 668	19	0.6	289698	75	US-60-242-679-216	Sequence 216, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 669	19	0.6	374732	21	US-09-739-449-216	Sequence 216, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 670	19	0.6	374732	21	US-09-739-449-216	Sequence 216, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 671	19	0.6	948061	14	US-09-012-031-317	Sequence 317, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 672	19	0.6	948061	14	US-09-012-031-317	Sequence 317, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 673	19	0.6	948061	14	US-09-012-031-317	Sequence 317, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 674	19	0.6	948061	17	US-09-335-032-12319	Sequence 12319, A	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 675	19	0.6	955191	17	US-09-528-2378-1340	Sequence 1340, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 676	18	0.6	21	33	US-09-864-921-155	Sequence 155, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 677	18	0.6	51	61	US-60-172-373-11118	Sequence 11118, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A
c 678	18	0.6	64	61	US-60-172-373-4164	Sequence 4164, App	18	0.6	141	25	US-09-684-016-375590	Sequence 375590, A

c 752	18	0.6	224	21	US-09-540-766-12455	Sequence 12455, A	c 825	18	0.6	255	37	US-09-985-678-284017	Sequence 284017, A
c 753	18	0.6	225	13	US-08-951-196A-1590	Sequence 1590, Ap	c 826	18	0.6	255	54	US-60-108-396-1337	Sequence 1337, Ap
c 754	18	0.6	225	20	US-09-534-846B-28014	Sequence 28014, A	c 827	18	0.6	256	13	US-08-992-868-2625	Sequence 2625, Ap
c 755	18	0.6	228	13	US-08-922-315-3126	Sequence 3126, Ap	c 828	18	0.6	256	17	US-09-304-517A-154602	Sequence 154602, A
c 756	18	0.6	228	20	US-09-534-846B-28044	Sequence 28044, A	c 829	18	0.6	256	17	US-09-304-517A-164386	Sequence 164386, A
c 757	18	0.6	233	14	US-09-015-080-3908	Sequence 3908, Ap	c 830	18	0.6	256	17	US-09-371-146A-154602	Sequence 154602, A
c 758	18	0.6	233	20	US-09-534-846B-28099	Sequence 28099, A	c 831	18	0.6	256	17	US-09-371-146A-154602	Sequence 154602, A
c 759	18	0.6	233	33	US-09-866-555-16289	Sequence 16289, A	c 832	18	0.6	256	21	US-09-540-764-39303	Sequence 39303, A
c 760	18	0.6	234	15	US-09-167-461-2202	Sequence 2202, Ap	c 833	18	0.6	256	37	US-09-985-678-154602	Sequence 154602, A
c 761	18	0.6	234	20	US-09-535-896-28336	Sequence 28336, A	c 834	18	0.6	256	37	US-09-985-678-164386	Sequence 164386, A
c 762	18	0.6	235	33	US-08-866-555-16284	Sequence 16284, A	c 835	18	0.6	257	16	US-09-244-000A-72260	Sequence 72260, A
c 763	18	0.6	236	14	US-09-035-169-2193	Sequence 2193, Ap	c 836	18	0.6	257	29	US-09-724-750-22097	Sequence 22097, A
c 764	18	0.6	236	21	US-09-540-766-46294	Sequence 46294, A	c 837	18	0.6	257	36	US-09-978-703-72260	Sequence 72260, A
c 765	18	0.6	236	47	US-60-039-415-2193	Sequence 2193, Ap	c 838	18	0.6	257	61	US-60-171-431-22097	Sequence 22097, A
c 766	18	0.6	238	14	US-09-035-169-675	Sequence 675, App	c 839	18	0.6	258	11	US-08-740-370-187	Sequence 187, App
c 767	18	0.6	238	21	US-09-540-766-2709	Sequence 2709, Ap	c 840	18	0.6	258	44	US-60-007-127-187	Sequence 187, App
c 768	18	0.6	238	47	US-60-039-415-675	Sequence 675, App	c 841	18	0.6	258	13	US-08-901-904-4164	Sequence 4164, Ap
c 769	18	0.6	239	12	US-08-865-291-2657	Sequence 2657, Ap	c 842	18	0.6	259	21	US-09-540-208-52282	Sequence 52282, A
c 770	18	0.6	239	13	US-08-903-474-1864	Sequence 1864, Ap	c 843	18	0.6	261	16	US-09-288-687-3335	Sequence 3335, Ap
c 771	18	0.6	239	20	US-09-534-846B-28025	Sequence 28025, A	c 844	18	0.6	261	21	US-09-540-229-179664	Sequence 179664, A
c 772	18	0.6	239	20	US-09-534-846B-28121	Sequence 28121, A	c 845	18	0.6	262	14	US-09-012-473-733	Sequence 733, App
c 773	18	0.6	240	12	US-08-865-291-2112	Sequence 2112, Ap	c 846	18	0.6	262	16	US-09-263-191-11864	Sequence 11864, A
c 774	18	0.6	240	20	US-09-534-846B-28120	Sequence 28120, A	c 847	18	0.6	262	20	US-09-534-846B-28105	Sequence 28105, A
c 775	18	0.6	240	20	US-10-138-145-82	Sequence 82, Appl	c 848	18	0.6	262	36	US-09-975-254-11864	Sequence 11864, A
c 776	18	0.6	241	12	US-08-879-863-1436	Sequence 1436, Ap	c 849	18	0.6	262	47	US-60-037-663-733	Sequence 733, App
c 777	18	0.6	241	12	US-08-879-863A-1436	Sequence 1436, Ap	c 850	18	0.6	263	13	US-08-986-693A-1572	Sequence 1572, Ap
c 778	18	0.6	241	12	US-09-540-213-11483	Sequence 11483, A	c 851	18	0.6	263	13	US-08-986-693A-1572	Sequence 1572, Ap
c 779	18	0.6	243	11	US-08-730-774-46	Sequence 46, Appl	c 852	18	0.6	263	20	US-09-534-846B-28000	Sequence 28000, A
c 780	18	0.6	243	11	US-08-730-774-46	Sequence 46, Appl	c 853	18	0.6	264	20	US-09-532-315-9273	Sequence 9273, Ap
c 781	18	0.6	244	15	US-09-534-846B-27998	Sequence 27998, A	c 854	18	0.6	265	12	US-08-884-508-387	Sequence 387, App
c 782	18	0.6	244	15	US-09-107-510-4368	Sequence 4368, Ap	c 855	18	0.6	265	21	US-09-540-208-48971	Sequence 48971, A
c 783	18	0.6	244	19	US-09-521-640-31592	Sequence 31592, A	c 856	18	0.6	265	46	US-60-020-690-387	Sequence 387, App
c 784	18	0.6	244	20	US-09-534-846B-24410	Sequence 24410, A	c 857	18	0.6	266	13	US-08-923-871-970	Sequence 970, App
c 785	18	0.6	245	12	US-08-858-221-1910	Sequence 1910, Ap	c 858	18	0.6	266	20	US-09-534-846B-28041	Sequence 28041, A
c 786	18	0.6	245	20	US-09-534-846B-20164	Sequence 20164, A	c 859	18	0.6	267	14	US-09-075-782-332	Sequence 332, App
c 787	18	0.6	245	25	US-09-534-846B-28006	Sequence 28006, A	c 860	18	0.6	267	18	US-09-417-507-10198	Sequence 10198, A
c 788	18	0.6	245	25	US-09-654-617-89856	Sequence 89856, A	c 861	18	0.6	267	21	US-09-540-766-4814	Sequence 4814, Ap
c 789	18	0.6	246	11	US-08-734-338-600	Sequence 600, App	c 862	18	0.6	267	48	US-60-046-624-332	Sequence 332, App
c 790	18	0.6	246	16	US-09-283-466-22438	Sequence 22438, A	c 863	18	0.6	269	5	US-08-137-951-293	Sequence 293, App
c 791	18	0.6	246	20	US-09-534-846B-20166	Sequence 20166, A	c 864	18	0.6	269	5	US-08-197-801A-293	Sequence 290, App
c 792	18	0.6	246	23	US-09-606-755-5195	Sequence 5195, Ap	c 865	18	0.6	269	6	US-08-237-491-290	Sequence 3287, Ap
c 793	18	0.6	246	44	US-60-007-078-600	Sequence 600, App	c 866	18	0.6	269	6	US-08-296-757B-3287	Sequence 3287, Ap
c 794	18	0.6	247	12	US-08-839-389-712	Sequence 712, App	c 867	18	0.6	269	20	US-09-534-846B-27973	Sequence 27973, A
c 795	18	0.6	247	20	US-09-534-846B-28040	Sequence 28040, A	c 868	18	0.6	270	17	US-09-304-517A-157833	Sequence 157833, A
c 796	18	0.6	249	20	US-09-534-846B-20168	Sequence 20168, A	c 869	18	0.6	270	17	US-09-304-517A-204771	Sequence 204771, A
c 797	18	0.6	250	5	US-08-137-951-900	Sequence 900, App	c 870	18	0.6	270	17	US-09-371-146A-157833	Sequence 157833, A
c 798	18	0.6	250	5	US-08-197-801A-900	Sequence 900, App	c 871	18	0.6	270	17	US-09-371-146A-204771	Sequence 204771, A
c 799	18	0.6	250	6	US-08-237-491-900	Sequence 900, App	c 872	18	0.6	270	25	US-09-654-617-47784	Sequence 47784, A
c 800	18	0.6	250	6	US-08-296-757B-3897	Sequence 3897, Ap	c 873	18	0.6	270	27	US-09-684-016-47784	Sequence 47784, A
c 801	18	0.6	250	15	US-09-107-909-3532	Sequence 3532, Ap	c 874	18	0.6	270	37	US-09-985-678-157833	Sequence 157833, A
c 802	18	0.6	250	20	US-09-534-846B-28032	Sequence 28032, A	c 875	18	0.6	270	37	US-09-985-678-157833	Sequence 204771, A
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c 805	18	0.6	251	17	US-09-370-505-246	Sequence 246, App	c 878	18	0.6	273	22	US-09-552-086-23274	Sequence 23274, A
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c 811	18	0.6	251	33	US-09-866-555-16317	Sequence 16317, A	c 884	18	0.6	274	25	US-09-654-617-93487	Sequence 93487, A
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c 813	18	0.6	251	53	US-60-096-463-246	Sequence 246, App	c 886	18	0.6	274	39	US-10-062-727-222	Sequence 222, App
c 814	18	0.6	253	16	US-09-293-655-1530	Sequence 1530, Ap	c 887	18	0.6	275	20	US-09-534-846B-28022	Sequence 28022, A
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c 817	18	0.6	254	20	US-09-534-846B-28050	Sequence 28050, A	c 890	18	0.6	276	55	US-60-111-749-143	Sequence 143, App
c 818	18	0.6	255	48	US-60-048-979-1822	Sequence 979, Appl	c 891	18	0.6	277	16	US-09-210-297-95	Sequence 95, Appl
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c 822	18	0.6	255	21	US-09-540-499-25086	Sequence 25086, A	c 895	18	0.6	278	20	US-09-534-853-17553	Sequence 17553, A
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c 824	18	0.6	255	22	US-09-565-306-23136	Sequence 23136, A	c 897	18	0.6	279	13	US-08-992-868-1842	Sequence 1842, Ap

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RESULT 3

US-09-841-739-3
; Sequence 3, Application US/09841739
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29

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 Db 2881 TTTGAGAACTTTAAGCAATTTAGTGTGTTTGTGACTTTTAGTACTAAGAAATTTCTACCTGAT 2940
 QY 2941 CCAGCATTTAGTCAGAAACTTACCAAGTGTATCCAAAGTTAACTTTCTGCAAGAGCT 3000
 Db 2941 CCAGCATTTAGTCAGAAACTTACCAAGTGTATCCAAAGTTAACTTTCTGCAAGAGCT 3000
 QY 3001 AGGCTTGTGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060
 Db 3001 AGGCTTGTGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060

QY 3061 CTAGTAACCTGCT 3072
 Db 3061 CTAGTAACCTGCT 3072

RESULT 4
 PCT-US00-29643-1
 ; Sequence 1. Application PC/TUS0029643
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 ; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
 ; FILE REFERENCE: 07334-136W01
 ; CURRENT APPLICATION NUMBER: PCT/US00/29643
 ; CURRENT FILING DATE: 2000-10-26
 ; PRIOR APPLICATION NUMBER: US 60/161,822
 ; PRIOR FILING DATE: 1999-10-27
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 3133
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (36)...(3107)
 PCT-US00-29643-1

Query Match 100.0%; Score 3072; DB 1; Length 3133;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3072; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCAATTTTCATTAAGGACAAATAGCCGAGCCCTATTCAAGATGGAATGGAATGCTGTATA 60
 Db 36 ATGAATTTTCATTAAGGACAAATAGCCGAGCCCTATTCAAGATGGAATGGAATGCTGTATA 95
 QY 61 AAGCAATCACAGATGACCTATTGTTGATGGAATGTTCTGAATCGCGAAGAACTTAAACATC 120
 Db 96 AAGCAATCACAGATGACCTATTGTTGATGGAATGTTCTGAATCGCGAAGAACTTAAACATC 155
 QY 121 ATTGCTGGAGAGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 180
 Db 156 ATTGCTGGAGAGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 215
 QY 181 AAGGTTTCAGAGTCCCTGTAACCTCTTTCTTAATCCCTTAAGAGTGGAACTATCCTCTA 240
 Db 216 AAGGTTTCAGAGTCCCTGTAACCTCTTTCTTAATCCCTTAAGAGTGGAACTATCCTCTA 275
 QY 241 TTTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAAGAGACTTTGGACGAT 300
 Db 276 TTTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAAGAGACTTTGGACGAT 335
 QY 301 TTGGCTCAGGATTTAAAGGACTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTT 360
 Db 336 TTGGCTCAGGATTTAAAGGACTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTT 395
 QY 361 GGTGAAGATATTGACATTTATTTTAACTTGAAGAACCCCTTCACAGAACTGTCTGTGG 420
 Db 396 GGTGAAGATATTGACATTTATTTTAACTTGAAGAACCCCTTCACAGAACTGTCTGTGG 455
 QY 421 AGGAAGGACCAACCATCACCCTGGAGCAGCTGACCCCTGAATGGCCCTCCCTGCGAGGCT 480
 Db 456 AGGAAGGACCAACCATCACCCTGGAGCAGCTGACCCCTGAATGGCCCTCCCTGCGAGGCT 515
 QY 481 CTTTCAGAGCCCTGCATCATTTGAAGGGGAACTGCGAAGAGCAAGTCCACTCTGCTGCAG 540
 Db 516 CTTTCAGAGCCCTGCATCATTTGAAGGGGAACTGCGAAGAGCAAGTCCACTCTGCTGCAG 575
 QY 541 CGCATTTGCCATGCTCTGGGGCTCCGGAAGTGCAGGCTCTGCACCAAGTTCAAAATTCGTC 600
 Db 576 CGCATTTGCCATGCTCTGGGGCTCCGGAAGTGCAGGCTCTGCACCAAGTTCAAAATTCGTC 635

Qy 601 TTCTTCCCTCCCTCAGCAGGCCCCAGGTGGACTTTTGAACCCCTGTGATCAACTC 660
Db 636 TTCCTCTCCGTCTCAGCAGGCCCCAGGTGGACTTTTGAACCCCTGTGATCAACTC 695
Qy 661 CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGCGCCATCTGCTGAAGCTGGG 720
Db 696 CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGCGCCATCTGCTGAAGCTGGG 755
Qy 721 CAGAGGGTCTTTTCCCTCTTGTATGGCTTACAAATGAATTCAGGCCCCAGAACTGCCCGAA 780
Db 756 CAGAGGGTCTTTTCCCTCTTGTATGGCTTACAAATGAATTCAGGCCCCAGAACTGCCCGAA 815
Qy 781 ATCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGGTCATCGTCACCACTACC 840
Db 816 ATCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGGTCATCGTCACCACTACC 875
Qy 841 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGATATG 900
Db 876 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGATATG 935
Qy 901 ACAGAAAGACAGGCCAGGCTCTCATCCGAGAAGTGCTGATCAAGGAGCTTGCTGAAGGC 960
Db 936 ACAGAAAGACAGGCCAGGCTCTCATCCGAGAAGTGCTGATCAAGGAGCTTGCTGAAGGC 995
Qy 961 TTGTTGCTCCAAATTCAGAAATCAGAGTCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020
Db 996 TTGTTGCTCCAAATTCAGAAATCAGAGTCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1055
Qy 1021 GTGGTFCATCTGTGCAATCCAGATGGGTGAAAGTGGAGTTCCACTCTCACACACAACA 1080
Db 1056 GTGGTFCATCTGTGCAATCCAGATGGGTGAAAGTGGAGTTCCACTCTCACACACAACA 1115
Qy 1081 ACGTGTGTTCCATACCTCTATGATCTGTTGTATACAGAAAAACAACACAAACATAAAGGT 1140
Db 1116 ACGTGTGTTCCATACCTCTATGATCTGTTGTATACAGAAAAACAACACAAACATAAAGGT 1175
Qy 1141 GTGGTGCAGTACTCATTCGGAGCTTGACCACTGTGGAGACCTAGCTCTGGAGGGT 1200
Db 1176 GTGGTGCAGTACTCATTCGGAGCTTGACCACTGTGGAGACCTAGCTCTGGAGGGT 1235
Qy 1201 GTGTTCTCCCAAGTTTGTATTTCCGAATCGCAGATGTGTCACGCTGAATGAGGATGTC 1260
Db 1236 GTGTTCTCCCAAGTTTGTATTTCCGAATCGCAGATGTGTCACGCTGAATGAGGATGTC 1295
Qy 1261 CTGCTGACAACTGGGCTCCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAA 1320
Db 1296 CTGCTGACAACTGGGCTCCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAA 1355
Qy 1321 TTCTTTACAAAGTCAATCCAGAGTACACAGCAGCAGCAAGTATTTGACG 1380
Db 1356 TTCTTTACAAAGTCAATCCAGAGTACACAGCAGCAGCAAGTATTTGACG 1415
Qy 1381 TCTCATGAGCCAGAGGAGTACCAAGGGGAATGGTTACTTGCAGAAATGGTTCCATT 1440
Db 1416 TCTCATGAGCCAGAGGAGTACCAAGGGGAATGGTTACTTGCAGAAATGGTTCCATT 1475
Qy 1441 TCGGACATTTACATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTCTATCTGTGGAA 1500
Db 1476 TCGGACATTTACATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTCTATCTGTGGAA 1535
Qy 1501 GCCACAGGGCTGTATGAAGCACTCGCAGCAGTGTATCAACACGGCTGCTCTCGGA 1560
Db 1536 GCCACAGGGCTGTATGAAGCACTCGCAGCAGTGTATCAACACGGCTGCTCTCGGA 1595
Qy 1561 CTTTCCATTCGCAAGAGGCCCTCTGGAGACAGGAATCTTTGCAAAAGTGTAAAAACACC 1620
Db 1596 CTTTCCATTCGCAAGAGGCCCTCTGGAGACAGGAATCTTTGCAAAAGTGTAAAAACACC 1655
Qy 1621 ACTGAGCAAGAAATCTTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680
Db 1656 ACTGAGCAAGAAATCTTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1715
Qy 1681 TTATATCAAGAGGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTCAA 1740

Db 1716 TTATTTCAAGAGAGTACATCCAAATCAGCCCTGAGCCAGAAATTTGAAGCTTTCTTCAA 1775
Qy 1741 GGTATAGCTTATATCAACTCAGGGAACATCCCGGATTAATTTGACTTCTTTGAA 1800
Db 1776 GGTATAGCTTATATCAACTCAGGGAACATCCCGGATTAATTTGACTTCTTTGAA 1835
Qy 1801 CATTTGCCAAATTTGCAAGTCTCTGGACTTCAATTAACATGGACTTTTATGGGGAGCT 1860
Db 1836 CATTTGCCAAATTTGCAAGTCTCTGGACTTCAATTAACATGGACTTTTATGGGGAGCT 1895
Qy 1861 ATGSC TTTATGGGAAAAGGCTGCAAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1920
Db 1896 ATGSC TTTATGGGAAAAGGCTGCAAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1955
Qy 1921 GAAAC TACATTTCCAGCAGGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGG 1980
Db 1956 GAAAC TACATTTCCAGCAGGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGG 2015
Qy 1981 ACTCTG GAGGTACAGCTCCCGGATTTTCAGCAAGTGTATTAAGCAAGATATCACATATCTG 2040
Db 2016 ACTCTG GAGGTACAGCTCCCGGATTTTCAGCAAGTGTATTAAGCAAGATATCACATATCTG 2075
Qy 2041 GGGAAATATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAAATAAAGAGATGTCTGGTGTG 2100
Db 2076 GGGAAATATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAAATAAAGAGATGTCTGGTGTG 2135
Qy 2101 GCTGGA AGCCTCAGTCTTGGTCTCCTCAGCACCTGTAAAGAACATTTATCTCTCATGGTGAA 2160
Db 2136 GCTGGA AGCCTCAGTCTTGGTCTCCTCAGCACCTGTAAAGAACATTTATCTCTCATGGTGAA 2195
Qy 2161 GCCAGTTCCTCAGCATAGAAGATGAGAGGCACATCACATCTGTAACAAACCTGAAAACC 2220
Db 2196 GCCAGTTCCTCAGCATAGAAGATGAGAGGCACATCACATCTGTAACAAACCTGAAAACC 2255
Qy 2221 TTGAGTCTTTCATGACCTACAGAAATCAACGGCTGCGGGTGTCTGACTGACAGCTTGGGT 2280
Db 2256 TTGAGTCTTTCATGACCTACAGAAATCAACGGCTGCGGGTGTCTGACTGACAGCTTGGGT 2315
Qy 2281 AACTTTGAGAACCCTTACAAAGCTCATATGATGAATCAACATTAAGATGAATGAAGAGATGCT 2340
Db 2316 AACTTTGAGAACCCTTACAAAGCTCATATGATGAATCAACATTAAGATGAATGAAGAGATGCT 2375
Qy 2341 ATAAAC TAGCTGAAGGCCCTGAAAACCTGAAGAGATGTCTTTATTTTCATTTGACCCAC 2400
Db 2376 ATAAAC TAGCTGAAGGCCCTGAAAACCTGAAGAGATGTCTTTATTTTCATTTGACCCAC 2435
Qy 2401 TTGCTGACATTTGAGAGGGNAATGGATACATAGTCAAGTCTCTGTCAGTGAACCCCTGT 2460
Db 2436 TTGCTGACATTTGAGAGGGNAATGGATACATAGTCAAGTCTCTGTCAGTGAACCCCTGT 2495
Qy 2461 GACCTTGAGAAATTCATTAAGTCTCTGCTGCTGCTGCAAAATGCAAGTGAATAATCCTA 2520
Db 2496 GACCTTGAGAAATTCATTAAGTCTCTGCTGCTGCTGCAAAATGCAAGTGAATAATCCTA 2555
Qy 2521 GCTCAGATCTTTCACAAATTTGGTCAAACTGAGCATTTCTTGATTTATCAGAAAAATACCTG 2580
Db 2556 GCTCAGATCTTTCACAAATTTGGTCAAACTGAGCATTTCTTGATTTATCAGAAAAATACCTG 2615
Qy 2581 GAAAAAGTGGAAATGAAGCTCTTTCATGAACATGATCGACAGAGATGAAGCTGCTAGAACAG 2640
Db 2616 GAAAAAGTGGAAATGAAGCTCTTTCATGAACATGATCGACAGAGATGAAGCTGCTAGAACAG 2675
Qy 2641 CTCACCGCTGATGCTGCCCTGGGGCTGTGACCTGCAAGCAGCCTGAGCAGCTGTG 2700
Db 2676 CTCACCGCTGATGCTGCCCTGGGGCTGTGACCTGCAAGCAGCCTGAGCAGCTGTG 2735
Qy 2701 AAACATTTTGAGGAGTCCCAACTCTGTCAGGCTGGGTGAAAAACTGGAGACTCACA 2760
Db 2736 AAACATTTTGAGGAGTCCCAACTCTGTCAGGCTGGGTGAAAAACTGGAGACTCACA 2795
Qy 2761 GATACAGATTTAGGTTGCAATTTTTCGAAGAACCTCTGAAAACTTCCAG 2820

Db 2796 GATACAGAGATTAGATTTTAGTGCAATTTTGGAAAGAACCCCTCTGAAAGAAATCCAG 2855
QY 2821 CAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGGCTTCCATGGGTGTA 2880
Db 2856 CAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGGCTTCCATGGGTGTA 2915
QY 2881 TTTGAGAATCTTAAGCAATTAGTGTGTTTGTGACTTTTAGTACTAAAGAAATTTCTACCTGAT 2940
Db 2916 TTTGAGAATCTTAAGCAATTAGTGTGTTTGTGACTTTTAGTACTAAAGAAATTTCTACCTGAT 2975
QY 2941 CCAGCATTAGTCAGAAACTTAGCAAGTGTATCCAGTTAACTTTTCTGCAAGAGCT 3000
Db 2976 CCAGCATTAGTCAGAAACTTAGCAAGTGTATCCAGTTAACTTTTCTGCAAGAGCT 3035
QY 3001 AGGCTTTGTTGGTGCAATTTTATGATGATGATCTCAGTGTATTTACAGGTGCTTTTAAA 3060
Db 3036 AGGCTTTGTTGGTGCAATTTTATGATGATGATCTCAGTGTATTTACAGGTGCTTTTAAA 3095
QY 3061 CTAGTAACGTCT 3072
Db 3096 CTAGTAACGTCT 3107

RESULT 5

US-09-697-089-1
; Sequence 1, Application US/09697089
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136001
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US/09/697,089
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-697-089-1

Query Match 100.0%; Score 3072; DB 27; Length 3133;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3072; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATTTTCATAAAGCAATAGCCGAGCCCTTATTCAGAGATGGGATGACTGTTATA 60
Db 36 ATGAATTTTCATAAAGCAATAGCCGAGCCCTTATTCAGAGATGGGATGACTGTTATA 95
QY 61 AAGCAATACAGATGACCTATTGTTATGGAATGTTCTGAATCGGGAAGTAACATC 120
Db 96 AAGCAATACAGATGACCTATTGTTATGGAATGTTCTGAATCGGGAAGTAACATC 155
QY 121 ATTGCTGGGAAGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAAA 180
Db 156 ATTGCTGGGAAGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAAA 215
QY 181 AAGGTTTCAGATCTCTGTAACTCTTTCTTAATCCCTTAAGGATGGAATCTCTTA 240
Db 216 AAGGTTTCAGATCTCTGTAACTCTTTCTTAATCCCTTAAGGATGGAATCTCTTA 275
QY 241 TTTTCAGGACTTGAATGGCAAAAGTCTTTTTCATCAGACATCAGAGGAGCTTGGACGAT 300
Db 276 TTTTCAGGACTTGAATGGCAAAAGTCTTTTTCATCAGACATCAGAGGAGCTTGGACGAT 335
QY 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACATTTTATCCCTT 360

Db 336 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACTTTTATCCCTT 395
QY 361 GGTGAAGATATTGACATTTATTTTAACTTTGAAAGCACTTCCACAGAACTCTCTCTGTGG 420
Db 396 GGTGAAGATATTGACATTTATTTTAACTTTGAAAGCACTTCCACAGAACTCTCTCTGTGG 455
QY 421 AGGAAGGACCAACACCATCACCGCGTGGAGCAGCTGACCCCTGAATGGGCTCTCTGAGGCT 480
Db 456 AGGAAGGACCAACACCATCACCGCGTGGAGCAGCTGACCCCTGAATGGGCTCTCTGAGGCT 515
QY 481 CTTTCAGAGCCCTGATCATTTGAAGGGGAATCTGCAAGAGCAAGTCCACTCTGTCGAG 540
Db 516 CTTTCAGAGCCCTGATCATTTGAAGGGGAATCTGCAAGAGCAAGTCCACTCTGTCGAG 575
QY 541 CGCATTTGCAATCTCTGGGGCTCCGAAAGTCAAGGCTCTCACCAAGTTCAAAATTCGTC 600
Db 576 CGCATTTGCAATCTCTGGGGCTCCGAAAGTCAAGGCTCTGACCAAGTTCAAAATTCGTC 635
QY 601 TTCTTCTCCGCTCTCAGCAGGGCCCAAGGCTGAGCTTTTGAAGCCCTCTGTGATCAATC 660
Db 636 TTCTTCTCCGCTCTCAGCAGGGCCCAAGGCTGAGCTTTTGAAGCCCTCTGTGATCAATC 695
QY 661 CTGGATATACCTGGGCACATCAGGAGCAGACATTCATGGCCATGCTGCTGAAGCTGGG 720
Db 696 CTGGATATACCTGGGCACATCAGGAGCAGACATTCATGGCCATGCTGCTGAAGCTGGG 755
QY 721 CAGAGGTTCTTTTCTTCTGATGGCTACAATGAATTAAGCCCAAGCTGCCCAGAA 780
Db 756 CAGAGGTTCTTTTCTTCTGATGGCTACAATGAATTAAGCCCAAGCTGCCCAGAA 815
QY 781 ATCGAAGCCCTGATAAAGGAAACCCGCTTCAAGAACATGGTCTGCTACCACTACC 840
Db 816 ATCGAAGCCCTGATAAAGGAAACCCGCTTCAAGAACATGGTCTGCTACCACTACC 875
QY 841 ACTGAGTCCCTCAGCAGACATACGCGAGTTTGGTCCCTGACTGCTGAGGTGGGGATAG 900
Db 876 ACTGAGTCCCTCAGCAGACATACGCGAGTTTGGTCCCTGACTGCTGAGGTGGGGATAG 935
QY 901 ACAGAGACAGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGGAGCTTCTGCTGAAGC 960
Db 936 ACAGAGACAGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGGAGCTTCTGCTGAAGC 995
QY 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTTGAGGAATCTCATGAAGACCCCTCTCTT 1020
Db 996 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTTGAGGAATCTCATGAAGACCCCTCTCTT 1055
QY 1021 GTGGTCATCATTGTGCAATCCAGATGGGTGAAGTGGTCCACTCTCACACAAACA 1080
Db 1056 GTGGTCATCATTGTGCAATCCAGATGGGTGAAGTGGTCCACTCTCACACAAACA 1115
QY 1081 AGGCTGTTCCATACCTCTCTATGATCTGTTGATACAGAAAACAAACACAAATAAAGT 1140
Db 1116 AGGCTGTTCCATACCTCTCTATGATCTGTTGATACAGAAAACAAACACAAATAAAGT 1175
QY 1141 GTGGCTGCAAGTGAATTCATTCGGAGCCCTGGACCACTGTGGAGACCTAGCTCTGGAGGT 1200
Db 1176 GTGGCTGCAAGTGAATTCATTCGGAGCCCTGGACCACTGTGGAGACCTAGCTCTGGAGGT 1235
QY 1201 GTGGTCTCCACAAAGTTTGAATTTCCAACTGCGAGGATGTGTCAGGCTGAATGAGGATGTC 1260
Db 1236 GTGGTCTCCACAAAGTTTGAATTTCCAACTGCGAGGATGTGTCAGGCTGAATGAGGATGTC 1295
QY 1261 CTGGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGCTTCAAGCAAGTATATAA 1320
Db 1296 CTGGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGCTTCAAGCAAGTATATAA 1355
QY 1321 TTTCTTTCAGAGTCAATTCAGGAGTACACAGCAGGACGAGGACTCAGCAGTTTATGAGC 1380
Db 1356 TTTCTTTCAGAGTCAATTCAGGAGTACACAGCAGGACGAGGACTCAGCAGTTTATGAGC 1415
QY 1381 TCTCATGAGCCAGAGGAGTGTACCAAGGGAATGTTACTTTCAGAAAAATGTTTCCATT 1440
Db 1416 TCTCATGAGCCAGAGGAGTGTACCAAGGGAATGTTACTTTCAGAAAAATGTTTCCATT 1475

QY 61 AAGCAATACAGATGACATATTTGATGGAATGTTCTGAATCGGAGAAAGTAAACATC 120
Db AAGCAATACAGATGACATATTTGATGGAATGTTCTGAATCGGAGAAAGTAAACATC 155
QY 121 ATTGCTCGGAGAGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAA 180
Db ATTGCTCGGAGAGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAA 215
QY 181 AAGGTTTCAGAGTCCCTGTAACCTCTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 240
Db AAGGTTTCAGAGTCCCTGTAACCTCTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 275
QY 241 TTTCAGGACTTGAATGGACAAGTCTTTTCATFAGACATCAAGAGGAGCTTGGACGAT 300
Db TTTCAGGACTTGAATGGACAAGTCTTTTCATFAGACATCAAGAGGAGCTTGGACGAT 335
QY 301 TTGGCTCAGGATTTAAGGACTTGTACCATACCCATCTTTCTGAACTTTTATCCCTT 360
Db TTGGCTCAGGATTTAAGGACTTGTACCATACCCATCTTTCTGAACTTTTATCCCTT 395
QY 361 GGTGAAGATATTGACATTTATTTTAACTTTGAAAAGCACCTTCACAGAACTGTCTGTGG 420
Db GGTGAAGATATTGACATTTATTTTAACTTTGAAAAGCACCTTCACAGAACTGTCTGTGG 455
QY 421 AGGAAGGACCAACACCATCACCGCGTGGAGCAGCTGACCTGAATGGCCCTCTGACAGCT 480
Db AGGAAGGACCAACACCATCACCGCGTGGAGCAGCTGACCTGAATGGCCCTCTGACAGCT 515
QY 481 CTTACAGGCCCTGCATCTGAAGGGGAATCTGGCAAGAGTCCACTCTGCTGCGAG 540
Db CTTACAGGCCCTGCATCTGAAGGGGAATCTGGCAAGAGTCCACTCTGCTGCGAG 575
QY 541 CGCATTTGCCATGCTCTGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAAAATTCGTC 600
Db CGCATTTGCCATGCTCTGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAAAATTCGTC 635
QY 601 TTCTTCCCTCGCTCAGCAGGCCCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTC 660
Db TTCTTCCCTCGCTCAGCAGGCCCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTC 695
QY 661 CTGGATATACCTGGCAATCAGGAGCAGACATTCATGGCCATGCTGTGAAGCTGGG 720
Db CTGGATATACCTGGCAATCAGGAGCAGACATTCATGGCCATGCTGTGAAGCTGGG 755
QY 721 CAGAGGTTCTTTTCTCTTGATGCTACAATGAATCAAGCCCCAGAACTGCCAGAA 780
Db CAGAGGTTCTTTTCTCTTGATGCTACAATGAATCAAGCCCCAGAACTGCCAGAA 815
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Db ATCGAAGCCCTGATAAAGGAAACCAACCGCTTCAAGAACATGTCATCGTCAACCACTAC 875
QY 841 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGTGGGGATATG 900
Db ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGTGGGGATATG 935
QY 901 ACAGAAGACAGGCCCGCAGCTCATCCGAGAGTCTGATCAAGGAGCTTGCTGAAGC 960
Db ACAGAAGACAGGCCCGCAGCTCATCCGAGAGTCTGATCAAGGAGCTTGCTGAAGC 995
QY 961 TTGTGCTCCAAATTCAGAAATCCAGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020
Db TTGTGCTCCAAATTCAGAAATCCAGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1055
QY 1021 GTGGTCATCATTTGCAATCCAGATGGGTGAAAGTGTGAGTTCACATCTCACACAAACA 1080
Db GTGGTCATCATTTGCAATCCAGATGGGTGAAAGTGTGAGTTCACATCTCACACAAACA 1115
QY 1081 ACCTGTTCCATACCTTCTATGATCTGTGATACAGAAACAAACACAAACATAAAGT 1140
Db ACCTGTTCCATACCTTCTATGATCTGTGATACAGAAACAAACACAAACATAAAGT 1175
QY 1141 GTGGCTGCAAGTACCTTTCATTCGGAGCCTGGACCACTGTGGAGACCTAGTCTGGAGG 1200

Db 1176 GTGGCTGCAAGTACCTTTCATTCGGAGCCTGGACCACTGTGGAGACCTAGTCTGGAGG 1235
QY 1201 GTGTTCTCCCAACAAGTTTTCATTTGAACTGCAAGATGCTGCCAGCGTGAATGAGGATGTC 1260
Db GTGTTCTCCCAACAAGTTTTCATTTGAACTGCAAGATGCTGCCAGCGTGAATGAGGATGTC 1295
QY 1261 CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAAGGTTCAAGCCAAAGTATAA 1320
Db CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAAGGTTCAAGCCAAAGTATAA 1355
QY 1321 TTCTTTCAAAAGTTCATTCAGGAGTACAGAGGAGGAGACTCAGCAGTTTATTGACG 1380
Db TTCTTTCAAAAGTTCATTCAGGAGTACAGAGGAGGAGACTCAGCAGTTTATTGACG 1415
QY 1381 TCTCATGACCCAGAGGAGTGCACCAAGGGAATGTTACTTGCAGAAAAATGGTTTCCATT 1440
Db TCTCATGACCCAGAGGAGTGCACCAAGGGAATGTTACTTGCAGAAAAATGGTTTCCATT 1475
QY 1441 TCGGACATTTACATCCACTTATAGCAGCTGCTCCGGTACACCTTGTGGTCACTGTGGA 1500
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QY 1501 GGCACAGGCTGTTTATGAAGCAGCTCGCAGCAGTGTATCAACACCGCTGCTTCTCGGA 1560
Db GGCACAGGCTGTTTATGAAGCAGCTCGCAGCAGTGTATCAACACCGCTGCTTCTCGGA 1595
QY 1561 CTTTCCATCGCAAGAGGCTCTCTCGAGACAGGAATCTTGCAGAACTGTGAACACAC 1620
Db CTTTCCATCGCAAGAGGCTCTCTCGAGACAGGAATCTTGCAGAACTGTGAACACAC 1655
QY 1621 ACTGAGCAAGAAATCTGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680
Db ACTGAGCAAGAAATCTGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1715
QY 1681 TTATATFCAAGAGATACATCCAATCAGCCCTGAGCAGAGAAATTTGAAGCTTTCTTTCAA 1740
Db TTATATFCAAGAGATACATCCAATCAGCCCTGAGCAGAGAAATTTGAAGCTTTCTTTCAA 1775
QY 1741 GGTAAAGCTTATATATCAACTCAGGAAACATCCCGATTTACTTTTACATCTCTTTGAA 1800
Db GGTAAAGCTTATATATCAACTCAGGAAACATCCCGATTTACTTTTACATCTCTTTGAA 1835
QY 1801 CATTTGCCCAATTTGTCAGTGTCTGAGCTTCATTTAACTGGACTTTTATGGGGAGCT 1860
Db CATTTGCCCAATTTGTCAGTGTCTGAGCTTCATTTAACTGGACTTTTATGGGGAGCT 1895
QY 1861 ATGGCTTCATGGGAAAAGGCTGCAGAAACACAGGTTGGAATCCATGGAAGAGGCCCA 1920
Db ATGGCTTCATGGGAAAAGGCTGCAGAAACACAGGTTGGAATCCATGGAAGAGGCCCA 1955
QY 1921 GAAACCTACATTTCCCGAGGCTGTATCTTGTCTTCAACTGGAAGCAGGAATTCAGG 1980
Db GAAACCTACATTTCCCGAGGCTGTATCTTGTCTTCAACTGGAAGCAGGAATTCAGG 2015
QY 1981 ACTCTGGAGTTCACACTCCGGGATTTTCAGCAAGTTTCAATTAAGCAAGATATCATATCTG 2040
Db ACTCTGGAGTTCACACTCCGGGATTTTCAGCAAGTTTCAATTAAGCAAGATATCATATCTG 2075
QY 2041 GGGAAATATTCAGCTTCTGCCAAGCCCTCAGGCTGCAAAATAAAGAGATGTGCTGTGTG 2100
Db GGGAAATATTCAGCTTCTGCCAAGCCCTCAGGCTGCAAAATAAAGAGATGTGCTGTGTG 2135
QY 2101 GCTGGAAGCCTCAGTTTGTCTCAGCAGCTGTAAAGCAATTTATTTCTCTCATGGTGGAA 2160
Db GCTGGAAGCCTCAGTTTGTCTCAGCAGCTGTAAAGCAATTTATTTCTCTCATGGTGGAA 2195
QY 2161 GCCAGTCCCTCACCATAGAAGATGAGGACATCACATCTGTAAACACCTGAAAC 2220
Db GCCAGTCCCTCACCATAGAAGATGAGGACATCACATCTGTAAACACCTGAAAC 2255
QY 2221 TTGAGTATTTCAGCTACAGAAATCAACGGCTGCCGGTGGTCTGACTGACAGCTTGGGT 2280

Db 2256 TTGAGTATTCATGACCTACAGAAATCAACGGCTGCGGGTGGTGTGACTGACAGCTTGGGT 2315
Qy 2281 AACTTTGAAGAACCTTACAAAGCTCATAATGGATACATAAAGATGAATGAAGAGATGCT 2340
Db 2316 AACTTTGAAGAACCTTACAAAGCTCATAATGGATACATAAAGATGAATGAAGAGATGCT 2375
Qy 2341 ATAAAACCTAGCTGAAGGCTGAAAGAACCTGAAGAGATGTGTTTATTTCAATTTGACCCAC 2400
Db 2376 ATAAAACCTAGCTGAAGGCTGAAAGAACCTGAAGAGATGTGTTTATTTCAATTTGACCCAC 2435
Qy 2401 TTGCTCTGACATTTGGAGAGGGAATGATTACATAGTCAAGTCTCTGCTCAAGTGAACCTGT 2460
Db 2436 TTGCTCTGACATTTGGAGAGGGAATGATTACATAGTCAAGTCTCTGCTCAAGTGAACCTGT 2495
Qy 2461 GACCTTTGAAGAAATCAATAGTCTCTGCTGCTGCTCAAGTGAACCTGTGCTCAAGTGAACCTGT 2520
Db 2496 GACCTTTGAAGAAATCAATAGTCTCTGCTGCTGCTCAAGTGAACCTGTGCTCAAGTGAACCTGT 2555
Qy 2521 GCTGAGATCTCAAAATTTGGTCAAGTGAACCTGAGCATTTGATTTATTCAGAAATTTACCTG 2580
Db 2556 GCTGAGATCTCAAAATTTGGTCAAGTGAACCTGAGCATTTGATTTATTCAGAAATTTACCTG 2615
Qy 2581 GAAAAGATGAAGTGAAGCTCTTCATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2640
Db 2616 GAAAAGATGAAGTGAAGCTCTTCATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2675
Qy 2641 CTCACCGCACTGATGCTGCCCTGGGCTGTGACGTGCAAGGAGCGCTGAGCAGCGCTGTG 2700
Db 2676 CTCACCGCACTGATGCTGCCCTGGGCTGTGACGTGCAAGGAGCGCTGAGCAGCGCTGTG 2735
Qy 2701 AAACATTTGGAGAGTGGTCCCACTGCTCAAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2760
Db 2736 AAACATTTGGAGAGTGGTCCCACTGCTCAAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2795
Qy 2761 GATACAGAGATAGAAATTTAGGTGCAATTTTGGTGAAGAACCTCTGAAAAAATTTCCAG 2820
Db 2796 GATACAGAGATAGAAATTTAGGTGCAATTTTGGTGAAGAACCTCTGAAAAAATTTCCAG 2855
Qy 2821 CAGTTGAATTTGGGGGAAATCGTGTGAGCAGTATGATGCTTGGCTTCAATGGTGTGTA 2880
Db 2856 CAGTTGAATTTGGGGGAAATCGTGTGAGCAGTATGATGCTTGGCTTCAATGGTGTGTA 2915
Qy 2881 TTTGAGATCTTAAGCAATTTAGTGTGTTTGTGCTTACTAGTAAAGATTTTCACTGAT 2940
Db 2916 TTTGAGATCTTAAGCAATTTAGTGTGTTTGTGCTTACTAGTAAAGATTTTCACTGAT 2975
Qy 2941 CCAGCATTTAGCAAAATTTAGCAAGTGTATCCCAAGTAACTTTCTGCAAGAGCT 3000
Db 2976 CCAGCATTTAGCAAAATTTAGCAAGTGTATCCCAAGTAACTTTCTGCAAGAGCT 3035
Qy 3001 AGCTTTGTTGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060
Db 3036 AGCTTTGTTGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3095
Qy 3061 CTAGTAATGCT 3072
Db 3096 CTAGTAATGCT 3107

RESULT 7
us-10-156-733-1
; Sequence 1, Application US/10156733
; GENERAL INFORMATION:
; APPLICANT: Alnemi, Ehad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; FILE OF INVENTION: FACTOR
; FILE REFERENCE: 480140.477
; CURRENT APPLICATION NUMBER: US/10/156,733
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ. ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO 1
; LENGTH: 3075

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(3075)
US-10-156-733-1

Query Match 95.0%; Score 2919; DB 41; Length 3075;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3069; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAATTCATTAAGGCAATAGCGGAGCCCTTATTCAGAAATGGGAAATGACACTGTATA 60
Db 1 ATGAATTCATTAAGGCAATAGCGGAGCCCTTATTCAGAAATGGGAAATGACACTGTATA 60
Qy 61 AAGCAATACAGATGACCTATTGTTATGGAATGTTCTGAATCGGAAAGATTAACATC 120
Db 61 AAGCAATACAGATGACCTATTGTTATGGAATGTTCTGAATCGGAAAGATTAACATC 120
Qy 121 ATTTGC TCGAAGAGGTGGAGCAGATGCTGCTAGAGGATCATTCACATGATTTGAAA 180
Db 121 ATTTGC TCGAAGAGGTGGAGCAGATGCTGCTAGAGGATCATTCACATGATTTGAAA 180
Qy 181 AAGGTT CAGAGTCTGTAACCTCTTTCTTAAATCCCTTAAAGGAGTGAACATGCTCTA 240
Db 181 AAGGTT CAGAGTCTGTAACCTCTTTCTTAAATCCCTTAAAGGAGTGAACATGCTCTA 240
Qy 241 TTTCAATGTAATGGACAAAGTCTTTTTCATCAGACATCAGAGGAGCTTGGACGAT 300
Db 241 TTTCAATGTAATGGACAAAGTCTTTTTCATCAGACATCAGAGGAGCTTGGACGAT 300
Qy 301 TTGGCT AGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACTTTTATCCCTT 360
Db 301 TTGGCT AGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACTTTTATCCCTT 360
Qy 361 GGTGAATATTTGACATTTTAACTTGAAGAGCCTTTCACAGAACTTCTGCTGG 420
Db 361 GGTGAATATTTGACATTTTAACTTGAAGAGCCTTTCACAGAACTTCTGCTGG 420
Qy 421 AGAAGGACCAACACCATCCCGCTGAGCAGCTGACCTGAAATGGCTCTCCAGCT 480
Db 421 AGAAGGACCAACACCATCCCGCTGAGCAGCTGACCTGAAATGGCTCTCCAGCT 480
Qy 481 CTTGAGA CCGCTGATGATTAAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGAG 540
Db 481 CTTGAGA CCGCTGATGATTAAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGAG 540
Qy 541 CGATTTG CATGCTCTGGGCTCCGGAAGTGAAGGCTCTGACCAAGTTCATTCGTC 600
Db 541 CGATTTG CATGCTCTGGGCTCCGGAAGTGAAGGCTCTGACCAAGTTCATTCGTC 600
Qy 601 TTTCTCC CCGCTCTCAGAGGCGCCAGGCTGAGCTTTTGAACCCCTCTGTGATCAACT 660
Db 601 TTTCTCC CCGCTCTCAGAGGCGCCAGGCTGAGCTTTTGAACCCCTCTGTGATCAACT 660
Qy 661 CTGATA ACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGG 720
Db 661 CTGATA ACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGG 720
Qy 721 CAGAGGGT TCTTTCTCTTGTGCTTACATGAATCAAGCCCGCAGAACTGCCAGAA 780
Db 721 CAGAGGGT TCTTTCTCTTGTGCTTACATGAATCAAGCCCGCAGAACTGCCAGAA 780
Qy 781 ATCAAGC CTTGATAAAGGAAACACCGCTTCAAGAACATGGTCACTGTCACCACTACC 840
Db 781 ATCAAGC CTTGATAAAGGAAACACCGCTTCAAGAACATGGTCACTGTCACCACTACC 840
Qy 841 ACTGAGTG CTGAGGCACATACGAGCTTTGGTCCCTGAGCTGCTGAGTGGGGATATG 900
Db 841 ACTGAGTG CTGAGGCACATACGAGCTTTGGTCCCTGAGCTGCTGAGTGGGGATATG 900
Qy 901 ACAGAAGA AGCGCCCGAGGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGTGAAGGC 960
Db 901 ACAGAAGA AGCGCCCGAGGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGTGAAGGC 960

Db	901	ACAGAGACAGCGCCGAGGCTCTCATCCGAGAAGTGCTGATCAAGGAGCTTGCTGTAAGGC	960
Qy	961	TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTTGAGGAATCTCATGAAGCCCTCTCTTT	1020
Db	961	TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTTGAGGAATCTCATGAAGCCCTCTCTTT	1020
Qy	1021	GTGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACAAACA	1080
Db	1021	GTGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACAAACA	1080
Qy	1081	ACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAACACAAACATATAAGGT	1140
Db	1081	ACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAACACAAACATATAAGGT	1140
Qy	1141	GTGGCTCAAGTGACTTCATTTCGGAGCCTGAGCACTCTGGAGACCTAGCTCTGGAGGT	1200
Db	1141	GTGGCTCAAGTGACTTCATTTCGGAGCCTGAGCACTCTGGAGACCTAGCTCTGGAGGT	1200
Qy	1201	GTGTTCTCCACAAGTTGATTTGCAAGTGCAGATGTGCCAGGTGAATGAGGATGTC	1260
Db	1201	GTGTTCTCCACAAGTTGATTTGCAAGTGCAGATGTGCCAGGTGAATGAGGATGTC	1260
Qy	1261	TCGTCGACACTGGGCTCTCTGTAATATACAGCTCAAAAGTTCAAGCCAAAGATATAA	1320
Db	1261	TCGTCGACACTGGGCTCTCTGTAATATACAGCTCAAAAGTTCAAGCCAAAGATATAA	1320
Qy	1321	TTCTTTTCACAAGTCATTCCAGGAGTACACAGCAGCAGCAAGACTCAGCAGTTATTACG	1380
Db	1321	TTCTTTTCACAAGTCATTCCAGGAGTACACAGCAGCAGCAAGACTCAGCAGTTATTACG	1380
Qy	1381	TCTCATGAGCCAGAGGAGTGACCAAGGGAAATGGTTACTTTGCAGAAATGGTTCCATT	1440
Db	1381	TCTCATGAGCCAGAGGAGTGACCAAGGGAAATGGTTACTTTGCAGAAATGGTTCCATT	1440
Qy	1441	TCGACATATACATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTCACTGTGGAA	1500
Db	1441	TCGACATATACATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTCACTGTGGAA	1500
Qy	1501	GCCACACGGGCTGTTATGAAGACCTCCGACAGTGTATCAACACGGCTGCCTTCGGA	1560
Db	1501	GCCACACGGGCTGTTATGAAGACCTCCGACAGTGTATCAACACGGCTGCCTTCGGA	1560
Qy	1561	CTTTTCATCGCCAAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACC	1620
Db	1561	CTTTTCATCGCCAAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACC	1620
Qy	1621	ACTGAGCAAGAAATTCGAAAGCCATAACATCAATTCCTTTGTAGAGTGTGGCATCCAT	1680
Db	1621	ACTGAGCAAGAAATTCGAAAGCCATAACATCAATTCCTTTGTAGAGTGTGGCATCCAT	1680
Qy	1681	TTATATCAAGAGAGTACATCCAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTCTTTCAA	1740
Db	1681	TTATATCAAGAGAGTACATCCAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTCTTTCAA	1740
Qy	1741	GGTAAAAGCTTATATCAACTCAGGAACATCCCGGATTACTTATTGTACTTCTTTGAA	1800
Db	1741	GGTAAAAGCTTATATCAACTCAGGAACATCCCGGATTACTTATTGTACTTCTTTGAA	1800
Qy	1801	CATTTCGCCAAATTTGCGAAGTGTCTGTGACTTCATTAACTGGACTTTTATGGGGAGCT	1860
Db	1801	CATTTCGCCAAATTTGCGAAGTGTCTGTGACTTCATTAACTGGACTTTTATGGGGAGCT	1860
Qy	1861	ATGGCTTCATGGGAAAAGGCTGCAAGACACAGGTGGAATCCACATGGGAAGAGGCCCA	1920
Db	1861	ATGGCTTCATGGGAAAAGGCTGCAAGACACAGGTGGAATCCACATGGGAAGAGGCCCA	1920
Qy	1921	GAACCTTACATTCGCCAGCGGGTGATCTTTGTTCTTCAACTGGAGCAGGAATTCAGG	1980
Db	1921	GAACCTTACATTCGCCAGCGGGTGATCTTTGTTCTTCAACTGGAGCAGGAATTCAGG	1980
Qy	1981	ACTCTGAGGTACACTCCGGGATTCAGCAAGTTGAATAAGCAAGATATCACATATCTG	2040
Db	1981	ACTCTGAGGTACACTCCGGGATTCAGCAAGTTGAATAAGCAAGATATCACATATCTG	2040

Qy	2041	GGGAAATATTTCAGCTCTGCCAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGTG	2100
Db	2041	GGGAAATATTTCAGCTCTGCCAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGTG	2100
Qy	2101	GCTGGAAGCCTCAGTTTGGTCTCAGCAGCTGTGAAGAACATTTATCTCTCATGGTGGAA	2160
Db	2101	GCTGGAAGCCTCAGTTTGGTCTCAGCAGCTGTGAAGAACATTTATCTCTCATGGTGGAA	2160
Qy	2161	GCCAGTCCCCTCACCATTAGAAGATGAGAGGCACATCACAATCTGTAAACAACCTGAAAAACC	2220
Db	2161	GCCAGTCCCCTCACCATTAGAAGATGAGAGGCACATCACAATCTGTAAACAACCTGAAAAACC	2220
Qy	2221	TTGAGTATTCAATGACCTACAGAATCAACGGCTGCCGGGTGCTCTGACTGACAGCTTGGGT	2280
Db	2221	TTGAGTATTCAATGACCTACAGAATCAACGGCTGCCGGGTGCTCTGACTGACAGCTTGGGT	2280
Qy	2281	AACCTTGGAAGAACCTTCAAAAGCTCAATAATGGATACATAAAGATGAATGAAGAGATGCT	2340
Db	2281	AACCTTGGAAGAACCTTCAAAAGCTCAATAATGGATACATAAAGATGAATGAAGAGATGCT	2340
Qy	2341	ATAAACTAGCTGAAGGCCTGAAAAACCTGGAAGAAGATGTGTATTTTCATTTCGACCCAC	2400
Db	2341	ATAAACTAGCTGAAGGCCTGAAAAACCTGGAAGAAGATGTGTATTTTCATTTCGACCCAC	2400
Qy	2401	TTGTCTGACATTTGGAGAGGAATGGATACATPAGTCAAGTCTCTGTCAAGTGAACCCCTGT	2460
Db	2401	TTGTCTGACATTTGGAGAGGAATGGATACATPAGTCAAGTCTCTGTCAAGTGAACCCCTGT	2460
Qy	2461	GACCTTGAAGAAATTCAAATTAGTCTCCTGCTGCTGCTGCANAATGCAAGTGAATAATCCTA	2520
Db	2461	GACCTTGAAGAAATTCAAATTAGTCTCCTGCTGCTGCTGCANAATGCAAGTGAATAATCCTA	2520
Qy	2521	GCTCAGAAATCTTCACAATTTGGTCAAACTGAGCATCTTGATTTATCAGAAAAATTCACCTG	2580
Db	2521	GCTCAGAAATCTTCACAATTTGGTCAAACTGAGCATCTTGATTTATCAGAAAAATTCACCTG	2580
Qy	2581	GAAAAAGATGGAATGAAGCTCTTCATGAACATGATCGACAGGATGAAGTCTGTAGAACAG	2640
Db	2581	GAAAAAGATGGAATGAAGCTCTTCATGAACATGATCGACAGGATGAAGTCTGTAGAACAG	2640
Qy	2641	CTCACCCGACTGATGCTGCCCTGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTGTTG	2700
Db	2641	CTCACCCGACTGATGCTGCCCTGGGCTGTGACGTGCAAGGCAGCCTGAGCAGCCTGTTG	2700
Qy	2701	AAACATTTGGAGGAGGTGCCAACATCTGCAAGCTTGGGTTGAAAACTGGAGACTCACA	2760
Db	2701	AAACATTTGGAGGAGGTGCCAACATCTGCAAGCTTGGGTTGAAAACTGGAGACTCACA	2760
Qy	2761	GATACAGAGATTAGAATTTTAGTGCAATTTTGGAAAGAACCCCTCTGAAAACTCCAG	2820
Db	2761	GATACAGAGATTAGAATTTTAGTGCAATTTTGGAAAGAACCCCTCTGAAAACTCCAG	2820
Qy	2821	CAGTTGAATTTGGCGGGAATCCTGTGACAGTGAATGGCTTGCCCTCATGGGTGTA	2880
Db	2821	CAGTTGAATTTGGCGGGAATCCTGTGACAGTGAATGGCTTGCCCTCATGGGTGTA	2880
Qy	2881	TTTGAGAAATCTTAAGCAATTAGTGTGTTTTTGTGACTTTAGTACTAAGAAATTTCTACCTGAT	2940
Db	2881	TTTGAGAAATCTTAAGCAATTAGTGTGTTTTTGTGACTTTAGTACTAAGAAATTTCTACCTGAT	2940
Qy	2941	CCAGCATTTAGTCAGAAACTTAGCCAAAGTGTATCCAGTTAACTTTTCTGCAAGAGCT	3000
Db	2941	CCAGCATTTAGTCAGAAACTTAGCCAAAGTGTATCCAGTTAACTTTTCTGCAAGAGCT	3000
Qy	3001	AGGCTTTGGTGGGCAATTTGATGATGATGATCTCAGTGTATTACAGGTGCTTTTAAA	3060
Db	3001	AGGCTTTGGTGGGCAATTTGATGATGATGATCTCAGTGTATTACAGGTGCTTTTAAA	3060
Qy	3061	CTAGTAACTGCT 3072	
Db	3061	CTAGTAACTGCT 3072	

RESULT 8
US-10-156-733-14
; Sequence 14, Application US/10156733
; GENERAL INFORMATION:
; APPLICANT: Alimemri, Enad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; FILE REFERENCE: 480140.477
; CURRENT APPLICATION NUMBER: US/10/156.733
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-156-733-14

Query Match 95.0%; Score 2919; DB 41; Length 3219;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3069; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATTTCAAAAGGCAATAGCCGAGCCCTTATTAAAGAAATGGGAATGACTGTTATA 60
Db |||||||
QY 61 AAGCAATTCACAGATGACCTATTGCTATGGATGCTTCAATCGGGAAGATGAACATC 120
Db |||||||
QY 121 ATTGCTCGGAGAAGGTGGAGCAGATGCTGTAGAGGATCATATTCATGATTTGAAA 180
Db |||||||
QY 241 TTTCAGGACTTGAATGACAAAGTCTTTTTCATCAGACATCAGAAAGGAGCTTGGACGAT 300
Db |||||||
QY 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTATCCCTT 360
Db |||||||
QY 361 GTTGAAGATATTGACATTTATTTAACTTGAAGCCACCTTCACAGAACCTGCTGTGG 420
Db |||||||
QY 505 GGTGAAGATATTGACATTTATTTAACTTGAAGCCACCTTCACAGAACCTGCTGTGG 564
QY 421 AGGAAGGACCAACACCATCAGCGGTGGAGCAGCTGACCCCTGAATGGCTCCTGAGGCT 480
Db |||||||
QY 565 AGGAAGGACCAACACCATCAGCGGTGGAGCAGCTGACCCCTGAATGGCTCCTGAGGCT 624
QY 481 CTTAGAGCCCTGTCATCATTTGAAGGGGAATCTGGCAAAGCAAGTCCACCTCTGCTGCAG 540
Db |||||||
QY 625 CTTAGAGCCCTGTCATCATTTGAAGGGGAATCTGGCAAAGCAAGTCCACCTCTGCTGCAG 684
QY 541 CGCATTTGCATGCTCTGGGGCTCCGGAAAGTGCAAGGCTCTGACCAAGTTCAAAATTCGTC 600
Db |||||||
QY 685 CGAATTTGCATGCTCTGGGGCTCCGGAAAGTGCAAGGCTCTGACCAAGTTCAAAATTCGTC 744
QY 601 TTTCTCCCTCCGTCACAGAGGCCACAGGTGAGCTTTTGAAGCCCTCTGTGATCAACTC 660
Db |||||||
QY 745 TTTCTCCCTCCGTCACAGAGGCCACAGGTGAGCTTTTGAAGCCCTCTGTGATCAACTC 804
QY 661 CTGGATATACCTGGCACATCAGGAAGCAGACATTCATGGCCATGCTGCAAGCTGGG 720
Db |||||||
QY 805 CTGGATATACCTGGCACATCAGGAAGCAGACATTCATGGCCATGCTGCAAGCTGGG 864
QY 721 CAGAGGTTCTTTCTCTGATGGCTTCAATCAAGTCAAGCCCGCAGAACTGCCGAA 780
Db |||||||

Db 865 CAGAG3GTTCTTTCTTTGCTGCTACAAATGAATTCAGAGCCCGAGAACTGCCCGAA 924
QY 781 ATCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGGTCATCGTCAACCACTACC 840
Db |||||||
QY 925 ATCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGGTCATCGTCAACCACTACC 984
QY 841 ACTGAATGCTGCTGAGGACATACGCGAGTTTGGTGCCTCTGACTGTGAGGTGGGGATATG 900
Db |||||||
QY 985 ACTGAATGCTGCTGAGGACATACGCGAGTTTGGTGCCTCTGACTGTGAGGTGGGGATATG 1044
QY 901 ACAGAGACAGCGCCCGAGGCTCTCATCCGAGAAGTGTCTGATCAAGGAGCTTGTCTGAAGGC 960
Db |||||||
QY 1045 ACAGAGACAGCGCCCGAGGCTCTCATCCGAGAAGTGTCTGATCAAGGAGCTTGTCTGAAGGC 1104
QY 961 TTGTTCTCCCAAAATTCAGAAATCCAGGTGCTTGAAGGAATCTCATGAAGACCCCTCTCTTT 1020
Db |||||||
QY 1105 TTGTTCTCCCAAAATTCAGAAATCCAGGTGCTTGAAGGAATCTCATGAAGACCCCTCTCTTT 1164
QY 1021 GTGCTCTATCACTTTGTCAATCCAGATGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1080
Db |||||||
QY 1165 GTGCTCTATCACTTTGTCAATCCAGATGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1224
QY 1081 ACGCTGTCCCAATACCTTCTATGATCTGTGATACAGAAAACAAACACAAACATAAAGGT 1140
Db |||||||
QY 1225 ACGCTGTCCCAATACCTTCTATGATCTGTGATACAGAAAACAAACACAAACATAAAGGT 1284
QY 1141 GTGCTCTCAAGTGTACTTTCGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1200
Db |||||||
QY 1285 GTGCTCTCAAGTGTACTTTCGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1344
QY 1201 GTGCTCTCAAGTGTACTTTCGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1260
Db |||||||
QY 1345 GTGCTCTCAAGTGTACTTTCGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1404
QY 1261 GTGCTCTCAAGTGTACTTTCGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1320
Db |||||||
QY 1405 GTGCTCTCAAGTGTACTTTCGAGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1464
QY 1321 TTTCTTTTCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1380
Db |||||||
QY 1465 TTTCTTTTCAAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1524
QY 1381 TCTCATAGCCAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1440
Db |||||||
QY 1525 TCTCATAGCCAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1584
QY 1441 TCGGACATACACTTATAGCAGCTGCTCCGGTACACCTGCTGGTCACTCTGTGGAA 1500
Db |||||||
QY 1585 TCGGACATACACTTATAGCAGCTGCTCCGGTACACCTGCTGGTCACTCTGTGGAA 1644
QY 1501 GCCACCA3GGCTGTATGAAGCAGCTCCGACAGTGTATCAACACGCGTGCCTTCTCGGA 1560
Db |||||||
QY 1645 GCCACCA3GGCTGTATGAAGCAGCTCCGACAGTGTATCAACACGCGTGCCTTCTCGGA 1704
QY 1561 CTTTCCA3CGCCAAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAGTGTGAAAACACC 1620
Db |||||||
QY 1705 CTTTCCA3CGCCAAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAGTGTGAAAACACC 1764
QY 1621 ACTGAGCTAGAAATCTTGAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680
Db |||||||
QY 1765 ACTGAGCTAGAAATCTTGAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1824
QY 1681 TTATATCTAGAGATACATCCAAATCAGCCTGAGCCCAAGAAATTTGAAGCTTTCTTCAA 1740
Db |||||||
QY 1825 TTATATCTAGAGATACATCCAAATCAGCCTGAGCCCAAGAAATTTGAAGCTTTCTTCAA 1884
QY 1741 GGTAAAGCTTATATCAACTCAGGAACATCCCGATTAATTTGACTTTCTTTGAA 1800
Db |||||||
QY 1885 GGTAAAGCTTATATCAACTCAGGAACATCCCGATTAATTTGACTTTCTTTGAA 1944
QY 1801 CATTTGCC3AATTTGTGCAAGTGTCTGGACTTCAATTAAGTGGACTTTTATGGGGAGCT 1860
Db |||||||
QY 1945 CATTTGCC3AATTTGTGCAAGTGTCTGGACTTCAATTAAGTGGACTTTTATGGGGAGCT 2004

QY 1861 ATGGCTTTCATGGGAAAGGCTGCAGAAAGACACAGAGTGGGAATCCACATGGAAGAGGCCCA 1920
|||||
Db 2005 ATGGCTTTCATGGGAAAGGCTGCAGAAAGACACAGAGTGGGAATCCACATGGAAGAGGCCCA 2064
QY 1921 GAAACCTACATCCCGAGGAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGG 1980
|||||
Db 2065 GAAACCTACATCCCGAGGAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGG 2124
QY 1981 ACTCTGGAGGTACACTCCGGGATTTCCAGCAAGTTGCAATAAGCAAGATATCATATCTG 2040
|||||
Db 2125 ACTCTGGAGGTACACTCCGGGATTTCCAGCAAGTTGCAATAAGCAAGATATCATATCTG 2184
QY 2041 GGGAAATATTCAGCTCTCCCAAGCCTCAGCTCAGCTCAATATAAGAGATGTCTGTGTG 2100
|||||
Db 2185 GGGAAATATTCAGCTCTCCCAAGCCTCAGCTCAGCTCAATATAAGAGATGTCTGTGTG 2244
QY 2101 GCTGGAAGCCTCAGTTTGGTCTCTCAGCACCCTGTGAAGACATTTATCTCTCATGTGGAA 2160
|||||
Db 2245 GCTGGAAGCCTCAGTTTGGTCTCTCAGCACCCTGTGAAGACATTTATCTCTCATGTGGAA 2304
QY 2161 GCCAGTCCCTCACCATAGAAATGAGAGGCACATCAGATCTGTAAACAACCTGAAACCC 2220
|||||
Db 2305 GCCAGTCCCTCACCATAGAAATGAGAGGCACATCAGATCTGTAAACAACCTGAAACCC 2364
QY 2221 TTGAGTATTTCATGACCTACAGATCAACGGCTGCCGGGTGGTCTGACTCACAGCTTGGCT 2280
|||||
Db 2365 TTGAGTATTTCATGACCTACAGATCAACGGCTGCCGGGTGGTCTGACTCACAGCTTGGCT 2424
QY 2281 AACTTGAAGAACCTTTACAAAGCTCAATATGGATACATAAAGATGAATGAAGAGATGCT 2340
|||||
Db 2425 AACTTGAAGAACCTTTACAAAGCTCAATATGGATACATAAAGATGAATGAAGAGATGCT 2484
QY 2341 ATAAACTAGCTGAAGCCCTGAAAACCTGAAGAAGATGTGTTTATTTGACCCAC 2400
|||||
Db 2485 ATAAACTAGCTGAAGCCCTGAAAACCTGAAGAAGATGTGTTTATTTGACCCAC 2544
QY 2401 TTGCTCGACATGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTG 2460
|||||
Db 2545 TTGCTCGACATGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTG 2604
QY 2461 GACCTTGAAGAAATTCATATAGTCTCCTGCTGTGCTGCTGCAAAATGCAATTCCTA 2520
|||||
Db 2605 GACCTTGAAGAAATTCATATAGTCTCCTGCTGCTGCTGCAAAATGCAATTCCTA 2664
QY 2521 GCTCAGAATCTTCACAAATTTGGTCAAACGAGCATCTTGATTATCAGAAATACCTG 2580
|||||
Db 2665 GCTCAGAATCTTCACAAATTTGGTCAAACGAGCATCTTGATTATCAGAAATACCTG 2724
QY 2581 GAAAAAGATGGAAATGAAGCTCTTCATGAACCTGATCGACAGGATGAACGCTGCTAGAACAG 2640
|||||
Db 2725 GAAAAAGATGGAAATGAAGCTCTTCATGAACCTGATCGACAGGATGAACGCTGCTAGAACAG 2784
QY 2641 CTCACCGCACTGATGCTGCCCTGGGCTGTGACGTGCAAGGAGCGCTGACGAGCCCTGTG 2700
|||||
Db 2785 CTCACCGCACTGATGCTGCCCTGGGCTGTGACGTGCAAGGAGCGCTGACGAGCCCTGTG 2844
QY 2701 AAACATTTTGGAGAGGTCCCAACTCGTCAGCTTGGGTTGAAAACCTGGAGACTCACA 2760
|||||
Db 2845 AAACATTTTGGAGAGGTCCCAACTCGTCAGCTTGGGTTGAAAACCTGGAGACTCACA 2904
QY 2761 GATACAGAGATTAGAAATTTTAGGTGCATTTTGTGGAAAGAACCCCTCTGAAAACCTGCCAG 2820
|||||
Db 2905 GATACAGAGATTAGAAATTTTAGGTGCATTTTGTGGAAAGAACCCCTCTGAAAACCTGCCAG 2964
QY 2821 CAGTTGAATTTGGCGGGAATCGTGTGAGCAGTGTGATGGCTTGCCCTTCATGGGTGTA 2880
|||||
Db 2965 CAGTTGAATTTGGCGGGAATCGTGTGAGCAGTGTGATGGCTTGCCCTTCATGGGTGTA 3024
QY 2881 TTTGAGAAATCTTAAGCAATTTAGTGTTTTGTGACTTTAGTACTTAAGAAATTTCTACCTGAT 2940
|||||
Db 3025 TTTGAGAAATCTTAAGCAATTTAGTGTTTTGTGACTTTAGTACTTAAGAAATTTCTACCTGAT 3084

QY 2941 CCAGCATTTAGTCAGAAAACCTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCT 3000
|||||
Db 3085 CCAGCATTTAGTCAGAAAACCTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAGCT 3144
QY 3001 AGCGTTGTTGGTGCGCAATTTGATGATGATGATCTCAGTGTATTATACAGGTGCTTTTAA 3060
|||||
Db 3145 AGCGTTGTTGGTGCGCAATTTGATGATGATGATCTCAGTGTATTATACAGGTGCTTTTAA 3204
QY 3061 CTAGTAACCTGCT 3072
|||||
Db 3205 CTAGTAACCTGCT 3216
|||

RESULT 9
US-09-491-404-1319
; Sequence 1319, Application US/09491404
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Slinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 785
; CURRENT APPLICATION NUMBER: US/09/491,404
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 3796
; SOFTWARE: pc_sp_genes Version 1.0
; SEQ ID NO 1319
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (781)...(916)
; OTHER INFORMATION: this location contains the signal peptide sequence,
; OTHER INFORMATION: MLWGSCKKALTKFKVFFLRSLRAQGLFETLCDQLLDIPGIR, Run with Signal
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (679)...(3279)
; OTHER INFORMATION: similar to gl3688110 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-491-404-1319

Query Match 95.0%; Score 2919; DB 18; Length 3545;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3069; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGACAAATAGCCGAGGCCCTTATTCAAAGAAATGGAATGACTGTATA 60
|||||
Db 232 ATGAATTTTCATAAAGGACAAATAGCCGAGGCCCTTATTCAAAGAAATGGAATGACTGTATA 291
QY 61 AAGCAAAATCACAGATGACCTATTTGTATGGAATGTTCTGAATCGCGGAAGATAAACATC 120
|||||
Db 292 AAGCAAAATCACAGATGACCTATTTGTATGGAATGTTCTGAATCGCGGAAGATAAACATC 351
QY 121 ATTTGCTCGGAGAAAGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGAA 180
|||||
Db 352 ATTTGCTCGGAGAAAGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGAA 411
QY 181 AAGGGTTACAGAGTCCTGTAAACCTCTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 240
|||||
Db 412 AAGGGTTACAGAGTCCTGTAAACCTCTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 471
QY 241 TTTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAAGAGACATTGGACGAT 300
|||||
Db 472 TTTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAAGAGACATTGGACGAT 531
QY 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACTTTTATCCCTT 360
|||||
Db 532 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACTTTTATCCCTT 591
|||||

Db 1252 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACAAACA 1311
Qy 1081 ACGTGTGTCCATACCTTCTATGATCTGTGTATACAGAAAAACAACATAAAGGT 1140
Db 1312 ACGTGTGTCCATACCTTCTATGATCTGTGTATACAGAAAAACAACATAAAGGT 1371
Qy 1141 GTGGCTGCAAGTGACTTCATTCGGAGGCTTGACCACTGTGGAGACCTAGCTCTGGAGGGT 1200
Db 1372 GTGGCTGCAAGTGACTTCATTCGGAGGCTTGACCACTGTGGATACCTAGCTCTGGAGGGT 1431
Qy 1201 GTGGTTCGCCACAAGTTTGATTTCCGAATCGCAGATGTGCCAGCTGAATGAGGATGC 1260
Db 1432 GTGGTTCGCCACAAGTTTGATTTCCGAATCGCAGATGTGCCAGCTGAATGAGGATGC 1491
Qy 1261 CTGGTGACAACTGGGCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAA 1320
Db 1492 CTGGTGACAACTGGGCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAA 1551
Qy 1321 TTCTTTTCAAGTCAATTCAGGAGTACACAGCAGGAGAGACATCAGCAGTTTATTCAGC 1380
Db 1552 TTCTTTTCAAGTCAATTCAGGAGTACACAGCAGGAGAGACATCAGCAGTTTATTCAGC 1611
Qy 1381 TCTCATGAGCCAGAGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAATGGTTTCCATT 1440
Db 1612 TCTCATGAGCCAGAGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAATGGTTTCCATT 1671
Qy 1441 TCGACATTTACATCCACTTATAGCAGGCTGCTCCGGTACACCTGTGGGTCACTGTGGAA 1500
Db 1672 TCGACATTTACATCCACTTATAGCAGGCTGCTCCGGTACACCTGTGGGTCACTGTGGAA 1731
Qy 1501 GCCACAGGGGTGTATGAAGCACTCGCAGCAGTGTATCAACACGGCTGCTTCTCGGA 1560
Db 1732 GCCACAGGGGTGTATGAAGCACTCGCAGCAGTGTATCAACACGGCTGCTTCTCGGA 1791
Qy 1561 CTTTTCATCGCAAGAGGCTCTCTGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1620
Db 1792 CTTTTCATCGCAAGAGGCTCTCTGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1851
Qy 1621 ACTGAGCAAGAAATCTGAAAGCCATAAATCAATCAATTCCTTTGTAGAGTGTGCAATCCAT 1680
Db 1852 ACTGAGCAAGAAATCTGAAAGCCATAAATCAATCAATTCCTTTGTAGAGTGTGCAATCCAT 1911
Qy 1681 TTATATCAAGAGTACATCAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAA 1740
Db 1912 TTATATCAAGAGTACATCAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAA 1971
Qy 1741 GGTAAGCTTATATATCAACTCAGGAACATCCCGATTAATTTGACTTCTTTGAA 1800
Db 1972 GGTAAGCTTATATATCAACTCAGGAACATCCCGATTAATTTGACTTCTTTGAA 2031
Qy 1801 CATTTGCCCAATTTGTCAAGTCTCTGGACTTCAATTAACCTGGAATTTATGGGGAGCT 1860
Db 2032 CATTTGCCCAATTTGTCAAGTCTCTGGACTTCAATTAACCTGGAATTTATGGGGAGCT 2091
Qy 1861 ATGGCTTTCATGGGAAAAGGCTGCAGAGACACAGGTGGAATPCCATGGAAGAGGCCCA 1920
Db 2092 ATGGCTTTCATGGGAAAAGGCTGCAGAGACACAGGTGGAATPCCATGGAAGAGGCCCA 2151
Qy 1921 GAAACCTTACATTCACAGCAGGCTGTATCTTTGTTCCTCAACTGGAAGCAGGAATTCAGG 1980
Db 2152 GAAACCTTACATTCACAGCAGGCTGTATCTTTGTTCCTCAACTGGAAGCAGGAATTCAGG 2211
Qy 1981 ACTCTGAGGTACACTCCGGGATTTTCAGCAAGTTTGAATAAGCAAGATATCACATATCTG 2040
Db 2212 ACTCTGAGGTACACTCCGGGATTTTCAGCAAGTTTGAATAAGCAAGATATCACATATCTG 2271
Qy 2041 GGGAAAATATTCAGCTCTGCCACAAGCTCAGGCTGCAAAATAAGAGATGTGCTGGGTG 2100
Db 2272 GGGAAAATATTCAGCTCTGCCACAAGCTCAGGCTGCAAAATAAGAGATGTGCTGGGTG 2331
Qy 2101 GCTGGAAGCTTCAGTTTGGTCTCAGCACTGTGAAGACATTTATCTCTCATGGTGGAA 2160
Db 2332 GCTGGAAGCTTCAGTTTGGTCTCAGCACTGTGAAGACATTTATCTCTCATGGTGGAA 2391

Qy 2161 GCCAGTCCCTCACATAGAGATGAGAGGCACATCATCTGTAAACAAACCTGAAAACC 2220
Db 2392 GCCAGTCCCTCACATAGAGATGAGAGGCACATCATCTGTAAACAAACCTGAAAACC 2451
Qy 2221 TTGAGATTCTATGACCTACAGAACTCAACGGCTGCGGGTGTCTGACTGACAGCTTGGGT 2280
Db 2452 TTGAGATTCTATGACCTACAGAACTCAACGGCTGCGGGTGTCTGACTGACAGCTTGGGT 2511
Qy 2281 AACCTTAAGAACCTTACAAAAGCTCATATATGATAAACAATAAGATGAATGAAGAAGATGCT 2340
Db 2512 AACCTTAAGAACCTTACAAAAGCTCATATATGATAAACAATAAGATGAATGAAGAAGATGCT 2571
Qy 2341 ATAAATAGCTGAGGCTCAAAAAGCTGAAAGATGATGTTTATTTTCATTTGACCCAC 2400
Db 2572 ATAAATAGCTGAGGCTGAAAGATGATGTTTATTTTCATTTGACCCAC 2631
Qy 2401 TTGCTGACATTTGAGAGGGAATGGATACATAGTCAAGTCTCTGTCGAAGTGAACCTGT 2460
Db 2632 TTGCTGACATTTGAGAGGGAATGGATACATAGTCAAGTCTCTGTCGAAGTGAACCTGT 2691
Qy 2461 GACCTTAAGAAATTCATATAGTCTCTGCTGCTGCTGCAAAATGAGTGAATAATGCTA 2520
Db 2692 GACCTTAAGAAATTCATATAGTCTCTGCTGCTGCTGCAAAATGAGTGAATAATGCTA 2751
Qy 2521 GCTCAGAACTTTCACAAATTTGGTCAAACTGAGCAATCTTGATTTATCAGAAAAATACCTG 2580
Db 2752 GCTCAGAACTTTCACAAATTTGGTCAAACTGAGCAATCTTGATTTATCAGAAAAATACCTG 2811
Qy 2581 GAAAAATATGAAATGAAGCTCTTCATGAATGATCGACAGGATGAACGCTGTAAGACAG 2640
Db 2812 GAAAAATATGAAATGAAGCTCTTCATGAATGATCGACAGGATGAACGCTGTAAGACAG 2871
Qy 2641 CTCACCTCAGTGTGCTGCTGCGGCTGTGACGTGCAAGCAGCCTGAGCAGCTGTG 2700
Db 2872 CTCACCTCAGTGTGCTGCTGCGGCTGTGACGTGCAAGCAGCCTGAGCAGCTGTG 2931
Qy 2701 AAACATTTGAGAGAGTCCACACACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACA 2760
Db 2932 AAACATTTGAGAGAGTCCACACACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACA 2991
Qy 2761 GATACATAGATTAAGATTTAGGTGCAATTTTGGAAAGACCTCTGAAAACTTCCAG 2820
Db 2992 GATACATAGATTAAGATTTAGGTGCAATTTTGGAAAGACCTCTGAAAACTTCCAG 3051
Qy 2821 CAGTTGATTGCGGGAATTCGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGTA 2880
Db 3052 CAGTTGATTGCGGGAATTCGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGTA 3111
Qy 2881 TTTGAGATCTTAAGCAATTAGTGTGTTTTGACHTTTAGTACTAAAGAAATTTCTACCTGAT 2940
Db 3112 TTTGAGATCTTAAGCAATTAGTGTGTTTTGACHTTTAGTACTAAAGAAATTTCTACCTGAT 3171
Qy 2941 CCAGCATAGTCAAGAACTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAAGCT 3000
Db 3172 CCAGCATAGTCAAGAACTTAGCCAAAGTGTATCCAAAGTTAACTTTTCTGCAAGAAAGCT 3231
Qy 3001 AGGCTTCTGGGTGGCAATTTGATGATGATGATCTCAGTGTATTACAGGTGCTTTTAAA 3060
Db 3232 AGGCTTCTGGGTGGCAATTTGATGATGATGATCTCAGTGTATTACAGGTGCTTTTAAA 3291
Qy 3061 CTAGTAATCTGCT 3072
Db 3292 CTAGTAATCTGCT 3303

RESULT 11
US-09-922-279A-1319
; Sequence 1319, Application US/09922279A
; GENERAL INFORMATION:
; APPLICANT: Tanji, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Siku, Ankura

APPLICANT: Liu, Chinghua
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 785
CURRENT APPLICATION NUMBER: US/09/922,279A
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 3796
SOFTWARE: pt_sp_genes Version 1.0
SEQ ID NO 1319
LENGTH: 3545
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (781)...(916)
OTHER INFORMATION: this location contains the signal peptide sequence,
OTHER INFORMATION: MLWGGKCKALTKFKFVFFLRLSRAGGLFETLCDQLLDIPGTR, Run with signalp
NAME/KEY: misc_feature
LOCATION: (679)...(3279)
OTHER INFORMATION: similar to q13688110 in the genepept database release 114,
OTHER INFORMATION: Run with FASTXY 3.3c00, default parameters
US-09-922-279A-1319

Query Match		95.0%;	Score 2919;	DB 34;	Length 3545;
Best Local Similarity		99.9%;	Pred. No. 0;		
Matches 3069;		Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	1	ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAGAATGGGAATGACTGTTATA	60		
DB	232	ATGAATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAGAATGGGAATGACTGTTATA	291		
QY	61	AAGCAATACACAGATCACCATTATTGTATGGAATGTTCTGAATCGCGAAGTAACATC	120		
DB	292	AAGCAATACACAGATCACCATTATTGTATGGAATGTTCTGAATCGCGAAGTAACATC	351		
QY	121	ATTTGCTCGGAGAGGTGGAGGAGTGTGCTAGAGGATCATTCACATGATTTTGA	180		
DB	352	ATTTGCTCGGAGAGGTGGAGGAGTGTGCTAGAGGATCATTCACATGATTTTGA	411		
QY	181	AAGGTTTCAGAGTCCCTTAACCTCTTTCTTAATCCCTTAAAGAGTGGAACTATCCTTA	240		
DB	412	AAGGTTTCAGAGTCCCTTAACCTCTTTCTTAATCCCTTAAAGAGTGGAACTATCCTTA	471		
QY	241	TTTCAGGACTTGAATGGCAAAAGTCTTTTCATCAGACATCAGAAGGAGCTTGGACGAT	300		
DB	472	TTTCAGGACTTGAATGGCAAAAGTCTTTTCATCAGACATCAGAAGGAGCTTGGACGAT	531		
QY	301	TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACCTTTATCCCTT	360		
DB	532	TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACCTTTATCCCTT	591		
QY	361	GGTGAAGATATTGACATATTTTAACTTGAAGAGCACCTTCACAGAACCTGTCTGTGG	420		
DB	592	GGTGAAGATATTGACATATTTTAACTTGAAGAGCACCTTCACAGAACCTGTCTGTGG	651		
QY	421	AGGAGGACCAACACCATCAGCGGTGGAGAGCTGACCCCTGAATGGCCCTCTGACGGCT	480		
DB	652	AGGAGGACCAACACCATCAGCGGTGGAGAGCTGACCCCTGAATGGCCCTCTGACGGCT	711		
QY	481	CTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG	540		
DB	712	CTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG	771		
QY	541	CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGGCTCTGACCAAGTTCAAATTCGTC	600		
DB	772	CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGGCTCTGACCAAGTTCAAATTCGTC	831		
QY	601	TTCTTCTCCGCTCAGCAGGCGCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTC	660		
DB	832	TTCTTCTCCGCTCAGCAGGCGCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTC	891		

QY	661	CTGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTCGG	720
DB	892	CTGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTCGG	951
QY	721	CAGAGGGTCTTTTCTCTTGTATGGCTACATGAATTCAGAGCCAGAACTGCCAGAA	780
DB	952	CAGAGGGTCTTTTCTCTTGTATGGCTACATGAATTCAGAGCCAGAACTGCCAGAA	1011
QY	781	ATCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGTCATCGTCACCACTACC	840
DB	1012	ATCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGTCATCGTCACCACTACC	1071
QY	841	ACTGAGTGCTTGAGGCACATACGGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATG	900
DB	1072	ACTGAGTGCTTGAGGCACATACGGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATG	1131
QY	901	ACAGAAGACAGCCGCCAGGCTCTCATCCAGAGAGTCTGATCAAGAGCTTGTCTGAAGC	960
DB	1132	ACAGAAGACAGCCGCCAGGCTCTCATCCGAGAAAGTCTGATCAAGAGCTTGTCTGAAGC	1191
QY	961	TTGTTCTCCAAATTCAGAAATCCAGGTGCTTCAGGAATCTCATGAAGACCCCTCTCTT	1020
DB	1192	TTGTTCTCCAAATTCAGAAATCCAGGTGCTTCAGGAATCTCATGAAGACCCCTCTCTT	1251
QY	1021	GTGGTCATCATTGTGCAATCCAGATGGGTGAAAGTCTGATCCACTCTCACACACAACA	1080
DB	1252	GTGGTCATCATTGTGCAATCCAGATGGGTGAAAGTCTGATCCACTCTCACACACAACA	1311
QY	1081	AGCTGTTCCATACCTTCTATGATCTGTGATACAGAAACAAACACAAACATAAAGT	1140
DB	1312	AGCTGTTCCATACCTTCTATGATCTGTGATACAGAAACAAACACAAACATAAAGT	1371
QY	1141	GTGGCTGCAAGTGACTTTCATTCGGAGCTGGACCTGTGGAGCTAGCTCTGGAGGT	1200
DB	1372	GTGGCTGCAAGTGACTTTCATTCGGAGCTGGACCTGTGGAGCTAGCTCTGGAGGT	1431
QY	1201	GTGTTCTCCACAAAGTTTGAATTCGAACTGCAGAGTGTGCCAGCTGATAGAGTATC	1260
DB	1432	GTGTTCTCCACAAAGTTTGAATTCGAACTGCAGAGTGTGCCAGCTGATAGAGTATC	1491
QY	1261	CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAAGTTCAGGCCAAAGTATAA	1320
DB	1492	CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAAGTTCAGGCCAAAGTATAA	1551
QY	1321	TTCTTTCAAGTCAATCCAGGAGTACACAGCAGGAGGAGACTCAGCAGTTTATTGACG	1380
DB	1552	TTCTTTCAAGTCAATCCAGGAGTACACAGCAGGAGGAGACTCAGCAGTTTATTGACG	1611
QY	1381	TCTCATGAGCCAGAGGAGGTGACCAAGGGAAATGGTTACTTGCAGAAAAATGGTTCCAT	1440
DB	1612	TCTCATGAGCCAGAGGAGGTGACCAAGGGAAATGGTTACTTGCAGAAAAATGGTTCCAT	1671
QY	1441	TCGGACATTACATPCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTATCTGTGGAA	1500
DB	1672	TCGGACATTACATPCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTATCTGTGGAA	1731
QY	1501	GCCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACAGGCTGCCCTTCGGA	1560
DB	1732	GCCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACAGGCTGCCCTTCGGA	1791
QY	1561	CTTTCCATCGCCAAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACC	1620
DB	1792	CTTTCCATCGCCAAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACC	1851
QY	1621	ACTGAGCAAGAAATCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCCAT	1680
DB	1852	ACTGAGCAAGAAATCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCCAT	1911
QY	1681	TTATATCAGAGAGTACATCCAAATCAGCCCTGAGCCAGGAATTTGAAGCTTCTTTCAA	1740
DB	1912	TTATATCAGAGAGTACATCCAAATCAGCCCTGAGCCCTGAGCCCTGAGCCCTTCTTTCAA	1971

QY 362 GTGAAGATATTGACATTTATTTTAACTTGAAAGACACCTTCACAGAACCTGTCTGTGGA 421
|||||
Db 500 GTGAAGATATTGACATTTATTTTAACTTGAAAGACACCTTCACAGAACCTGTCTGTGGA 559
|||||
QY 422 GGAAGACCAACACCATCATCCGGTGGAGACGTGACCCCTGAATGGCTTCTGCGAGGCTC 481
|||||
Db 560 GGAAGACCAACACCATCATCCGGTGGAGACGTGACCCCTGAATGGCTTCTGCGAGGCTC 619
|||||
QY 482 TTCAGAGCCCTGTCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCACG 541
|||||
Db 620 TTCAGAGCCCTGTCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCACG 679
|||||
QY 542 GCATTGCCATGCTTGGGGCTCCGGAAAGTGCAAGGCTCTGCACCAAGTTCAAAATTCGTCT 601
|||||
Db 680 GAATTGCCATGCTTGGGGCTCCGGAAAGTGCAAGGCTCTGCACCAAGTTCAAAATTCGTCT 739
|||||
QY 602 TCTTCTCCGCTCAGCAGGGCCAGGGTGGAGCTTTTGAACCCCTCTGTGATCAACTCC 661
|||||
Db 740 TCTTCTCCGCTCAGCAGGGCCAGGGTGGAGCTTTTGAACCCCTCTGTGATCAACTCC 799
|||||
QY 662 TGSATATACCTGSCACAANTCAGSAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGCG 721
|||||
Db 800 TGSATATACCTGSCACAANTCAGSAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGCG 859
|||||
QY 722 AGAGGGTCTCTTTTCCCTTCTTGATGGCTACAATGAATTCAGGCCCCAGAACTGCCAGAAA 781
|||||
Db 860 AGAGGGTCTCTTTTCCCTTCTTGATGGCTACAATGAATTCAGGCCCCAGAACTGCCAGAAA 919
|||||
QY 782 TCGAAGCCCTGATAAAGGAAAACCCAGCGCTTCAAGAACATGCTCATCGCTACCCACTACCA 841
|||||
Db 920 TCGAAGCCCTGATAAAGGAAAACCCAGCGCTTCAAGAACATGCTCATCGCTACCCACTACCA 979
|||||
QY 842 CTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGGATATCA 901
|||||
Db 980 CTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGGATATCA 1039
|||||
QY 902 CAGAAGACAGCCCGCAGGCTCTCATCCGAGAAAGTGTGATCAAGGAGCTTGCTGAAGGCT 961
|||||
Db 1040 CAGAAGACAGCCCGCAGGCTCTCATCCGAGAAAGTGTGATCAAGGAGCTTGCTGAAGGCT 1099
|||||
QY 962 TGTGTCTCCAAATTCAGAAATCCAGGTGCTTGAAGAAATCTCATGAAGACCCCTCTCTTTG 1021
|||||
Db 1100 TGTGTCTCCAAATTCAGAAATCCAGGTGCTTGAAGAAATCTCATGAAGACCCCTCTCTTTG 1159
|||||
QY 1022 TGSCTCATCTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACACAACAA 1081
|||||
Db 1160 TGSCTCATCTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACACAACAA 1219
|||||
QY 1082 CGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACAAACATAAAGGTG 1141
|||||
Db 1220 CGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACATAAAGGTG 1279
|||||
QY 1142 TGGCTGCAAGTGACTTCATTCGGAGCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTG 1201
|||||
Db 1280 TGGCTGCAAGTGACTTCATTCGGAGCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTG 1339
|||||
QY 1202 TGTCTCCACAAAGTTTGATTTTCGAACCTCAGGATGTGTCCAGCGTGAATGAGGATGTCC 1261
|||||
Db 1340 TGTCTCCACAAAGTTTGATTTTCGAACCTCAGGATGTGTCCAGCGTGAATGAGGATGTCC 1399
|||||
QY 1262 TGCTGACAACTGGGCTCTCTTAATATACAGCTCAAAAGTTCAAGGCCAAAGATATAAT 1321
|||||
Db 1400 TGCTGACAACTGGGCTCTCTTAATATACAGCTCAAAAGTTCAAGGCCAAAGATATAAT 1459
|||||
QY 1322 TCTTTTCAGAACTTCAGGAGTACACAGAGGAGGAGACTCAGAGCTTATTGACGT 1381
|||||
Db 1460 TCTTTTCAGAACTTCAGGAGTACACAGAGGAGGAGACTCAGAGCTTATTGACGT 1519
|||||
QY 1382 CTCATGAGCCAGAGGAGTACCAAGGGGAATGGTTACTTTCAGAAAAATGGTTCCATTT 1441
|||||
Db 1520 CTCATGAGCCAGAGGAGTACCAAGGGGAATGGTTACTTTCAGAAAAATGGTTCCATTT 1579
|||||

QY 1442 CGGACATTTACATCCACTTATAGACGCTCTGCTCGGTACACCTGTGGGTCAATCTGTGGAAG 1501
|||||
Db 1580 CGGACATTTACATCCACTTATAGACGCTCTGCTCGGTACACCTGTGGGTCAATCTGTGGAAG 1639
|||||
QY 1502 CCACCAAGGCTGTTATGAAGCACCCTCGCAGCAGTGTATCAACACGCTGCCCTCTCGGAC 1561
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Db 1640 CCACCAAGGCTGTTATGAAGCACCCTCGCAGCAGTGTATCAACACGCTGCCCTCTCGGAC 1699
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QY 1622 CTGAGCAAGAAATCTTGAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCAATT 1681
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QY 1682 TATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTCAAG 1741
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Db 1820 TATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTCAAG 1879
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QY 1802 ATTTGGCCCAATTTGTCAAGTGTCTGGACTTTCATTTAAACTGGACTTTTATGGGGAGCTA 1861
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QY 1862 TGGCTTATCGGAAAGGCTGCAGAAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAG 1921
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Db 2000 TGGCTTATCGGAAAGGCTGCAGAAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAG 2059
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QY 1922 AAACCTTACATTCACAGCAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGA 1981
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QY 2042 GGAATAATTTACGTCTGCCACAAGCCTCAGGCTGCAATTAAGAAAGATGTGCTGGTGTGG 2101
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QY 2102 CTGGAGCCCTCAGTTTGGTCTCAGCACCTGTAAAGAACTTTATTTCTCATCGTGGGAAG 2161
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QY 2222 TGAGTATTCATGACCTCAGAAATCAGGCTGCCGGGTGCTGACTGACAGCTGGGTA 2281
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QY 2282 ACTTGAAGAACCTTCAAAAGCTCATAATGGATAAAGATGAATGAAGATGCTA 2341
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QY 2342 TAAAACTAGCTGAAGCCCTGAAAAACCTGAAAGAGATGTGTTTATTTTCATTTGACCCACT 2401
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Db 3020 TTGAGAACTTTAAGCAATTTAGTGTTTGTGACTTTTACTTAAAGAAATTTCTACCTGATC 3079
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Db 3080 CAGCATTTAGTCAGAAAATTTAGCCAACTGTATCCAAAGTTAACTTTCTGCAAGAAGCTA 3139
Qy 3002 GCCTGTGGTGGCAATTTGATGATGATGATCTCAGTGTATTTACAGGTGCTTTTAAAC 3061
Db 3140 GCCTGTGGTGGCAATTTGATGATGATGATCTCAGTGTATTTACAGGTGCTTTTAAAC 3199
Qy 3062 TAGTAACTGCT 3072
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RESULT 13

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US-10-221-097-23
; Sequence 23, Application US/10221097
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/10/221,097
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-221-097-23
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Query Match 95.0%; Score 2918; DB 42; Length 3213;
Best Local Similarity 99.9%; Pred. No. 0;

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Db 140 TGAATTTTCATAAAGGACAATAGCGGAGCCCTTATTTCAAAAGTAATGGGAATGACTCTTTATAA 199
Qy 62 AGCAATTCACAGATGACCTATTTGTATGGAATGTTCTGGAATCGCGAAGAGTAAACATCA 121
Db 200 AGCAATTCACAGATGACCTATTTGTATGGAATGTTCTGGAATCGCGAAGAGTAAACATCA 259
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Db 260 TTTGCTCGCGAAGAGGTGGAGCAGATGCTGCTAGAGGATCAATTCACATGATTTTGAATA 319
Qy 182 AGGTTTCAGAGTCCCTGTAACCTCTTTCTTAAATCCCTTAAGGAGTGAAGCTATCTCTAT 241
Db 320 AGGTTTCAGAGTCCCTGTAACCTCTTTCTTAAATCCCTTAAGGAGTGAAGCTATCTCTAT 379
Qy 242 TTCAGGACTTGAATTTGAGCAAAAGTCTTTTTCATCAGACATCAGAAGGAGACTTTGACGAT 301
Db 380 TTCAGGACTTGAATTTGAGCAAAAGTCTTTTTCATCAGACATCAGAAGGAGACTTTGACGAT 439
Qy 302 TGGCTCAGGATTTAAAGGACTTTGACCATACCCCATCTTTTCTGAACTTTTATCCCTTG 361
Db 440 TGGCTCAGGATTTAAAGGACTTTGACCATACCCCATCTTTTCTGAACTTTTATCCCTTG 499
Qy 362 GTGAAGTATATGACATTTTAACTTTGAAAGCACTTTCACAGAACCTGTCTCTGGGA 421
Db 500 GTGAAGTATATGACATTTTAACTTTGAAAGCACTTTCACAGAACCTGTCTCTGGGA 559
Qy 422 GGAAGTCCCAACACCATCACCGGTGGAGCAGCTGACCTGAAATGGGCTCTCTGAGGCTC 481
Db 560 GGAAGTCCCAACACCATCACCGGTGGAGCAGCTGACCTGAAATGGGCTCTCTGAGGCTC 619
Qy 482 TTCAGACTCCCTGTGATCATTTGAAGGGAAATCTTGCAAAAGGCAAGTCCACATCTGTGTCAGC 541
Db 620 TTCAGACTCCCTGTGATCATTTGAAGGGAAATCTTGCAAAAGGCAAGTCCACATCTGTGTCAGC 679
Qy 542 GCATTCATGCTCTGGGCTCCGGAAGTGCAGAGCTCTGACCAAGTCTCAAAATTCGCT 601
Db 680 GCATTCATGCTCTGGGCTCCGGAAGTGCAGAGCTCTGACCAAGTCTCAAAATTCGCT 739
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Db 740 TCTTCCCTCGTCTCAGCAGGGCCCGAGGTGGACTTTTGAACCCCTCTGTGATCAACTCC 799
Qy 662 TGGATATCTCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGGC 721
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Db 920 TCGAAGCTCTGATTAAGGAACACCGCTTCAAGAACATGGTCTGTCACCACTACCA 979
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Db 1160 TGTGCTATCACTTGTGCAATCCAGATGGGTGAAAGTGAAGTCCACTCTCAGACACAAACAA 1219
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; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Olivella, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: Novel Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(3348)
; US-09-864-921-96
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Query Match 93.4%; Score 2868; DB 33; Length 3396;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3068; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGAAATTCATAAAGGACAATAGCGAGCCCTTATTCAAAGAAATGGGAATGACTGTTATA 60
DB 277 ATGAAATTCATAAAGGACAATAGCGAGCCCTTATTCAAAGAAATGGGAATGACTGTTATA 336

QY 61 AAGCAAAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAATAACATC 120
DB 337 AAGCAAAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAATAACATC 396

QY 121 ATTTGCTCGGAGAAGTGGAGCAGGATGCTGTACAGGAGTCAATCACATGATTTTGAA 180
DB 397 ATTTGCTCGGAGAAGTGGAGCAGGATGCTGTACAGGAGTCAATCACATGATTTTGAA 456

QY 181 AAGGGTTCAGAGTCTGTAACTCTTTCTTAAATCCCTTAAAGGAGTGAACATATCCTCTA 240
DB 457 AAGGGTTCAGAGTCTGTAACTCTTTCTTAAATCCCTTAAAGGAGTGAACATATCCTCTA 516

QY 241 TTTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGACGAT 300
DB 517 TTTTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGACGAT 576

QY 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATTTTCTGAATTTTATCCCTT 360
DB 577 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATTTTCTGAATTTTATCCCTT 636

QY 361 GGTGAAGATATGACATATTTTAACTTGAAGACCTTTCACAGACCTGCTCTGTGG 420
DB 637 GGTGAAGATATGACATATTTTAACTTGAAGACCTTTCACAGACCTGCTCTGTGG 696

QY 421 AGGAAGACCAACACCATCACCGCTGGAGCAGTGCACCCCTGAATGGCTCTCTGAGGCT 480
DB 697 AGGAAGACCAACACCATCACCGCTGGAGCAGTGCACCCCTGAATGGCTCTCTGAGGCT 756

QY 481 CTTTCAGACCCCTGCATCATTTGAAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGAG 540
DB 757 CTTTCAGACCCCTGCATCATTTGAAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGAG 816

QY 541 CGCATTTGCATGCTCTGGGGCTCCGGAAGTGCAAGGCTCTGACCAAGTTCAAAATTCGTC 600
DB 817 CGCATTTGCATGCTCTGGGGCTCCGGAAGTGCAAGGCTCTGACCAAGTTCAAAATTCGTC 876

QY 601 TTTCTCCCTCCGCTCTCAGCAGGCGCCAGGCTGACTTTTGAACCCCTCTGTGATCAACTC 660
DB 876 TTTCTCCCTCCGCTCTCAGCAGGCGCCAGGCTGACTTTTGAACCCCTCTGTGATCAACTC 2016
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QY 841 ACTGAJTGCCCTGAGGCACATAGCGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGATATG 900
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DB 1957 GTGGTATFACATGTGCAATCCAGATGGGTGAAAGTGGAGTTCCTCATCACACAAACA 2016
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QY 320 ACTGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGTGTAAGATATTGACATTA 379
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QY 380 TTTTAACTTGAAGACACTTTCACAGAACCTGTCTGTGGAGGAAGGACCACACACCATC 439
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QY 500 TTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAAGCGCATTCGCATGCTCTGGG 559
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QY 1700 CCAATTCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTCAAGGTAAAGCTTATATATCA 1759
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Db 1976 CCAATTCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTCAAGGTAAAGCTTATATATCA 2035
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QY 1760 ACTCA3GGAAACATCCCGGATTAATTTGACTTCTTTGAACATTTTGGCCAAATTTGCA 1819
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Db 2036 ACTCA3GGAAACATCCCGGATTAATTTGACTTCTTTGAACATTTTGGCCAAATTTGCA 2095
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QY 1820 GTGCTTTGGACTTCAATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGG 1879
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|||||
QY 1880 CTGCA3AAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAAACCTACATTTCCAGCA 1939
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Db 2156 CTGCA3AAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAAACCTACATTTCCAGCA 2215
|||||
QY 1940 GGGCTTTATCTTTTGTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTCAACCTCC 1999
|||||
Db 2216 GGGCTTTATCTTTTGTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTCAACCTCC 2275
|||||
QY 2000 GGGATTTCAAGCAAGTGAATAAGCAAGATATCACATATCTCTGGGAAAAATTTACGCTCG 2059
|||||
Db 2276 GGGATTTCAAGCAAGTGAATAAGCAAGATATCACATATCTCTGGGAAAAATTTACGCTCG 2335
|||||
QY 2060 CCACAGCCTCAGGCTGCAAAATAAAGAGATGCTGGTGTGGCTGGAAGCCCTCAGTTTG 2119
|||||
Db 2336 CCACAGCCTCAGGCTGCAAAATAAAGAGATGCTGGTGTGGCTGGAAGCCCTCAGTTTG 2395
|||||
QY 2120 TCCTCTGCACCTGTGAAGACATTTATCTCTCATGGTGGAGCCAGTCCCTCCACATAG 2179
|||||
Db 2396 TCCTCTGCACCTGTGAAGACATTTATCTCTCATGGTGGAGCCAGTCCCTCCACATAG 2455
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QY 2180 AAGATCAGAGGCACATCAGATCTGTAACAAACCTGAAAACCTTGAGTATTCATGACCTAC 2239
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Db 2456 AAGATCAGAGGCACATCAGATCTGTAACAAACCTGAAAACCTTGAGTATTCATGACCTAC 2515
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QY 2240 AGAATCAGCGGTGCGGGTGGTCTGACTGACAGCTTTGGGTAACTTGAAGAACCCTTACAA 2299
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Db 2516 AGAATCAGCGGTGCGGGTGGTCTGACTGACAGCTTTGGGTAACTTGAAGAACCCTTACAA 2575
|||||
QY 2300 AGCTCTAATATGATTAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGGCC 2359
|||||
Db 2576 AGCTCTAATATGATTAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGGCC 2635
|||||
QY 2360 TGAATAACCTGAAGAAGATGCTGTTTATTTTCATTTTCCACCCACTGTCTGACATTTGAGAGG 2419
|||||
Db 2636 TGAATAACCTGAAGAAGATGCTGTTTATTTTCATTTTCCACCCACTGTCTGACATTTGAGAGG 2695
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QY 2420 GAATGATATACATGCTGAGTCTGCTCAAGTGAAACCTGACCTTGAGAAATTCAT 2479
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Db 2696 GAATGATATACATGCTGAGTCTGCTCAAGTGAAACCTGACCTTGAGAAATTCAT 2755
|||||
QY 2480 TAGTCTCTGCTGCTTCTGCAAAATGCAAGTGAATAATCCTAGCTCAGAACTTTCACAAT 2539
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Db 2756 TAGTCTCCCTGCTGTGCTCAAAATGCAGTGAATAATCTAGCTCAGAAATCTTCAAAAT 2815
QY 2540 TGGTCAAACTGAGCATCTTTGATTTATCAGAAAATACCTGGAAGAAGATGGAATGAAG 2599
Db 2816 TGGTCAAACTGAGCATCTTTGATTTATCAGAAAATACCTGGAAGAAGATGGAATGAAG 2875
QY 2600 CTCCTCATGAACATGATGCAGAGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGC 2659
Db 2876 CTCCTCATGAACATGATGCAGAGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGC 2935
QY 2660 CTTGGGGCTGTGACGTGCAAGCAGCCTGAGCAGCCTGTGAAACATTTGGAGGAGTCC 2719
Db 2936 CTTGGGGCTGTGACGTGCAAGCAGCCTGAGCAGCCTGTGAAACATTTGGAGGAGTCC 2995
QY 2720 CACAACCTCGTCAAGCTTTGGGTTGAAAACCTGGAGACTCACAGATACAGAGATTAGAAATTT 2779
Db 2996 CACAACCTCGTCAAGCTTTGGGTTGAAAACCTGGAGACTCACAGATACAGAGATTAGAAATTT 3055
QY 2780 TAGGTGCATTTTTTGGAAAGAACCCCTCTGAAAACCTCCAGCAGTTGAAATTTGGCGGAA 2839
Db 3056 TAGGTGCATTTTTTGGAAAGAACCCCTCTGAAAACCTCCAGCAGTTGAAATTTGGCGGAA 3115
QY 2840 ATCGTGTGAGCAGTATGATGGCTTGCCTTCATGGGTGTATTTGAGAATCTTAAGCAAT 2899
Db 3116 ATCGTGTGAGCAGTATGATGGCTTGCCTTCATGGGTGTATTTGAGAATCTTAAGCAAT 3175
QY 2900 TAGTGTTTTTTGACTTTTACTACTAAAGAAATTTCTACCTGATCAGCATTTAGTCAGAAAAC 2959
Db 3176 TAGTGTTTTTTGACTTTTACTACTAAAGAAATTTCTACCTGATCAGCATTTAGTCAGAAAAC 3235
QY 2960 TTAGCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAACTAGGCTTGTGGTGCCAAT 3019
Db 3236 TTAGCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAACTAGGCTTGTGGTGCCAAT 3295
QY 3020 TTGATGATGATGATCTCAGTGTATTACAGTGCCTTTTAACTAGTAACTGCT 3072
Db 3296 TTGATGATGATGATCTCAGTGTATTACAGTGCCTTTTAACTAGTAACTGCT 3348

RESULT 16

PCT-US01-14826-66
; Sequence 66, Application PC/TUS0114826
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-103
; CURRENT APPLICATION NUMBER: PCT/US01/14826
; PRIOR FILING DATE: 2001-05-16
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/677,298<151> 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,781<151> 2000-10-24
; PRIOR APPLICATION NUMBER: 09/715,869<151> 2000-11-17
; PRIOR APPLICATION NUMBER: 09/775,330<151> 2001-02-01
; NUMBER OF SEQ ID NOS: 864
; SOFTWARE: Custom
; SEQ ID NO 66
; LENGTH: 3260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)...(3226)
PCT-US01-14826-66

Query Match 90.0%; Score 2765; DB 1; Length 3260;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3065; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 TGAATTTCAAAAGGACAAATAGCCGAGCCCTTATTCAAAAGATGGGAATGACTGTATATA 61
Db 156 TGAATTTCAAAAGGACAAATAGCCGAGCCCTTATTCAAAAGATGGGAATGACTATTATA 215

QY 62 AGCAAAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGATAACATCA 121
Db 216 AGCAAAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGATAACATCA 275
QY 122 TTTTGTGCGAGAAAGTGGAGCAGGATGCTGTAGAGGGATCATTCACATGATTTTGAATA 181
Db 276 TTTTGTGCGAGAAAGTGGAGCAGGATGCTGTAGAGGGATCATTCACATGATTTTGAATA 335
QY 182 AGGGTTACAGATGCTCTGTAACCTCTTTTAAATCCCTTAAAGGAGTGGAACTATCCTCTAT 241
Db 336 AGGGTTACAGATGCTCTGTAACCTCTTTTAAATCCCTTAAAGGAGTGGAACTATCCTCTAT 395
QY 242 TTTAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAAGAGACTTTGACGATT 301
Db 396 TTTAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAAGAGACTTTGACGATT 455
QY 302 TGGCTCAGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTTTG 361
Db 456 TGGCTCAGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTTTG 515
QY 362 GTGAAGATATTGACATTTATTTTAACTTGAAAAGCACCCTTCACAGAACCTGTCTCTGGA 421
Db 516 GTGAAGATATTGACATTTATTTTAACTTGAAAAGCACCCTTCACAGAACCTGTCTCTGGA 575
QY 422 GGAAGGACCAACACCATCACCCTGGAGCAGCTGACCCCTGAATGGCCCTCCTGCAGGCTC 481
Db 576 GGAAGGACCAACACCATCACCCTGGAGCAGCTGACCCCTGAATGGCCCTCCTGCAGGCTC 635
QY 482 TTCAGAGCCCTTGCAATTTGAAGGGAAATCTGGCAAGAGCAAGTCCACTCTGCTGCAGC 541
Db 636 TTCAGAGCCCTTGCAATTTGAAGGGAAATCTGGCAAGAGCAAGTCCACTCTGCTGCAGC 695
QY 542 GCATTTGCCATGCTCTGGGGCTCGGAAAGTGCAGAGCTCTGACCAAGTTTCAAAATTCGTCT 601
Db 696 GAATTTGCCATGCTCTGGGGCTCGGAAAGTGCAGAGCTCTGACCAAGTTTCAAAATTCGTCT 755
QY 602 TCTTCTCCCTCTCAGCAGGGCCAGGGTGGACTTTTTTGAACCCCTCTGTGATCAACTCC 661
Db 756 TCTTCTCCCTCTCAGCAGGGCCAGGGTGGACTTTTTTGAACCCCTCTGTGATCAACTCC 815
QY 662 TGGATATACCTGGCAAAATCAGGAAGCAGACATTTATGCGCATGCTGCTGAAGCTGGGGC 721
Db 816 TGGATATACCTGGCAAAATCAGGAAGCAGACATTTATGCGCATGCTGCTGAAGCTGGGGC 875
QY 722 AGAGGGTCTCTTTTCTCTTGTGCTACAATCAATTCAGGCCCCAGAACTGCCAGAAA 781
Db 876 AGAGGGTCTCTTTTCTCTTGTGCTACAATCAATTCAGGCCCCAGAACTGCCAGAAA 935
QY 782 TCGAAGCCCTGTATAAAGGAAAACACCGCTTCAAGAACATGGTCACTGCCACTACCA 841
Db 936 TCGAAGCCCTGTATAAAGGAAAACACCGCTTCAAGAACATGGTCACTGCCACTACCA 995
QY 842 CTGAGTGCCTGAGGCACATACGGCAGTTGGTGGCCCTGACTGCTGAGGTGGGGGATATGA 901
Db 996 CTGAGTGCCTGAGGCACATACGGCAGTTGGTGGCCCTGACTGCTGAGGTGGGGGATATGA 1055
QY 902 CAGAAGACAGCGCCAGGCTCTCATCCGAGAAAGTGTGTATCAGGAGCTTGTGAAGGCT 961
Db 1056 CAGAAGACAGCGCCAGGCTCTCATCCGAGAAAGTGTGTATCAGGAGCTTGTGAAGGCT 1115
QY 962 TGTGTCTCAAAATTCAGAAATCAGGTGCTTGAGGAATCTCTGAAGACCCCTCTCTTTG 1021
Db 1116 TGTGTCTCAAAATTCAGAAATCAGGTGCTTGAGGAATCTCTGAAGACCCCTCTCTTTG 1175
QY 1022 TGGTCATCACTTTGTGCAATCCAGATGGGTGAAAGTGAAGTGTCCACTCTCACACAAAACAA 1081
Db 1176 TGGTCATCACTTTGTGCAATCCAGATGGGTGAAAGTGAAGTGTCCACTCTCACACAAAACAA 1235
QY 1082 CGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAACAACATTAAGGTG 1141
Db 1236 CGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAACAACATTAAGGTG 1295
QY 1142 TGGCTCAAGTGACTTTCATTCGGAGCCTGGACCCTGTGGAGACCTAGCTCTGGAGGGTG 1201

Db	1296	 TGCTCGAAGTGA	 CTTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTCGAGGGTG	 	1355
Qy	1202	TGTTTCCCAAGAAGTTTGATTTTCGAACATGCAAGATGTGTCCAGCGTGAATGAGGATGTCC	 	1361	
Db	1356	TGTTTCCCAAGAAGTTTGATTTTCGAACATGCAAGATGTGTCCAGCGTGAATGAGGATGTCC	 	1415	
Qy	1262	TGCTGACAACTGGGCTCCCTCTCTAAATATACAGCTCAAAGGTTTCAAGCCAAAAGTATAAAT	 	1321	
Db	1416	TGCTGACAACTGGGCTCCCTCTCTAAATATACAGCTCAAAGGTTTCAAGCCAAAAGTATAAAT	 	1475	
Qy	1322	TCNTTTCACAAGTCATTCCAGGAGTACACAGCAGGACGAAAGACTCAGCAGATTTTATTGACGT	 	1381	
Db	1476	TCNTTTCACAAGTCATTCCAGGAGTACACAGCAGGACGAAAGACTCAGCAGATTTTATTGACGT	 	1535	
Qy	1382	CTCATGAGCCAGAGAGGTGACCAAGGGGAATGGTTACTTCGACAAAATGGTTTCCATTTT	 	1441	
Db	1536	CTCATGAGCCAGAGAGGTGACCAAGGGGAATGGTTACTTCGACAAAATGGTTTCCATTTT	 	1595	
Qy	1442	CGGACATATACATCCACTTATAGCAGCCTGTCTCCGGTACACCTGTGGGTGCATCTGTGGAG	 	1501	
Db	1596	CGGACATATACATCCACTTATAGCAGCCTGTCTCCGGTACACCTGTGGGTGCATCTGTGGAG	 	1655	
Qy	1502	CCACCAGGGCTGTATTGAAGCACCTCGCAGCAGTGTATCAACACGGTGCTCTCTCGGAC	 	1561	
Db	1656	CCACCAGGGCTGTATTGAAGCACCTCGCAGCAGTGTATCAACACGGTGCTCTCTCGGAC	 	1715	
Qy	1562	TTTCCATCGCAAGAGGCTCTCTCGAGACAGGAATCTTTCGAAGTGTGAAACACCA	 	1621	
Db	1716	TTTCCATCGCAAGAGGCTCTCTCGAGACAGGAATCTTTCGAAGTGTGAAACACCA	 	1775	
Qy	1622	CTGAGCAAGAAATCTGAAAGCCATAAATCAATCTCTTTGATAGTGTGGATCCATTT	 	1681	
Db	1776	CTGAGCAAGAAATCTGAAAGCCATAAATCAATCTCTTTGATAGTGTGGATCCATTT	 	1835	
Qy	1682	TATATCAAGAGTAGATCCAAATCAGCCCTGAGCCAGAAATTTGAAGCTTCTTTCCAG	 	1741	
Db	1836	TATATCAAGAGTAGATCCAAATCAGCCCTGAGCCAGAAATTTGAAGCTTCTTTCCAG	 	1895	
Qy	1742	GTAAGAAGCTTATATATCAACTCAGGAGACATCCCCGATTACTTATTTGACTCTTTGAAC	 	1801	
Db	1896	GTAAGAAGCTTATATATCAACTCAGGAGACATCCCCGATTACTTATTTGACTCTTTGAAC	 	1955	
Qy	1802	ATTTGCCCAATTTGCAAGTGTCTGGACTTCATATAACTGGACTTTTATGGGGAGCTA	 	1861	
Db	1956	ATTTGCCCAATTTGCAAGTGTCTGGACTTCATATAACTGGACTTTTATGGGGAGCTA	 	2015	
Qy	1862	TGGCTTCATGGGAAAGGCTGCAGAAGACACAGGTGGAAATCCACATGGAAGAGCCCCAG	 	1921	
Db	2016	TGGCTTCATGGGAAAGGCTGCAGAAGACACAGGTGGAAATCCACATGGAAGAGCCCCAG	 	2075	
Qy	1922	AAACCTACATTCGCCAGCAGGCTGTATCTTTGCTTCAACTGGAAGCAGGAATTCAGGA	 	1981	
Db	2076	AAACCTACATTCGCCAGCAGGCTGTATCTTTGCTTCAACTGGAAGCAGGAATTCAGGA	 	2135	
Qy	1982	CTCTGGAGGTCACACTCCGGGATTTTCAGCAAGTTGAATGAAGCAAGATATCACATATCTGG	 	2041	
Db	2136	CTCTGGAGGTCACACTCCGGGATTTTCAGCAAGTTGAATGAAGCAAGATATCACATATCTGG	 	2195	
Qy	2042	GGAATATTCAGCTCTGCCACAAGCCCTCAGCTGCAATTAAGAGATGTCTGGTGTGG	 	2101	
Db	2196	GGAATATTCAGCTCTGCCACAAGCCCTCAGCTGCAATTAAGAGATGTCTGGTGTGG	 	2255	
Qy	2102	CTGGAAGCCTCAGTTTGGTCTCAGCACCTGTAGAAGCATTTTATCTCATGTGGAG	 	2161	
Db	2256	CTGGAAGCCTCAGTTTGGTCTCAGCACCTGTAGAAGCATTTTATCTCATGTGGAG	 	2315	
Qy	2162	CCAGTCCCTCACCATPAGAAGATGAGGACATCACATCTGTAAACAACTGAAACCT	 	2221	
Db	2316	CCAGTCCCTCACCATPAGAAGATGAGGACATCACATCTGTAAACAACTGAAACCT	 	2375	
Qy	2222	TGAGTATTCACTGACCTACAGATCAACGGCTGCCGGGTGGTCTGACTGACAGCTTGGGTA	 	2281	

Db	2376	TGAGT	VTTCATGACCTACAGATCAACGGCTGCCGGGTGGTCTGACTGACAGCTTGGGTA	2435
Qy	2382	ACTTGT	AGAAACCTTACAAAGCTCATAAATGGATAACATAAAGATGAATGAAGAAGATGCTA	2341
Db	2436	ACTTGT	AGAAACCTTACAAAGCTCATAAATGGATAACATAAAGATGAATGAAGAAGATGCTA	2495
Qy	2434	TAAAA	TAGCTGAAGCGCTGAAAACCTGAAGAAGATGTGTTTATTTTATTTCATTGACCCACT	2401
Db	2496	TAAAA	TAGCTGAAGCGCTGAAAACCTGAAGAAGATGTGTTTATTTTATTTCATTGACCCACT	2555
Qy	2402	TGCTCT	ACATTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGTG	2461
Db	2556	TGCTCT	ACATTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGTG	2615
Qy	2462	ACCTTG	RAGAAATTCAAATTAGTCTCCTCGCTGCTGTCTGCAAAATGCAGTGAAAATCCTAG	2521
Db	2616	ACCTTG	RAGAAATTCAAATTAGTCTCCTCGCTGCTGTCTGCAAAATGCAGTGAAAATCCTAG	2675
Qy	2522	CTCAGA	ATCTTCACAATTTGGTCAAACTGAGCATTTCTTGATTATATCAGAAAATTAACCTGG	2581
Db	2676	CTCAGA	ATCTTCACAATTTGGTCAAACTGAGCATTTCTTGATTATATCAGAAAATTAACCTGG	2735
Qy	2582	AAAAAG	VTGGAATGAAGCTCTTCATGAACTGATCGACAGAGTGAACGCTGTAGAACAGC	2641
Db	2736	AAAAAG	VTGGAATGAAGCTCTTCATGAACTGATCGACAGAGTGAACGCTGTAGAACAGC	2795
Qy	2642	TCACCG	ACTGTAGTGCCTCTGGGGCTGTGACGTGCAAGCAGCGCTGAGCAGCCTGTGTA	2701
Db	2796	TCACCG	ACTGTAGTGCCTCTGGGGCTGTGACGTGCAAGCAGCGCTGAGCAGCCTGTGTA	2855
Qy	2702	AACATT	GGAGGAGGTCCTCCACAACTCGTCAGACCTTGGGTTGAAAACCTGAGAGATCAAG	2761
Db	2856	AACATT	GGAGGAGGTCCTCCACAACTCGTCAGACCTTGGGTTGAAAACCTGAGAGATCAAG	2915
Qy	2762	ATACAG	GATTAGAAATTTTAGTGTGATTTTTTTGGAAAGAACCCCTCTGAAAAACTTCCAGC	2821
Db	2916	ATACAG	GATTAGAAATTTTAGTGTGATTTTTTTGGAAAGAACCCCTCTGAAAAACTTCCAGC	2975
Qy	2822	AGTTGAA	TTTGGCGGGAAATCGTGTGACGAGTGAATGCGCTTGCCTTCATGGGTCTAT	2881
Db	2976	AGTTGAA	TTTGGCGGGAAATCGTGTGACGAGTGAATGCGCTTGCCTTCATGGGTCTAT	3035
Qy	2882	TTGAGAA	TCATTAAAGCAATTAGTGTGTTTTTTTGACCTTTAGTACTAAAGAAATTTCTACCTGAT	2941
Db	3036	TTGAGAA	TCATTAAAGCAATTAGTGTGTTTTTTTGACCTTTAGTACTAAAGAAATTTCTACCTGAT	3095
Qy	2942	CAGCAT	ATGTCAGAAAACCTTAGCCAGTGCTTATCCAAAGTTAACTTTTCTGCAAGAAGCTA	3001
Db	3096	CAGCAT	ATGTCAGAAAACCTTAGCCAGTGCTTATCCAAAGTTAACTTTTCTGCAAGAAGCTA	3155
Qy	3002	GGCTTGT	GGGTGGCAATTTGATGATGATGATCTCAGTGTGTTATATACAGGTGCTTTTAAAC	3061
Db	3156	GGCTTGT	GGGTGGCAATTTGATGATGATGATCTCAGTGTGTTATATACAGGTGCTTTTAAAC	3215
Qy	3062	TAGTAAC	GCCT 3072	
Db	3216	TAGTAAC	GCCT 3226	

RESULT 17
US-09-667-298-66
; Sequence 66, Application US/09667298
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyang
; APPLICANT: Zhao, Qing A.
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aiding J.
; APPLICANT: Wan, Jian-Rui
; APPLICANT: Chen, Rui-hong

APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 792CIP2A
CURRENT APPLICATION NUMBER: US/09/667,298
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 178
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 66
LENGTH: 3260
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (29)..(3229)
US-09-667-298-66

Query Match 90.0%; Score 2765; DB 26; Length 3260;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3065; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 TGAATTCATAAAGGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTATTATAA 61
Db 156 TGAATTCATAAAGGACAATAGCCGAGCCCTTATTCAAAGAATGGGAATGACTATTATAA 215
QY 62 AGCAATACAGATGACCTATTGTATGGAATGTTCTGAATCGGAAGATTAACATCA 121
Db 216 AGCAATACAGATGACCTATTGTATGGAATGTTCTGAATCGGAAGATTAACATCA 275
QY 122 TTGTCTCGAAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTGAAAA 181
Db 276 TTGTCTCGAAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTGAAAA 335
QY 182 AGGTTACAGAGTCTGTAACTCTTTCTTAAATCCCTTAAAGGAGTGAATCTCTCTAT 241
Db 336 AGGTTACAGAGTCTGTAACTCTTTCTTAAATCCCTTAAAGGAGTGAATCTCTCTAT 395
QY 242 TTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAGGAGCTTGGACGATT 301
Db 396 TTCAGGACTTGAATGGACAAGTCTTTTTCATCAGACATCAGAGGAGCTTGGACGATT 455
QY 302 TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACTTTTATCCCTTG 361
Db 456 TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACTTTTATCCCTTG 515
QY 362 GTGAAGATATGACATTTATTTTAACTTTGAAAGCACCCTTTCAGAACCTGTCTGTGGA 421
Db 516 GTGAAGATATGACATTTATTTTAACTTTGAAAGCACCCTTTCAGAACCTGTCTGTGGA 575
QY 422 GGAAGGACCAACCACTACCCGCTGGAGCAGCTGACCCCTGAATGGCTCTCTGCAGGCTC 481
Db 576 GGAAGGACCAACCACTACCCGCTGGAGCAGCTGACCCCTGAATGGCTCTCTGCAGGCTC 635
QY 482 TTCAGAGCCCTGCATCATTTAAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGC 541
Db 636 TTCAGAGCCCTGCATCATTTAAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGC 695
QY 542 GCATTGCCATGCTCTGGGGCTCCGGAAGTGAAGGCTGCAAGGCTTCAAAATTCGTCT 601
Db 696 GAATTGCCATGCTCTGGGGCTCCGGAAGTGAAGGCTTCAAAATTCGTCT 755
QY 602 TCTTCTCCCTCTCAGCAGGGCCAGGGTGGACTTTTGTAAACCCCTCTGTGATCAACTCC 661
Db 756 TCTTCTCCCTCTCAGCAGGGCCAGGGTGGACTTTTGTAAACCCCTCTGTGATCAACTCC 815
QY 662 TGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGGC 721
Db 816 TGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGGC 875
QY 722 AGAGGGTCTTTCTTCTTGTATGGCTACAAATGAATTCGAAGCCCAAGAACTGCCCAAAA 781
|||||

Db 876 AGAGGGTCTTTCTTCTTGTATGGCTACAAATGAATTCAGCCCAAGAACTGCCCAAAA 935
QY 782 TCGAAGCCCTGATAAAGGAAAAACACCCGCTTCAAGAACTGGTCTCATCGTCACTACTACCA 841
Db 936 TCGAAGCCCTGATAAAGGAAAAACACCCGCTTCAAGAACTGGTCTCATCGTCACTACTACCA 995
QY 842 CTGAGTGCCTGAGGCACATACGGCAGTTTGTGTCCTGACTGTGAGGTGGGGATATGA 901
Db 996 CTGAGTGCCTGAGGCACATACGGCAGTTTGTGTCCTGACTGTGAGGTGGGGATATGA 1055
QY 902 CAGAAGACAGCCCGCCAGGCTCTCATCCAGAAGTGTGATCAAGGAGCTTGTCTGAAGGCT 961
Db 1056 CAGAAGACAGCCCGCCAGGCTCTCATCCAGAAGTGTGATCAAGGAGCTTGTCTGAAGGCT 1115
QY 962 TGTGTCTCCAAATTCAGAAATCCAGGTGCTTGAAGATCTCATGAAGACCCCTCTCTTTG 1021
Db 1116 TGTGTCTCCAAATTCAGAAATCCAGGTGCTTGAAGATCTCATGAAGACCCCTCTCTTTG 1175
QY 1022 TGTGTCTCTTGTGCAATCCAGATGGGTGAAAGTGAAGTTCCTACTCTCACACACAAACAA 1081
Db 1176 TGTGTCTCTTGTGCAATCCAGATGGGTGAAAGTGAAGTTCCTACTCTCACACACAAACAA 1235
QY 1082 CGCTGTCTTCCATACCTTCTATGATCTGTGTATACAGAAAAACAAACACAAATAAAGGTG 1141
Db 1236 CGCTGTCTTCCATACCTTCTATGATCTGTGTATACAGAAAAACAAACACAAATAAAGGTG 1295
QY 1142 TGGCTGCAAGTGAATTCATTCGGAGCCTGGACCACCTGTGGAGACCTAGCTGTGGAGGTG 1201
Db 1296 TGGCTGCAAGTGAATTCATTCGGAGCCTGGACCACCTGTGGAGACCTAGCTGTGGAGGTG 1355
QY 1202 TGTCTCTCCCAAAATTTGATTTTGAATTCGAGTGTGTCCAGCGTGAATGAGGATGCTC 1261
Db 1356 TGTCTCTCCCAAAATTTGATTTTGAATTCGAGTGTGTCCAGCGTGAATGAGGATGCTC 1415
QY 1262 TGTGTCAACTGGGCTCTCTGTAAATATACAGCTCAAAGTTTCAAGCCAAAGTATTAAT 1321
Db 1416 TGTGTCAACTGGGCTCTCTGTAAATATACAGCTCAAAGTTTCAAGCCAAAGTATTAAT 1475
QY 1322 TCTTTTCAAGTTCATTCAGGAGTACACACAGSACCAAGACTCAGCAGTTTATTTGACGT 1381
Db 1476 TCTTTTCAAGTTCATTCAGGAGTACACACAGSACCAAGACTCAGCAGTTTATTTGACGT 1535
QY 1382 CTCATGAGCCAGAGGAGTGAACCAAGGGGAATGGTTACTTTGCAGAAAATGGTTTCCATTT 1441
Db 1536 CTCATGAGCCAGAGGAGTGAACCAAGGGGAATGGTTACTTTGCAGAAAATGGTTTCCATTT 1595
QY 1442 CGGACATTAATCCATTTATAGAGCCTGTCCGGTACACCTGTGGGTCTATCTGTGGAAG 1501
Db 1596 CGGACATTAATCCATTTATAGAGCCTGTCCGGTACACCTGTGGGTCTATCTGTGGAAG 1655
QY 1502 CCACGAGGCTGTTATGAAGCACCCTCCGACAGTGTATCAACAGCGCTGCTTCTCGGAC 1561
Db 1656 CCACGAGGCTGTTATGAAGCACCCTCCGACAGTGTATCAACAGCGCTGCTTCTCGGAC 1715
QY 1562 TTTTCCATCGCAAGAGGCTCTCTTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCA 1621
Db 1716 TTTTCCATCGCAAGAGGCTCTCTTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCA 1775
QY 1622 CTGAGCAAGAAATCTGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCCATT 1681
Db 1776 CTGAGCAAGAAATCTGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCCATT 1835
QY 1682 TATATCAAGAGTGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTTCAAG 1741
Db 1836 TATATCAAGAGTGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTTCAAG 1895
QY 1742 GTAAAAGCTTATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTTGAAC 1801
Db 1896 GTAAAAGCTTATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTTGAAC 1955
QY 1802 ATTTGCCCAATTTGCAAGTGTCTGTGACCTTCATTAACCTGGACTTTTATGGGGGAGCTA 1861
Db 1956 ATTTGCCCAATTTGCAAGTGTCTGTGACCTTCATTAACCTGGGCTTTTATGGGGGAGCTA 2015
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QY 1862 TGGCTTCATGGGAAAGGCTGCAGAAAGACACAGAGTGGGAATCCACATGGAAGAGGCCCCAG 1921
Db 2016 TGGCTTCATGGGAAAGGCTGCAGAAAGACACAGAGTGGGAATCCACATGGAAGAGGCCCCAG 2075
QY 1922 AAACCTACATCCCGAGGCGGTGATCTTTCTTCAACTGGAAGCAGGAAATTCAGGA 1981
Db 2076 AAACCTACATCCCGAGGCGGTGATCTTTCTTCAACTGGAAGCAGGAAATTCAGGA 2135
QY 1982 CTCTGAGGTACACTCCGGGATTTTCAGCAAGTTTGAATGAAGCAAGATATACATATCTGG 2041
Db 2136 CTCTGAGGTACACTCCGGGATTTTCAGCAAGTTTGAATGAAGCAAGATATACATATCTGG 2195
QY 2042 GGAATAATTCAGCTCTGCACAAGCCTCAGGCTGCAATAAAGAGATGCTGCTGGTGG 2101
Db 2196 GGAATAATTCAGCTCTGCACAAGCCTCAGGCTGCAATAAAGAGATGCTGCTGGTGG 2255
QY 2102 CTGGAAGCCTCAGTTTGGTCTCAGCACCTGTGAAGCAATTTATCTCTCATGTTGGAG 2161
Db 2256 CTGGAAGCCTCAGTTTGGTCTCAGCACCTGTGAAGCAATTTATCTCTCATGTTGGAG 2315
QY 2162 CCAGTCCCTCACCATGAGAGATGAGGCGACATCACATCTCTTAACAACCTGAAACCT 2221
Db 2316 CCAGTCCCTCACCATGAGAGATGAGGCGACATCACATCTCTTAACAACCTGAAACCT 2375
QY 2222 TCAGTATTCATCACTACAGATCAACGGCTCCGGGTGCTGACTGACGCTTGGGTA 2281
Db 2376 TCAGTATTCATCACTACAGATCAACGGCTCCGGGTGCTGACTGACGCTTGGGTA 2435
QY 2282 ACTTGAAGAACCTTCAAGCTCATTAATGGATPAACATAAAGATGAATGAAGAGATGCTA 2341
Db 2436 ACTTGAAGAACCTTCAAGCTCATTAATGGATPAACATAAAGATGAATGAAGAGATGCTA 2495
QY 2342 TAAACTAGCTGAAGGCTGAAACCTGAAGAGATGTGTTTATTTTCAATTTGACCCACT 2401
Db 2496 TAAACTAGCTGAAGGCTGAAACCTGAAGAGATGTGTTTATTTTCAATTTGACCCACT 2555
QY 2402 TGTCTGACATTTGGAGGGAATGGATTACATAGTCAAGTCTCTGTCAGAGTGAACCTGTG 2461
Db 2556 TGTCTGACATTTGGAGGGAATGGATTACATAGTCAAGTCTCTGTCAGAGTGAACCTGTG 2615
QY 2462 ACCTTTGAAGAAATTCAAATTAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2521
Db 2616 ACCTTTGAAGAAATTCAAATTAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2675
QY 2522 CTCAGAATCTTCACAAATTTGGTCAACCTGAGCATTTGATTTATCAGAAATTTACCTGG 2581
Db 2676 CTCAGAATCTTCACAAATTTGGTCAACCTGAGCATTTGATTTATCAGAAATTTACCTGG 2735
QY 2582 AAAAGATGGAATGAAGCTCTTCATGAACCTGATCGACAGGATGAAGTGTAGAACAGC 2641
Db 2736 AAAAGATGGAATGAAGCTCTTCATGAACCTGATCGACAGGATGAAGTGTAGAACAGC 2795
QY 2642 TCACGCACTGATGCTGCCCTGGGCTGTGAGTGCAGAGGAGCCTGACAGCCTGTTGA 2701
Db 2796 TCACGCACTGATGCTGCCCTGGGCTGTGAGTGCAGAGGAGCCTGACAGCCTGTTGA 2855
QY 2702 AACATTTGGAGAGTCCCAACCTCGTCAAGCTTTGGTGTGAAAACTGGAGACTCACAG 2761
Db 2856 AACATTTGGAGAGTCCCAACCTCGTCAAGCTTTGGTGTGAAAACTGGAGACTCACAG 2915
QY 2762 ATACAGATTTAGAATTTTAGTGTGATTTTGGAAAAACCCCTCTGAAAACTTCCAGC 2821
Db 2916 ATACAGATTTAGAATTTTAGTGTGATTTTGGAAAAACCCCTCTGAAAACTTCCAGC 2975
QY 2822 AGTTGAATTTGGCGGAATTCGTGTGAGCAGTGTGATGGCTTCCCTTCATGGGTGAT 2881
Db 2976 AGTTGAATTTGGCGGAATTCGTGTGAGCAGTGTGATGGCTTCCCTTCATGGGTGAT 3035
QY 2882 TTGAGAATCTTAAGCAATTAAGTGTGTTTTTTTGTAGTCTTACTAAAGAAATTTTACCTGATC 2941
Db 3036 TTGAGAATCTTAAGCAATTAAGTGTGTTTTTTTGTAGTCTTACTAAAGAAATTTTACCTGATC 3095
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QY 2942 CAGC:TTAGTCTAGAAAACCTTAGCCAAAGTGTATCCAAAGTTAACTTTCTGCAAGAGCTA 3001
Db 3096 CAGC:TTAGTCTAGAAAACCTTAGCCAAAGTGTATCCAAAGTTAACTTTCTGCAAGAGCTA 3155
QY 3002 GGCTTGTGGGTGGCAATTTGATGATGATCTCTCAGTGTGTTATTACAGTGTCTTTAAAC 3061
Db 3156 GGCTTGTGGGTGGCAATTTGATGATGATCTCTCAGTGTGTTATTACAGTGTCTTTAAAC 3215
QY 3062 TAGTAACTGCT 3072
Db 3216 TAGTAACTGCT 3226

RESULT 18
US-09-697-089-6
; Sequence 6, Application US/09697089
; GENERAL INFORMATION:
; APPLICANT: Bobison, Keith E.
; APPLICANT: Bobison, Keith E.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-134001
; CURRENT APPL. CATION NUMBER: US/09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; NUMBER OF SEQ. ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-697-089-6
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Query Match 85.7%; Score 2634; DB 27; Length 3612;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 263 GTCTTTTCATCAGACATCAGAAAGGAGACTTGGAGATTTGGCTCAGGATTTAAAGGACT 322
Db 734 GTCTTTTCATCAGACATCAGAAAGGAGACTTGGAGATTTGGCTCAGGATTTAAAGGACT 793
QY 323 GTTACCTACCCCATCTTTCTGAACTTTTATCCCTTGTGTAAGATTTGACATTTATTT 382
Db 794 GTTACCTACCCCATCTTTCTGAACTTTTATCCCTTGTGTAAGATTTGACATTTATTT 853
QY 383 TTAACCTGAAAAGACCTTTCACAGAACCTGCTGTGGAGGAGGACCAACACCATCACC 442
Db 854 TTAACCTGAAAAGACCTTTCACAGAACCTGCTGTGGAGGAGGACCAACACCATCACC 913
QY 443 GCGTGGTGCAGTGCACCTGAAATGGCTCCTGTCAGAGCTCTTCAGAGCCCTGCATCAT 502
Db 914 GCGTGGTGCAGTGCACCTGAAATGGCTCCTGTCAGAGCTCTTCAGAGCCCTGCATCAT 973
QY 503 AAGGGGAATCTGGCAAGGCAAGTCCACTCTGTCAGCGCATTTGCCATGCTCTGGGGCT 562
Db 974 AAGGGGAATCTGGCAAGGCAAGTCCACTCTGTCAGCGCATTTGCCATGCTCTGGGGCT 1033
QY 563 CCGGAAAATGCAAGGCTCTGACAAAGTTCAAAATTCGTCTTCTCTGCTCTCAGCAGG 622
Db 1034 CCGGAAAATGCAAGGCTCTGACAAAGTTCAAAATTCGTCTTCTCTGCTCTCAGCAGG 1093
QY 623 CCAGGGTGGACTTTTGAACCCCTGTCGATCAACTCTCTGATATACCTGCAACAATCA 682
Db 1094 CCAGGGTGGACTTTTGAACCCCTGTCGATCAACTCTCTGATATACCTGCAACAATCA 1153
QY 683 GGAAGCAACATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 742
Db 1154 GGAAGCAACATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1213
QY 743 ATGGCTAACATTCAGCCCGCAAGTCCCAAGAAATTCGAAGCCCTGATAAGAGGAAA 802
Db 1214 ATGGCTAACATTCAGCCCGCAAGTCCCAAGAAATTCGAAGCCCTGATAAGAGGAAA 1273
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QY 803 ACCACCGCTTCAAGAACATGGTCATCGTCACCACTACCACCTAGTGCTGAGGSCATAC 862
DB 1274 ACCACCGCTTCAAGAACATGGTCATCGTCACCACTACCACCTAGTGCTGAGGSCATAC 1333
QY 863 GGCAGTTTGGTGGCCCTGACTGCTGAGTGGGGGATATGACAGAAAGACAGCGCCAGGCTC 922
DB 1334 GGCAGTTTGGTGGCCCTGACTGCTGAGTGGGGATATGACAGAAAGACAGCGCCAGGCTC 1393
QY 923 TCATCCGAGAGTGCATGATCAAGGAGCTTGCTGAAGGCTTGTGCTCCAAATTCAGAAAT 982
DB 1394 TCATCCGAGAGTGCATGATCAAGGAGCTTGCTGAAGGCTTGTGCTCCAAATTCAGAAAT 1453
QY 983 CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTGTTGGTCACTCTGTGCAATCC 1042
DB 1454 CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTGTTGGTCACTCTGTGCAATCC 1513
QY 1043 AGATGGGTGAAGTGAAGTTCCTACTCTCACACAAACAAACGCTGTGTTCCATACCTTCTATG 1102
DB 1514 AGATGGGTGAAGTGAAGTTCCTACTCTCACACAAACAAACGCTGTGTTCCATACCTTCTATG 1573
QY 1103 ATCTGTTGATACAGAAACAAACACAAACATAAAGGTGTGGCTGCAAGTGACTTTCATTC 1162
DB 1574 ATCTGTTGATACAGAAACAAACACAAACATAAAGGTGTGGCTGCAAGTGACTTTCATTC 1633
QY 1163 GGAGCCTGGACCACCTGTGGAGACCTAGCTCTGGAGGCTGTGTTCTCCCAAGTTTGATT 1222
DB 1634 GGAGCCTGGACCACCTGTGGAGACCTAGCTCTGGAGGCTGTGTTCTCCCAAGTTTGATT 1693
QY 1223 TCGAAGTGAAGTGTCCAGGCTGAATGAGAGTGTCTGCTGCAAGTGGGCTCCTCT 1282
DB 1694 TCGAAGTGAAGTGTCTCAGCGTGAATGAGGATGCTGCTGCAAGTGGGCTCCTCT 1753
QY 1283 GTAATATACAGTCAAGGTTCAAGCCAAAGTATATAATCTTTCACAGTCAATTCACG 1342
DB 1754 GTAATATACAGTCAAGGTTCAAGCCAAAGTATATAATCTTTCACAGTCAATTCACG 1813
QY 1343 AGTACACAGCAGCAGCAGCAGCAGCTTATTTGACGCTCTCATGAGCAGAGAGGTGA 1402
DB 1814 AGTACACAGCAGCAGCAGCAGCAGCTTATTTGACGCTCTCATGAGCAGAGAGGTGA 1873
QY 1403 CCNAGGGGAATGGTTACTTTCGAGAAATGGTTTCCATTTTCGGACATTAATCCACTATA 1462
DB 1874 CCNAGGGGAATGGTTACTTTCGAGAAATGGTTTCCATTTTCGGACATTAATCCACTATA 1933
QY 1463 GCAGCTGCTCCGGTACACTGTGGGTCACTCTGGAAGCCACAGGCGCTGTATCAAGC 1522
DB 1934 GCAGCTGCTCCGGTACACTGTGGGTCACTCTGGAAGCCACAGGCGCTGTATCAAGC 1993
QY 1523 ACCTCGCAGAGTGTATCAACAGCGCTGCTTCTCGGACTTTCATCGCAAGAGGCGCTC 1582
DB 1994 ACCTCGCAGAGTGTATCAACAGCGCTGCTTCTCGGACTTTCATCGCAAGAGGCGCTC 2053
QY 1583 TCTGGAGACAGNATCTTTGCAAGTGTGAATAACCACTACTGAGCAAGAAATTCGAAAG 1642
DB 2054 TCTGGAGACAGNATCTTTGCAAGTGTGAATAACCACTACTGAGCAAGAAATTCGAAAG 2113
QY 1643 CCATAAACATCAATTCCTTTGTAGAGTGGCATCCATTTATATCAAGAGATACATCCA 1702
DB 2114 CCATAAACATCAATTCCTTTGTAGAGTGGCATCCATTTATATCAAGAGATACATCCA 2173
QY 1703 AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCCTTCAAGGTAAGAGCTTATATCAACT 1762
DB 2174 AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCCTTCAAGGTAAGAGCTTATATCAACT 2233
QY 1763 CAGGGAACATCCCGAATTAATTTGACTTCTTTGAACATTTGCCCCAATTTGCAAGTG 1822
DB 2234 CAGGGAACATCCCGAATTAATTTGACTTCTTTGAACATTTGCCCCAATTTGCAAGTG 2293
QY 1823 CTTGAGCTTCAATAACCTGAGCTTTTATGGGGAGCTATGCTTCATGGGAAAGGCTG 1882
DB 2294 CCTGAGCTTCAATAACCTGAGCTTTTATGGGGAGCTATGCTTCATGGGAAAGGCTG 2353

QY 1883 CAGAAGACACAGGTGGAATCCACATCGAAGAGGCCCCAGAAACCTTACATTTCCAGCAGG 1942
DB 2354 CAGAAGACACAGGTGGAATCCACATCGAAGAGGCCCCAGAAACCTTACATTTCCAGCAGG 2413
QY 1943 CTGTATCTTTGTTTCAACTTGAAGCAGGAATTCAGGACTCTGAGGCTCACACTCCGGG 2002
DB 2414 CTGTATCTTTGTTTCAACTTGAAGCAGGAATTCAGGACTCTGAGGCTCACACTCCGGG 2473
QY 2003 ATTTTCAGCAAGTGAATAAGCAGAGATATCACATATCTGGGGAATAATTCAGCTCTGCCA 2062
DB 2474 ATTTTCAGCAAGTGAATAAGCAGAGATATCACATATCTGGGGAATAATTCAGCTCTGCCA 2533
QY 2063 CAAAGCCTCAGGCTGCAATAAAGAGATGTGCTGGTGGCTGGAAGCCCTCAGTTTGGTCC 2122
DB 2534 CAAAGCCTCAGGCTGCAATAAAGAGATGTGCTGGTGGCTGGAAGCCCTCAGTTTGGTCC 2593
QY 2123 TCAGCACTCTGAAGACATTTATTTCTCATGTTGGAAGCCAGTCCCTTCACCATAGAAG 2182
DB 2594 TCAGCACTCTGAAGACATTTATTTCTCATGTTGGAAGCCAGTCCCTTCACCATAGAAG 2653
QY 2183 ATGAGAGGCACATCACATCTGTAACAAACCTGAAACCTTGAGTATTCATGACCTACAGA 2242
DB 2654 ATGAGAGGCACATCACATCTGTAACAAACCTGAAACCTTGAGTATTCATGACCTACAGA 2713
QY 2243 ATCAACGGCTGCCGGTGGTCTGACTGACAGCTTTGGGTAACTTTGAAGAACCCTTACAAAGC 2302
DB 2714 ATCAACGGCTGCCGGTGGTCTGACTGACAGCTTTGGGTAACTTTGAAGAACCCTTACAAAGC 2773
QY 2303 TCATAATGATTAACATATAAGATGAATGAAGAGATGCTATATAACCTAGCTGAAGGCTGA 2362
DB 2774 TCATAATGATTAACATATAAGATGAATGAAGAGATGCTATATAACCTAGCTGAAGGCTGA 2833
QY 2363 AAAACCTGAAGAGATGTGTTATTTCTATTTGACCCACTTGTCTGACATTTGGAGAGGGAA 2422
DB 2834 AAAACCTGAAGAGATGTGTTATTTCTATTTGACCCACTTGTCTGACATTTGGAGAGGGAA 2893
QY 2423 TGGATTACATAGTCAAGTCTCTGCTCAAGTGAACCCCTGTGACCTTTGAAGAAATTCATATAG 2482
DB 2894 TGGATTACATAGTCAAGTCTCTGCTCAAGTGAACCCCTGTGACCTTTGAAGAAATTCATATAG 2953
QY 2483 TCTCCTGCTGCTTGTCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2542
DB 2954 TCTCCTGCTGCTTGTCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 3013
QY 2543 TCAAACTGAGCATCTTTGATTTATCAGAAATTTACCTGGAAGAGATGGAATGGAAGTCA 2602
DB 3014 TCAAACTGAGCATCTTTGATTTATCAGAAATTTACCTGGAAGAGATGGAATGGAAGTCA 3073
QY 2603 TTCATGAAGTGAATGAGGATGAACGCTGTAGAACAGCTCACCCAGCTGATGCTGCCCT 2662
DB 3074 TTCATGAAGTGAATGAGGATGAACGCTGTAGAACAGCTCACCCAGCTGATGCTGCCCT 3133
QY 2663 GGGGCTGACGCTGCAAGCAGGCTGAGCAGCTGTTGAAACATTTGGAGAGGTTCCAC 2722
DB 3134 GGGGCTGACGCTGCAAGCAGGCTGAGCAGCTGTTGAAACATTTGGAGAGGTTCCAC 3193
QY 2723 AACTCCTCAAGCTTTGGGTTGAAAACTGGAGACTCACAGATACAGAGATTAGAAATTTAG 2782
DB 3194 AACTCCTCAAGCTTTGGGTTGAAAACTGGAGACTCACAGATACAGAGATTAGAAATTTAG 3253
QY 2783 GTGCATTTTTTGGAAAGAACCCCTCTGAAACCTTCCAGCAGTTGAATTTGGCGGGAATC 2842
DB 3254 GTGCATTTTTTGGAAAGAACCCCTCTGAAACCTTCCAGCAGTTGAATTTGGCGGGAATC 3313
QY 2843 GTGTGAGCAGTGAATGGCTTGCCTTCATGGGTGATTTGAGAAATCTTAAGCAATTTAG 2902
DB 3314 GTGTGAGCAGTGAATGGCTTGCCTTCATGGGTGATTTGAGAAATCTTAAGCAATTTAG 3373
QY 2903 TGTTTTTTTCACCTTACTACTAAAGAAATTTCTACCTCATCCAGCATTTAGTCAGAAACTTA 2962
DB 3374 TGTTTTTTTCACCTTACTACTAAAGAAATTTCTACCTCATCCAGCATTTAGTCAGAAACTTA 3433
QY 2963 GCCAAGTGTATCCAAAGTTAACTTTTCTGCAAGAGCTAGGCTTTGTTGGTGGCAATTTG 3022

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Db 3434 GCCAAGTGTATCCAGTTAACTTTTCGCAAGAGCTAGGCTTGTGGTGGCAATTG 3493
QY 3023 ATGATGATGATCTCAGTGTATTACAG 3049
Db 3494 ATGATGATGATCTCAGTGTATTACAG 3520

RESULT 19

US-09-841-739-6
; Sequence 6, Application US/09841739
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-6

Query Match 85.7%; Score 2634; DB 32; Length 3612;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 263 GTCCTTTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 322
Db 734 GTCCTTTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 793
QY 323 TGTACCATACCCCACTTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATTAATT 382
Db 794 TGTACCATACCCCACTTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATTAATT 853
QY 383 TTAACCTTCAAAAGCACTTTCACAGAACCTGCTGTGGAGGAAGCAACACCATCAC 442
Db 854 TTAACCTTCAAAAGCACTTTCACAGAACCTGCTGTGGAGGAAGCAACACCATCAC 913
QY 443 GCGTGGACGCTGACCTGAATGCTTCCCTGAGGCTCTTCAGAGCCCTGCAATCAT 502
Db 914 GCGTGGACGCTGACCTGAATGCTTCCCTGAGGCTCTTCAGAGCCCTGCAATCAT 973
QY 503 AAGGGATCTGGCAAGGCAAGTCCACTCTGCTGACGCGCATTTGCCATGCTCTGGGCT 562
Db 974 AAGGGATCTGGCAAGGCAAGTCCACTCTGCTGACGCGCAATTTGCCATGCTCTGGGCT 1033
QY 563 CCGMAAGTGAAGCTCTGACCAAGTTCAAATTCGCTTCTTCCCTGCTCAGCAGG 622
Db 1034 CCGMAAGTGAAGCTCTGACCAAGTTCAAATTCGCTTCTTCCCTGCTCAGCAGG 1093
QY 623 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCGATATACCTGGCAATCA 682
Db 1094 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCGATATACCTGGCAATCA 1153
QY 683 GGAAGCAGACATTCATGGCCATGCTGTGAAGCTGCGGCAGAGGGTTCTTTTCTCTTG 742
Db 1154 GGAAGCAGACATTCATGGCCATGCTGTGAAGCTGCGGCAGAGGGTTCTTTTCTCTTG 1213
QY 743 ATGGCTACAATGAATTCGAAGCCCGAGAACTGCCAGAAATCGAAGCCCTGATAAGGAAA 802
Db 1214 ATGGCTACAATGAATTCGAAGCCCGAGAACTGCCAGAAATCGAAGCCCTGATAAGGAAA 1273
QY 803 ACCACCGCTTCAAGAACATGCTCATCGTCAACCTACCACTGAGTGGTCCGACATAC 862
Db 1274 ACCACCGCTTCAAGAACATGCTCATCGTCAACCTACCACTGAGTGGTCCGACATAC 1333

QY 863 GGCAGTTTGTGGCCCTGACTGCTGAGGTGGGGATATACAGAGACAGCGCCAGGCTC 922
Db 1334 GGCAGTTTGTGGCCCTGACTGCTGAGGTGGGGATATACAGAGACAGCGCCAGGCTC 1393
QY 923 TCATC TGAGAAAGTGTCTGATCAAGGAGCTTGTCTGAAGGCTTGTCTCCAAATTCAGAAAT 982
Db 1394 TCATC TGAGAAAGTGTCTGATCAAGGAGCTTGTCTGAAGGCTTGTCTCCAAATTCAGAAAT 1453
QY 983 CGCTTGAGGAATCTCATGAAGACCCCTCTCTTTTGTGTGTCATCATCTTGTGCAATCC 1042
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QY 1043 AGATG:GTGAAAGTGAAGTTCACACTCTCACACAAACACGCTGTTCATACCTTCTTATG 1102
Db 1514 AGATG:GTGAAAGTGAAGTTCACACTCTCACACAAACACGCTGTTCATACCTTCTTATG 1573
QY 1103 ATCTG:TCATACAGAAAACAAACACAAACATAAAGGTGTGCTGCAAGTCACTTCATTC 1162
Db 1574 ATCTG:TCATACAGAAAACAAACACAAACATAAAGGTGTGCTGCAAGTCACTTCATTC 1633
QY 1163 GAGG:TTGGACCACTGTGGACACTAGCTCTGGAGGTGTGTTCTCCCAAGTTTGAT 1222
Db 1634 GAGG:TTGGACCACTGTGGACACTAGCTCTGGAGGTGTGTTCTCCCAAGTTTGAT 1693
QY 1223 TCGAAC TGCAGGATGTCAGAGCTGAATGAGATGTCTCTGCTGACAACTGGGCTCTCT 1282
Db 1694 TCGAAC TGCAGGATGTCAGAGCTGAATGAGATGTCTCTGCTGACAACTGGGCTCTCT 1753
QY 1283 GTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAATCTTTTTCACAAAGTCACTTCCAG 1342
Db 1754 GTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAATCTTTTTCACAAAGTCACTTCCAG 1813
QY 1343 AGTACA TAGCAGGAGGAGACTCAGCAGTTTATTGACCTCTCATGAGCAGAGGAGTGA 1402
Db 1814 AGTACA TAGCAGGAGGAGACTCAGCAGTTTATTGACCTCTCATGAGCAGAGGAGTGA 1873
QY 1403 CCAAGG TGAATGGTACTTTCAGAAAATGGTTTCCATTTCCGACATTAACATCCACTATA 1462
Db 1874 CCAAGG TGAATGGTACTTTCAGAAAATGGTTTCCATTTCCGACATTAACATCCACTATA 1933
QY 1463 GCAGCC TGTCCGCTGACACTGTGGTCTCTGTGGAAGCCACAGGCTGTGTTGAAGC 1522
Db 1934 GCAGCC TGTCCGCTGACACTGTGGTCTCTGTGGAAGCCACAGGCTGTGTTGAAGC 1993
QY 1523 ACCTCG:AGCAGTGTATCAACACGCTGCCCTCTCGGACTTTCCATCCCAAGAGGCTC 1582
Db 1994 ACCTCG:AGCAGTGTATCAACACGCTGCCCTCTCGGACTTTCCATCCCAAGAGGCTC 2053
QY 1583 TCTGGATACAGAACTTTTGCAAAAGTGTGAAAACACACACTGAGCAAGAAATTCGAAAG 1642
Db 2054 TCTGGATACAGAACTTTTGCAAAAGTGTGAAAACACACACTGAGCAAGAAATTCGAAAG 2113
QY 1643 CATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 1702
Db 2114 CATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 2173
QY 1703 AATCAGC CTTGAGCCAAAGATTTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT 1762
Db 2174 AATCAGC CTTGAGCCAAAGATTTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT 2233
QY 1763 CAGGGAATATCCCGGATTAATTTGACTTCTTTTGAACATTTGCCCAATTTGTGCAAGTG 1822
Db 2234 CAGGGAATATCCCGGATTAATTTGACTTCTTTTGAACATTTGCCCAATTTGTGCAAGTG 2293
QY 1823 CTCTGGA TTTCAATTAACCTGACTTTTATGGGGAGCTGTGGCTTCATGGGAAAAGGCTG 1882
Db 2294 CTCTGGA TTTCAATTAACCTGACTTTTATGGGGAGCTGTGGCTTCATGGGAAAAGGCTG 2353
QY 1883 CAGAAGATACAGGTTGAATCCACATGGAAGAGCCCAAGAACTACATTTCCAGCAGG 1942
Db 2354 CAGAAGATACAGGTTGAATCCACATGGAAGAGCCCAAGAACTACATTTCCAGCAGG 2413
QY 1943 CTGTATC:TTGTTCTTCTTCACTGGAAGCAGGAATTCAGGACTCTGAGGCTCACATCCGGG 2002

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Db 2414 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTCAACATCCGGG 2473
QY 2003 ATTTTCAGCAAGTTGAATTAAGCAAGATATACATATCTGGGGAATATATTCAGCTTGCCA 2062
Db 2474 ATTTTCAGCAAGTTGAATTAAGCAAGATATACATATCTGGGGAATATATTCAGCTTGCCA 2533
QY 2063 CAAGCCTCAGGCTGCAATTAAGAGATGTCTGGTGGCTGGAAGCCTCAGTTGGTCC 2122
Db 2534 CAAGCCTCAGGCTGCAATTAAGAGATGTCTGGTGGCTGGAAGCCTCAGTTGGTCC 2593
QY 2123 TCAGCAGCTGTGAAGCAATTTATCTCATGTTGGTGAAGCAGTCCCTCACCATAGAG 2182
Db 2594 TCAGCAGCTGTGAAGCAATTTATCTCATGTTGGTGAAGCAGTCCCTCACCATAGAG 2653
QY 2183 ATGAGAGGCACATCATCTGTAAACAACTGAAACCTTGAGTATTCATGACCTACAGA 2242
Db 2654 ATGAGAGGCACATCATCTGTAAACAACTGAAACCTTGAGTATTCATGACCTACAGA 2713
QY 2243 ATCAAGCCTGCGGCTGCTGACTGACAGCTTGGTAACTTGAAGAACCTTCAAAAGC 2302
Db 2714 ATCAAGCCTGCGGCTGCTGACTGACAGCTTGGTAACTTGAAGAACCTTCAAAAGC 2773
QY 2303 TCATATGATTAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGCCCTGA 2362
Db 2774 TCATATGATTAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGCCCTGA 2833
QY 2363 AAAACCTGAAGAGATGTTTATTTATTTGACCTTGGTAACTTGAAGAACCTTCAAAAGC 2422
Db 2834 AAAACCTGAAGAGATGTTTATTTATTTGACCTTGGTAACTTGAAGAACCTTCAAAAGC 2893
QY 2423 TGGATTACATAGTCAAGTCTCTGTCAGTGAAGTGAACCTTGGTAACTTGAAGAACCTTCAAAAGC 2482
Db 2894 TGGATTACATAGTCAAGTCTCTGTCAGTGAAGTGAACCTTGGTAACTTGAAGAACCTTCAAAAGC 2953
QY 2483 TCTCTGCTGCTGCTGCAAAATGAGTGAAGTGAACCTTGGTAACTTGAAGAACCTTCAAAAGC 2542
Db 2954 TCTCTGCTGCTGCTGCAAAATGAGTGAAGTGAACCTTGGTAACTTGAAGAACCTTCAAAAGC 3013
QY 2543 TCAACTGAGCATCTTGTATTTATCAGAAATTTACCTGGAAGAACCTTGAAGAACCTTCAAAAGC 2602
Db 3014 TCAACTGAGCATCTTGTATTTATCAGAAATTTACCTGGAAGAACCTTGAAGAACCTTCAAAAGC 3073
QY 2603 TTCATGAATGATGACAGGATGAACGTCTAGAACAGCTCAGCAGCTGATGCTGCCCT 2662
Db 3074 TTCATGAATGATGACAGGATGAACGTCTAGAACAGCTCAGCAGCTGATGCTGCCCT 3133
QY 2663 GGGGCTGACGTGCAAGCAGCCTGAGCAGCCTGTGAAACATTTGGAGGAGTCCAC 2722
Db 3134 GGGGCTGACGTGCAAGCAGCCTGAGCAGCCTGTGAAACATTTGGAGGAGTCCAC 3193
QY 2723 AACTGCTCAAGCTTGGTGTGAAGAACTGGAGACTCACAGATACAGATTAAGATTTAG 2782
Db 3194 AACTGCTCAAGCTTGGTGTGAAGAACTGGAGACTCACAGATACAGATTAAGATTTAG 3253
QY 2783 GTGCATTTTGGAAAGAACCTCTGAAACCTCCAGCAGTTGAATTTGGCGGAAATC 2842
Db 3254 GTGCATTTTGGAAAGAACCTCTGAAACCTCCAGCAGTTGAATTTGGCGGAAATC 3313
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Db 3314 GTGTGAGCAGTATGATGGCTTGCTTCAATGGGTGATTTGAGATCTTAAAGCAATTTAG 3373
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RESULT 20
PCT-US00-29643-4
; Sequence 4, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3612)
PCT-US00-29643-4
Query Match 85.7%; Score 2634; DB 1; Length 3615;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 263 GTCTTTTTCATCAGACATCAGAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 322
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QY 323 TGTACCATACCCCTCTTTTCTGAACCTTTATCCCTTGGTGAAGATATGACATATTT 382
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QY 383 TTAACCTGAAAGACACCTTTCACAGAACCTTCTGTGGAGGAGGACCAACACCATCACC 442
Db 854 TTAACCTGAAAGACACCTTTCACAGAACCTTCTGTGGAGGAGGACCAACACCATCACC 913
QY 443 GCGTGAGCAGCTGACCCCTGAATGGCCTCTTCAGAGCCTCTTCAGAGCCCTGCATCATTTG 502
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QY 503 AAGGGAAATCTGGCAAGGCAAGTCCACTCTCTGCAGGCGATTTGCCATGCTCTGGGGCT 562
Db 974 AAGGGAAATCTGGCAAGGCAAGTCCACTCTCTGCAGGCGAATTTGCCATGCTCTGGGGCT 1033
QY 563 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTCTTCTTCCCTCAGCAGG 622
Db 1034 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTCTTCTTCCCTCAGCAGG 1093
QY 623 CCCAGGTTGAGCTTTTGAACCCCTCTGTGATCAACTCTCTGGATATPACCTGCACAATCA 682
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Db 1154 GGAAGCAGACATTCATGCGCATGTCTGTAAGTCTGGGAGGAGGTTCTTTTCTTCTTGG 1213
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Db 1214 ATGGCTACAAATTCAGCCCAAGACTGCCAGAAATCAAGCCCTGATTAAGGAA 1273
QY 803 ACCACCGCTTCAAGAACATGTCTGTCACCACTACCACTGAGTCCCTGAGGACATAC 862
Db 1274 ACCACCGCTTCAAGAACATGTCTGTCACCACTACCACTGAGTCCCTGAGGACATAC 1333
QY 863 GGCAGTTTGGTCCCTGACTGCTGAGGTTGGGGATATGACAGAAGACACGCGCCAGGCTC 922
Db 1334 GGCAGTTTGGTCCCTGACTGCTGAGGTTGGGGATATGACAGAAGACACGCGCCAGGCTC 1393

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Db 1454 CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTGTGGTTCATCACATTGTCGAATCC 1513
QY 1043 AGATGGGTGAAAGTGAAGTTCACATCTCACACAAACAGCTGTTCCATACCTTCTATG 1102
Db 1514 AGATGGGTGAAAGTGAAGTTCACATCTCACACAAACAGCTGTTCCATACCTTCTATG 1573
QY 1103 ATCTGTTGATACAGAAACAAACACAAACATAAAGCTGTGGCTGCAAGTGATCTTATTC 1162
Db 1574 ATCTGTTGATACAGAAACAAACACAAACATAAAGCTGTGGCTGCAAGTGATCTTATTC 1633
QY 1163 GGAGCCTGGACCATGTGGAGACCTAGCTCTGGAGGCTGTCTCCACAAAGTTTGATTC 1222
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QY 1223 TCGAATCTGAGGATGTCTCAGCGTGAATGAGGATGTCTGCTGACAACTGGGGCTCTCT 1282
Db 1694 TCGAATCTGAGGATGTCTCAGCGTGAATGAGGATGTCTGCTGACAACTGGGGCTCTCT 1753
QY 1283 GTAATATACAGCTCAAAGSTCAAGCCAAAGATATAAATCTTTTCAAAAGTCATTCGAGG 1342
Db 1754 GTAATATACAGCTCAAAGSTCAAGCCAAAGATATAAATCTTTTCAAAAGTCATTCGAGG 1813
QY 1343 AGTACACAGCAGGACGAGACTCAGCAGTATTTATTGAGCTCTCATGAGCCAGAGGAGGTGA 1402
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QY 1463 GCAGCCTGCTCCGCTACACCTGTGGGTCACTGTGGAAGCCACCAGGCTGTATGAAGC 1522
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QY 1523 ACCTCGCAGCAGTGTATCAACAGCGCTGCCCTCTCGGACTTTCCATCGCAAGAGGCTC 1582
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QY 1703 AATCAGCCCTGAGCCAAAGATTTGAAGCTTCTTTCAGGTAAAGCTTATATATCAACT 1762
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QY 1763 CAGGAACATCCCGATTAATTTGACTTCTTTGAACATTTGCCCCAATTTGTGCAAGTG 1822
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QY 1823 CTCTGGACTTCATTAATGACTTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTG 1882
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QY 1883 CAGAAGACAGGTGGAATCCACATGGAAGAGGCCAGAAACCTACATTTCCAGAGAGG 1942
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Db 2414 CTGTATCTTTTCTTCACTGGAGCAGGAATTCAGGACTCTGGAGGTACACTCCGGG 2473

QY 2003 ATTTTC IGCAAGTTGAATTAAGCAAGATATCACATATCTGGGAAATATTCAGCTCTGCCA 2062
Db 2474 ATTTTC IGCAAGTTGAATTAAGCAAGATATCACATATCTGGGAAATATTCAGCTCTGCCA 2533
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QY 2123 TCAGC:CTCTGTGAAGCAATTTATTTCTCTCATGGTGAAGCAGTCCCTCACCATAGAG 2182
Db 2594 TCAGC:CTCTGTGAAGCAATTTATTTCTCTCATGGTGAAGCAGTCCCTCACCATAGAG 2653
QY 2183 ATGAG:GGCAGATACACATCTGTAAACACCTGAAACCTTTGAGTATTTCATGACCTACAGA 2242
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QY 2243 ATCAA:GGCTGCCGGGTGGTCTGACTGACAGCTTGGGTAACTTGAAGAACCTTCAAGC 2302
Db 2714 ATCAA:GGCTGCCGGGTGGTCTGACTGACAGCTTGGGTAACTTGAAGAACCTTCAAGC 2773
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Db 2894 TGGATTACATAGTCAAGTCTCTGTCAAAGTGAACCCCTGTGACCTTTGAAGAAATTCATATAG 2953
QY 2483 TCTCCT 3CTGCTGTCTGCAAAATGCAGTGAAGTCCCTAGCTCAGAAATCTTCAAAATTTGG 2542
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QY 2603 TTCATG:ACTGTGACAGGATGAACGTGTAGAACAGCTCAGCAGCTCAGCAGCTGATGCTGCCCT 2662
Db 3074 TTCATG:ACTGTGACAGGATGAACGTGTAGAACAGCTCAGCAGCTCAGCAGCTGATGCTGCCCT 3133
QY 2663 GGGCT:GTGAGTGAAGCAGCTGAGCAGCTGTTGAAACATTTGGAGAGGCTCCAC 2722
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QY 2783 GTGCAT:TTTTGGAAAGAACCTCTGAAACCTTCCAGAGCTTGAATTTGGCGGGAATC 2842
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QY 2903 TGTGTTT:IGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTTAGTCAGAAACTTA 2962
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Db 3494 ATGATGA:GATCTCAGTGTATTACAG 3520

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RESULT 21
PCT-US00-29643-6/c
; Sequence 6, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-29643-6

Query Match      85.7%; Score 2634; DB 1; Length 3615;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 263 GTCTTTTTCATCAGACATCAGAAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 322
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QY 323 TGTACCATACCCCATCTTTTCTGAACATTTATCCCTTGGTGAAGATATTTGACATTTATTT 382
DB 2822 TGTACCATACCCCATCTTTTCTGAACATTTATCCCTTGGTGAAGATATTTGACATTTATTT 2763
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DB 2762 TTAACCTTGAAGAACACCTTCACAGAACCTCTCCTGTGGAGGAGGACCAACACCATCAC 2703
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QY 503 AAGGGGAATCTGCAAGGCAAGTCCACTCTGCTGAGGCGCATTTGCCATGCTCTGGGGCT 562
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DB 2582 CCGGAAGTGCAGAGCTCTGACCAACTTCAAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2523
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Db 1022 TCAGCACCTGTGAAGAACATTTATTTCTCATGGTGGAGGAGGAGTCCCTCCACCATAGAAG 963
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Db 962 ATGAGAGGCACATCATCTCTGTAAACAACTGAAACCTTGAGTATTTATGACGCTACAGAG 903
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Db 902 ATCAACGGGTGCGGGTGTCTGACTGACAGCTTGGGTAACTTGAAGAACCTTACAAAGC 843
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Qy 2483 TCTCTGCTGCTTGTCTGCAATGAGTGAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2542
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Db 602 TCAAACTGAGCANTCTTGATTTATCAGAAATTAACCTGGAAGAGATGGAATGAAGCTC 543
Qy 2603 TTCATGAATGATGACAGGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCT 2662
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Qy 2903 TGTTTTTTGACTTTAGTACTAAGAAATTTTACCTGATCCAGCATTTAGTCAGAAACTTA 2962
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Qy 2963 GCCAAGTGTATCCAAAGTAACTTTTCTGCAAGAGAGCTAGGCTTGTGGGTGGCAATTTG 3022
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Db 122 ATGATGATGATCTCAGTGTATTACAG 96

RESULT 22
US-09-697-089-4
; Sequence 4, Application US/09697089
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136001
; CURRENT APPLICATION NUMBER: US/09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CD3
; LOCATION: (1)...(3612)
US-09-697-089-4

Query Match 85.7%; Score 2634; DB 27; Length 3615;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 263 GTCCTTTTCATCAGACATCAGAGAGACTTGGAGGATTTGGCTCAGGATTTAAAGGACT 322
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Qy 383 TTAACCTGAAAGACACCTTACAGAACCTGCTCTGTGGAGGAGGACCAACACCATCACC 442
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Qy 443 GCGTGGTSCAGCTGACCTGATGGCTTCCCTGAGAGCTTTCAGAGCCCTTCATCATTTG 502
Db 914 GCGTGGTSCAGCTGACCTGATGGCTTCCCTGAGAGCTTTCAGAGCCCTTCATCATTTG 973
Qy 503 AAGGGGTATCTGGGAAAGGCAAGTCCACTGCTGCTGAGGATTTGCCATGCTCTGGGCT 562
Db 974 AAGGGGTATCTGGGAAAGGCAAGTCCACTGCTGCTGAGGATTTGCCATGCTCTGGGCT 1033
Qy 563 CCGGAAATGTGCAAGGCTCTGACCAAGTTCAAAATTCGCTCTCTCCCTGCTCAGCAGGG 622
Db 1034 CCGGAAATGTGCAAGGCTCTGACCAAGTTCAAAATTCGCTCTCTCCCTGCTCAGCAGGG 1093
Qy 623 CCCAGGGTGGACTTTTTCAGAACCTCTGCTGATCACTCTCGATATACCTGGCACAATCA 682
Db 1094 CCCAGGGTGGACTTTTTCAGAACCTCTGCTGATCACTCTCGATATACCTGGCACAATCA 1153
Qy 683 GGAAGCAACATTCATGCGCATGCTGCTGAAGCTGGCGCAGAGGTTCTTTTCTCTCTTG 742
Db 1154 GGAAGCAACATTCATGCGCATGCTGCTGAAGCTGGCGCAGAGGTTCTTTTCTCTCTTG 1213
Qy 743 ATGCTATTAATGAATTCAGCCCTCAGAACTGCCAGAAATCCAGCCCTGTATTAAGGAAA 802
Db 1214 ATGCTATTAATGAATTCAGCCCTCAGAACTGCCAGAAATCCAGCCCTGTATTAAGGAAA 1273
Qy 803 ACCACCGTTTCAAGAAATTCATGCTGCTGACACTTACCACTGAGTGCCTGAGGACATAC 862
Db 1274 ACCACCGTTTCAAGAAATTCATGCTGCTGACACTTACCACTGAGTGCCTGAGGACATAC 1333
Qy 863 GGCAGTTTGGTCCCTGACTGCTGAGGTGGGGATATACAGAGACAGCGCCAGGCTC 922
Db 1334 GGCAGTTTGGTCCCTGACTGCTGAGGTGGGGATATACAGAGACAGCGCCAGGCTC 1393
Qy 923 TCATCCGTAAGTGTGATCAAGGCTTGTCTGAGGCTTGTCTCCAAATTCAGAAAT 982
Db 1394 TCATCCGTAAGTGTGATCAAGGCTTGTCTGAGGCTTGTCTCCAAATTCAGAAAT 1453
Qy 983 CCAGGTGCTTGAAGAAATTCATGAAGACCTCTCTTTGTTGGTCTATCATCTTGTGCAATCC 1042
Db 1454 CCAGGTGCTTGAAGAAATTCATGAAGACCTCTCTTTGTTGGTCTATCATCTTGTGCAATCC 1513

QY 1043 AGATGGGTGAAAGTGAGTTCCACTCTCACACAAACAAACGCTGTTCCTACCTCTCTATG 1102
Db 1514 AGATGGGTGAAAGTGAGTTCCACTCTCACACAAACAAACGCTGTTCCTACCTCTCTATG 1573
QY 1103 ATCTGTTGATACAGAAAACAAACAAACAAATAAAGGTGTGGCTGCAAGTACTTCATTTC 1162
Db 1574 ATCTGTTGATACAGAAAACAAACAAACAAATAAAGGTGTGGCTGCAAGTACTTCATTTC 1633
QY 1163 GGAGCTGGACCACTGTGGAGACCTAGCTCTCGAGGGTGTCTCCCAACAGTTTGATT 1222
Db 1634 GGAGCTGGACCACTGTGGAGACCTAGCTCTCGAGGGTGTCTCCCAACAGTTTGATT 1693
QY 1223 TCGAACTCGAGGATGTGTCAGCGTGAATGAGGATGTCTGCTGCAACACTGGGCTCCTCT 1282
Db 1694 TCGAACTCGAGGATGTGTCAGCGTGAATGAGGATGTCTGCTGCAACACTGGGCTCCTCT 1753
QY 1283 GTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAAATCTTTTCAACAGTCAATCCAGG 1342
Db 1754 GTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAAATCTTTTCAACAGTCAATCCAGG 1813
QY 1343 AGTACACACGACGACCAAGACTCAGCAGTTTATGACGTCTCATGAGCCAGAGGAGTGA 1402
Db 1814 AGTACACACGACGACCAAGACTCAGCAGTTTATGACGTCTCATGAGCCAGAGGAGTGA 1873
QY 1403 CCAAGGGGAATGGTTACTTTCAGAAAATGGTTTCCATTTTCGGACATTCATACCTTATA 1462
Db 1874 CCAAGGGGAATGGTTACTTTCAGAAAATGGTTTCCATTTTCGGACATTCATACCTTATA 1933
QY 1463 GCAGCTGTCGGGTACACCTGTGGGTCACTGTGGAAGCCACCAGGGGTGTATGAAGC 1522
Db 1934 GCAGCTGTCGGGTACACCTGTGGGTCACTGTGGAAGCCACCAGGGGTGTATGAAGC 1993
QY 1523 ACCTGCACGCTGATCAACAGGCTGCTCTCGAGCTTTCATCGCCAGAGGCCCTC 1582
Db 1994 ACCTGCACGCTGATCAACAGGCTGCTCTCGAGCTTTCATCGCCAGAGGCCCTC 2053
QY 1583 TCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAACACCACTGAGCAAGAAATCTGAAAG 1642
Db 2054 TCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAACACCACTGAGCAAGAAATCTGAAAG 2113
QY 1643 CCATTAACATCAATCTCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGATACATCCA 1702
Db 2114 CCATTAACATCAATCTCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGATACATCCA 2173
QY 1703 AATCAGCCCTGAGCAAGAAATTTGAAGCTTCTTCAAGGTAAAGCTTATATATCAACT 1762
Db 2174 AATCAGCCCTGAGCAAGAAATTTGAAGCTTCTTCAAGGTAAAGCTTATATATCAACT 2233
QY 1763 CAGGGAACATCCCGATTACTTTATTTGACTTCTTTGAACATTTGCCCAATTTGTCAAGTG 1822
Db 2234 CAGGGAACATCCCGATTACTTTATTTGACTTCTTTGAACATTTGCCCAATTTGTCAAGTG 2293
QY 1823 CTCGTGACTTCATTAACCTGGACTTTTATGGGGAGCTATGCGTTCATGGGAAAAGGCTG 1882
Db 2294 CCTCGACTTCATTAACCTGGACTTTTATGGGGAGCTATGCGTTCATGGGAAAAGGCTG 2353
QY 1883 CAGAGACACAGCTGGAATCCACATGGAAGAGGCCCCAGAAACCTTACATTCGCCAGCAGG 1942
Db 2354 CAGAGACACAGCTGGAATCCACATGGAAGAGGCCCCAGAAACCTTACATTCGCCAGCAGG 2413
QY 1943 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTTCACACTCCGGG 2002
Db 2414 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTTCACACTCCGGG 2473
QY 2003 ATTTTCAAGCAAGTTGAATGAAGATATACATATCTCGGGGAAATATTCAGCTCTGCCA 2062
Db 2474 ATTTTCAAGCAAGTTGAATGAAGATATACATATCTCGGGGAAATATTCAGCTCTGCCA 2533
QY 2063 CAAGCTCAGGCTGCAAAATAAAGAGATGTGCTGGGTGGCTGGAAGCCCTCAGTTTGGTCC 2122
Db 2534 CAAGCTCAGGCTGCAAAATAAAGAGATGTGCTGGGTGGCTGGAAGCCCTCAGTTTGGTCC 2593

QY 2123 TCAGCACCTGTGAAGACATTTATTTCTCATGTTGGAGCCAGTCCCTCACCATTAGAAG 2182
Db 2594 TCAGCACCTGTGAAGACATTTATTTCTCATGTTGGAGCCAGTCCCTCACCATTAGAAG 2653
QY 2183 ATGAGAGGCACATCAGATCTGTAAACAACTGAAAACCTTGAGTATTGATGACCTACAGA 2242
Db 2654 ATGAGAGGCACATCAGATCTGTAAACAACTGAAAACCTTGAGTATTGATGACCTACAGA 2713
QY 2243 ATCAACGGCTGCCGGTGTGCTGACTGACAGCTTGGGTAACTTGAAGAACCCTTACAAAGC 2302
Db 2714 ATCAACGGCTGCCGGTGTGCTGACTGACAGCTTGGGTAACTTGAAGAACCCTTACAAAGC 2773
QY 2303 TCATAATGGATAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGGCCCTGA 2362
Db 2774 TCATAATGGATAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGGCCCTGA 2833
QY 2363 AAAACCTGAAGAAGATGTGTTTATTTTCAATTTGACCCACTTGTCTGACATTTGAGAGGGAA 2422
Db 2834 AAAACCTGAAGAAGATGTGTTTATTTTCAATTTGACCCACTTGTCTGACATTTGAGAGGGAA 2893
QY 2423 TGGATTACATAGTCAAGTCTCTGCAAGTGAACCTGTGACCTTGAAGAAATTCATATTAG 2482
Db 2894 TGGATTACATAGTCAAGTCTCTGCAAGTGAACCTGTGACCTTGAAGAAATTCATATTAG 2953
QY 2483 TCTCCTGCTGCTTGTGCAAAATGCAGTGAAGAAATCCTAGCTCAGATCTTCACAAATTTGG 2542
Db 2954 TCTCCTGCTGCTTGTGCAAAATGCAGTGAAGAAATCCTAGCTCAGATCTTCACAAATTTGG 3013
QY 2543 TCAAACTGAGCAATCTTGATTTATCAGAAATTTACCTGGAAAAGATGAAATGAAGCTC 2602
Db 3014 TCAAACTGAGCAATCTTGATTTATCAGAAATTTACCTGGAAAAGATGAAATGAAGCTC 3073
QY 2603 TTCATGAACCTGATCAGCAGGATGAAGTCTAGAACAGCTCACCAGCTGATGCTGCCCT 2662
Db 3074 TTCATGAACCTGATCAGCAGGATGAAGTCTAGAACAGCTCACCAGCTGATGCTGCCCT 3133
QY 2663 GGGGCTGTGACGTGCAAGGAGCCTGAGCAGCCTGTTGAAACATTTTGGAGGAGTCCCAC 2722
Db 3134 GGGGCTGTGACGTGCAAGGAGCCTGAGCAGCCTGTTGAAACATTTTGGAGGAGTCCCAC 3193
QY 2723 AACTGCTCAAGCTTGGTTGAAAACCTGGAGACTCAGATACAGATACAGATTTAGATTAG 2782
Db 3194 AACTGCTCAAGCTTGGTTGAAAACCTGGAGACTCAGATACAGATACAGATTTAGATTAG 3253
QY 2783 GTGCATTTTGTGAAGAAGCCTCTGAAAACCTTCCAGCAGTTGAATTTGGCGGGAATC 2842
Db 3254 GTGCATTTTGTGAAGAAGCCTCTGAAAACCTTCCAGCAGTTGAATTTGGCGGGAATC 3313
QY 2843 GTGTGAGCAGTGTGATGGCTTGGCTTCATGGGTGATTTTGAAGATCTTAAGCAATTAG 2902
Db 3314 GTGTGAGCAGTGTGATGGCTTGGCTTCATGGGTGATTTTGAAGATCTTAAGCAATTAG 3373
QY 2903 TGTGTTTGTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGATTTAGTCAGAAACTTA 2962
Db 3374 TGTGTTTGTGACTTTAGTACTAAAGAAATTTCTACCTGATCCAGCAATTTAGTCAGAAACTTA 3433
QY 2963 GCCAAGTGTATCCAAAGTAACTTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATTTG 3022
Db 3434 GCCAAGTGTATCCAAAGTAACTTTTCTGCAAGAAGCTAGGCTTGTGGTGGCAATTTG 3493
QY 3023 ATGATGATGATCTCAGTGTATTACAG 3049
Db 3494 ATGATGATGATCTCAGTGTATTACAG 3520

RESULT 23

US-09-697-089-12/c
; Sequence 12, Application US/09697089
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF


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; FILE REFERENCE: 07334-136001
; CURRENT APPLICATION NUMBER: US/09/697,089
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-697-089-12

Query Match
Best Local Similarity 85.7%; Score 2634; DB 27; Length 3615;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 263 GTCCTTTTTCATCAGACATCAGAAGGAGACTTGGAGGATTTGGCTCAGGATTTAAAGGACT 322
Db 2882 GTCCTTTTTCATCAGACATCAGAAGGAGACTTGGAGGATTTGGCTCAGGATTTAAAGGACT 2823

Qy 323 TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATTCACATTTATTT 382
Db 2822 TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATTCACATTTATTT 2763

Qy 383 TTAACCTGAAAAGCACCTTCACAGAACCTGCTGTTGGAGGAAGGACCAACACCATCACC 442
Db 2762 TTAACCTGAAAAGCACCTTCACAGAACCTGCTGTTGGAGGAAGGACCAACACCATCACC 2703

Qy 443 GCGTGGAGCAGCTGACCTGAAATGGCCCTCTGCGAGGCTCTTTCAGAGCCCTGCAATATG 502
Db 2702 GCGTGGAGCAGCTGACCTGAAATGGCCCTCTGCGAGGCTCTTTCAGAGCCCTGCAATATG 2643

Qy 503 AAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCGAGGCTCTTTCAGAGCCCTGCAATATG 562
Db 2642 AAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCGAGGCTCTTTCAGAGCCCTGCAATATG 2583

Qy 563 CCGGAAAGTGAAGGCTCTGACCAAGTCAAAATTCGCTCTTCTCGCTCGTCTCAGCAGGG 622
Db 2582 CCGGAAAGTGAAGGCTCTGACCAAGTCAAAATTCGCTCTTCTCGCTCGTCTCAGCAGGG 2523

Qy 623 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTGATATACCTGGATATACCTGGCAATCA 682
Db 2522 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTGATATACCTGGCAATCA 2463

Qy 683 GGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGGAGGAGGCTTCTTCTCTCTTG 742
Db 2462 GGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGGAGGAGGCTTCTTCTCTCTTG 2403

Qy 743 ATGGCTACAATGAATTCAGCCCCCAGAACTGCTCCAGAAATCGAAGCCCTGATAAAGGAAA 802
Db 2402 ATGGCTACAATGAATTCAGCCCCCAGAACTGCTCCAGAAATCGAAGCCCTGATAAAGGAAA 2343

Qy 803 ACCACCGCTTCAGAAATGCTATCGTCACTACCTAGTGTGCTGAGGCAATAC 862
Db 2342 ACCACCGCTTCAGAAATGCTATCGTCACTACCTAGTGTGCTGAGGCAATAC 2283

Qy 863 GGCAGTTTGTGGCCCTGACTGCTGAGGTGGGGATATGACAGAAAGACAGCCCGCAGGCTC 922
Db 2282 GGCAGTTTGTGGCCCTGACTGCTGAGGTGGGGATATGACAGAAAGACAGCCCGCAGGCTC 2223

Qy 923 TCATCCGAGAAAGTGTGATCAAGAGCTTGTGTAAGCTTGTGCTCCAAATTCAGAAAT 982
Db 2222 TCATCCGAGAAAGTGTGATCAAGAGCTTGTGTAAGCTTGTGCTCCAAATTCAGAAAT 2163

Qy 983 CCAGGTGCTTGAGGAATCTCATGAAGCCCTCTCTTGTGGTCACTACATGTGCAATCC 1042
Db 2162 CCAGGTGCTTGAGGAATCTCATGAAGCCCTCTCTTGTGGTCACTACATGTGCAATCC 2103

Qy 1043 AGATGGGTGAAGTGAAGTTCACATTCACAGAAAGAGGCTTTCATACCTCTATG 1102
Db 2102 AGATGGGTGAAGTGAAGTTCACATTCACAGAAAGAGGCTTTCATACCTCTATG 2043
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Qy 1103 ATCTG TGTATACAGAAAAACAAACACAAACATAAAGGTGTGGCTGCAAGTCACTTCATTC 1162
Db 2042 ATCTG TGTATACAGAAAAACAAACACAAACATAAAGGTGTGGCTGCAAGTCACTTCATTC 1983

Qy 1163 GGAGC TGGACCACTGTGGAGACCTAGCTCTGGAGGTGTGTCTCCACAAAGTTTGANT 1222
Db 1982 GGAGC TGGACCACTGTGGAGACCTAGCTCTGGAGGTGTGTCTCCACAAAGTTTGANT 1923

Qy 1223 TCGAA TGCAGGATGTCTCCAGCGTGAATGAGGATGTCTCTGCTGACAACTGGGCTCTCT 1282
Db 1922 TCGAA TGCAGGATGTCTCCAGCGTGAATGAGGATGTCTCTGCTGACAACTGGGCTCTCT 1863

Qy 1283 GTAAATATACAGCTCAAGGTTCAAGCAAAAGTATAAATCTTTCAAAAGTCATTCCAGG 1342
Db 1862 GTAAATATACAGCTCAAGGTTCAAGCAAAAGTATAAATCTTTCAAAAGTCATTCCAGG 1803

Qy 1343 AGTAC CAGCAGGACGAAGACTCAGCAGCTTATTTAGCTCTCATGAGCCAGAGGATGA 1402
Db 1802 AGTAC CAGCAGGACGAAGACTCAGCAGCTTATTTAGCTCTCATGAGCCAGAGGATGA 1743

Qy 1403 CCAAGG GGAATGGTTACTTTCAGAAATGGTTCCATTCGGACATTCACATCCACTTATA 1462
Db 1742 CCAAGG GGAATGGTTACTTTCAGAAATGGTTCCATTCGGACATTCACATCCACTTATA 1683

Qy 1463 GCAGCC TGTCCGCTACACCTGTGGGTCTATCTGTGGAAGCCACAGGGCTGTGTATGAAGC 1522
Db 1682 GCAGCC TGTCCGCTACACCTGTGGGTCTATCTGTGGAAGCCACAGGGCTGTGTATGAAGC 1623

Qy 1523 ACTCG AGCAGTGTATCAACACGGCTGCCCTCTCTCGGACTTTCATCGCCAAAGAGGCTC 1582
Db 1522 ACTCG AGCAGTGTATCAACACGGCTGCCCTCTCTCGGACTTTCATCGCCAAAGAGGCTC 1563

Qy 1583 TCTGGA ACAGGAATCTTTGCAAAAGTGTGAAACACACACTGAGCAAGAAATTCGAAAG 1642
Db 1562 TCTGGA ACAGGAATCTTTGCAAAAGTGTGAAACACACACTGAGCAAGAAATTCGAAAG 1503

Qy 1643 CCATAA CATCAATCTCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 1702
Db 1502 CCATAA CATCAATCTCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 1443

Qy 1703 AATCAG CCTGAGCAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT 1762
Db 1442 AATCAG CCTGAGCAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT 1383

Qy 1763 CAGGGA CATCCCGATACTTATTTGACCTCTTTGACATTTGCAATTTGCCAATTTGCAAGTG 1822
Db 1382 CAGGGA CATCCCGATACTTATTTGACCTCTTTGACATTTGCAATTTGCCAATTTGCAAGTG 1323

Qy 1823 CTCTGG ATTCAATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1882
Db 1322 CCTTGG ATTCAATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1263

Qy 1883 CAGAAG ACAGGTGGAATCCACATGGAAGAGGCCCCAGAAACCTACATTTCCCAAGCAGGG 1942
Db 1262 CAGAAG ACAGGTGGAATCCACATGGAAGAGGCCCCAGAAACCTACATTTCCCAAGCAGGG 1203

Qy 1943 CTGTATC TTTGTTCTTCAACTTGAAGCAGGAATTCAGGACTCTCGAGGTCACTCCGGG 2002
Db 1202 CTGTATC TTTGTTCTTCAACTTGAAGCAGGAATTCAGGACTCTCGAGGTCACTCCGGG 1143

Qy 2003 ATTTTCA GAGTTGAATTAAGCAAGATATACATATCTGGGAAAATATTTCAGCTTCGCCA 2062
Db 1142 ATTTTCA GAGTTGAATTAAGCAAGATATACATATCTGGGAAAATATTTCAGCTTCGCCA 1083

Qy 2063 CAGCCTC AGGCTCAATTAAGAGATGTCTGTGTGGTGGAGCCTTCAGTTTGGTCC 2122
Db 1082 CAGCCTC AGGCTCAATTAAGAGATGTCTGTGTGGTGGAGCCTTCAGTTTGGTCC 1023

Qy 2123 TCAGCAC TGTAAAGACATTTATCTCTCATGGTGGAGCCAGTCCCTCCACATAGAG 2182
Db 1022 TCAGCAC TGTAAAGACATTTATCTCTCATGGTGGAGCCAGTCCCTCCACATAGAG 963

Qy 2183 ATGAGAG CACATCACATCTGTAAACACCTGAAACCTTGAGGATTTTCATGACCTACAGA 2242
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Db 962 ATGAGAGGCACATCACATCTGTAACAAACCTTGAAACACCTTGAGTATTGATGACCTACAGA 903
QY 2243 ATCAACGGCTCGGGGTGCTGACTGACAGCTTGGGTAACTTGAAGAACCTTACAAAGC 2302
Db 902 ATCAACGGCTCGGGGTGCTGACTGACAGCTTGGGTAACTTGAAGAACCTTACAAAGC 843
QY 2303 TCATAATGATTAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGGCTGA 2362
Db 842 TCATAATGATTAACATAAAGATGAATGAAGAAGATGCTATAAACTAGCTGAAGGCTGA 783
QY 2363 AAAACCTGAAGAAGATGCTGTTATTTCAATTTGACCCACTTGCTGACATTTGAGAGGGAA 2422
Db 782 AAAACCTGAAGAAGATGCTGTTATTTCAATTTGACCCACTTGCTGACATTTGAGAGGGAA 723
QY 2423 TGGATTACATAGTCAAGTCTCTGTCAGTGAACCCCTGTCACCTTGGAAGAAATTCATTTAG 2482
Db 722 TGGATTACATAGTCAAGTCTCTGTCAGTGAACCCCTGTCACCTTGGAAGAAATTCATTTAG 663
QY 2483 TCTCTGCTGCTTGTCTGCAAAATGCAATGCAATCTAGCTCAGAAATCTTCAAAATTTGG 2542
Db 662 TCTCTGCTGCTTGTCTGCAAAATGCAATGCAATCTAGCTCAGAAATCTTCAAAATTTGG 603
QY 2543 TCAAACTAGCAATCTTGTATTTATCAGAAATTTACCTGGAAGAAATGCAATGCAATGCAAT 2602
Db 602 TCAAACTAGCAATCTTGTATTTATCAGAAATTTACCTGGAAGAAATGCAATGCAATGCAAT 543
QY 2603 TTCATGAACCTGATGACAGAGTGAAGTCTGAGAGAGCTGAGAGAGTGAAGTGAAGTGAAG 2662
Db 542 TTCATGAACCTGATGACAGAGTGAAGTCTGAGAGAGCTGAGAGAGTGAAGTGAAGTGAAG 483
QY 2663 GGGGCTGTGACGTGCAAGCAGCCTGAGCAGCCTGTTGAAACATTTGGAGAGGTCCTCAC 2722
Db 482 GGGGCTGTGACGTGCAAGCAGCCTGAGCAGCCTGTTGAAACATTTGGAGAGGTCCTCAC 423
QY 2723 AACTGCTGAAGCTTGGGTTGAAAACCTGGAGACTCACAGATCAGAGATTAAGATTTTATG 2782
Db 422 AACTGCTGAAGCTTGGGTTGAAAACCTGGAGACTCACAGATCAGAGATTAAGATTTTATG 363
QY 2783 GTGCATTTTGTGAAGAACCTCTGAAAACCTCCAGAGTGAATTTGGCGGGAATTC 2842
Db 362 GTGCATTTTGTGAAGAACCTCTGAAAACCTCCAGAGTGAATTTGGCGGGAATTC 303
QY 2843 GTGTGACAGTATGATGGCTTGGCTTCATGGGTGATTTGAGATCTTAAAGCAATTTAG 2902
Db 302 GTGTGACAGTATGATGGCTTGGCTTCATGGGTGATTTGAGATCTTAAAGCAATTTAG 243
QY 2903 TGTTTTGTGACTTTGTACTAAGAAATTTCTACCTGATCCAGATTAAGCAATTTAG 2962
Db 242 TGTTTTGTGACTTTGTACTAAGAAATTTCTACCTGATCCAGATTAAGCAATTTAG 183
QY 2963 GCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAGCTAGGCTGTTGGTGGCAATTTG 3022
Db 182 GCCAAGTGTATCCAAAGTTAACTTTCTGCAAGAGCTAGGCTGTTGGTGGCAATTTG 123
QY 3023 ATGATGATGATCTCAGTGTATTACAG 3049
Db 122 ATGATGATGATCTCAGTGTATTACAG 96

RESULT 24
US-09-841-739-4
; Sequence 4, Application US/09841739
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27

; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(3612)
US-09-841-739-4

Query Match 85.7%; Score 2634; DB 32; Length 3615;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 263 GTCTTTTTCATCAGACATCAGAGGAGACTTGGACCATTTGGCTCAGGATTTAAAGGACT 322
Db 734 GTCTTTTTCATCAGACATCAGAGGAGACTTGGACCATTTGGCTCAGGATTTAAAGGACT 793
QY 323 TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATTGACATTTAT 382
Db 794 TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATTGACATTTAT 853
QY 383 TTAACCTTGAAGAGCACCTTTCACAGAACCTGTCTGTGAGAGAGGACCAACACCATCAC 442
Db 854 TTAACCTTGAAGAGCACCTTTCACAGAACCTGTCTGTGAGAGAGGACCAACACCATCAC 913
QY 443 GGGTGGAGCAGCTGACCCCTGAATGGCTCTGCAGGCTCTTCAGAGCCCTTCATCATTTG 502
Db 914 GGGTGGAGCAGCTGACCCCTGAATGGCTCTGCAGGCTCTTCAGAGCCCTTCATCATTTG 973
QY 503 AAGGGGAATCTGGCAAGGCAAGTCCACATCTGCTGAGCGCATTTGCCATGCTCTGGGGCT 562
Db 974 AAGGGGAATCTGGCAAGGCAAGTCCACATCTGCTGAGCGAATTTGCCATGCTCTGGGGCT 1033
QY 563 CCGGAAGTGCAGGGCTCTGACCAAGTTCAAAATTCGTCCTTCTTCCTCCCTCTCAGCAGGG 622
Db 1034 CCGGAAGTGCAGGGCTCTGACCAAGTTCAAAATTCGTCCTTCTTCCTCCCTCTCAGCAGGG 1093
QY 623 CCAGGGTGGACTTTTGAACCCCTGTGATCACTCTCGATATACCTGGATATACCTGGCACAAATCA 682
Db 1094 CCAGGGTGGACTTTTGAACCCCTGTGATCACTCTCGATATACCTGGATATACCTGGCACAAATCA 1153
QY 683 GGAAGCAGACATTCATGGCCATGCTGCTGAAAGCTGGCGAGAGGGTCTCTTCTCTCTTG 742
Db 1154 GGAAGCAGACATTCATGGCCATGCTGCTGAAAGCTGGCGAGAGGGTCTCTTCTCTCTTG 1213
QY 743 ATGGGTACAAATGAATTCAGAGCCCAAGACTGCCAGAAATTCGAAGCCCTGTATAAGGAAA 802
Db 1214 ATGGGTACAAATGAATTCAGAGCCCAAGACTGCCAGAAATTCGAAGCCCTGTATAAGGAAA 1273
QY 803 ACCACCGCTTCAAGRACATGGTCACTGCACCACTACCCTGCTGCTGCTGAGGCGCACATAC 862
Db 1274 ACCACCGCTTCAAGRACATGGTCACTGCACCACTACCCTGCTGCTGCTGAGGCGCACATAC 1333
QY 863 GGCAGTTTGGTGCCTGACTGCTGAGTGGGGATATGACAGAAAGACAGCGCCAGGCTC 922
Db 1334 GGCAGTTTGGTGCCTGACTGCTGAGTGGGGATATGACAGAAAGACAGCGCCAGGCTC 1393
QY 923 TCATCCGAAAGTGTGTGATCAAGGAGCTTGCTGAAAGGCTTTGTGCTCCAAATTCAGAAAT 982
Db 1394 TCATCCGAAAGTGTGTGATCAAGGAGCTTGCTGAAAGGCTTTGTGCTCCAAATTCAGAAAT 1453
QY 983 CCAGGTGCTTGAAGATCTCATGAAGACCCCTCTCTTTTGGTTCATCATCTTGGCAATCC 1042
Db 1454 CCAGGTGCTTGAAGATCTCATGAAGACCCCTCTCTTTTGGTTCATCATCTTGGCAATCC 1513
QY 1043 AGATGGTGAAGTGTGATTTCCACTCTCAGACACAAACAGCTGTGCTCCATACCTTCTATG 1102
Db 1514 AGATGGTGAAGTGTGATTTCCACTCTCAGACACAAACAGCTGTGCTCCATACCTTCTATG 1573
QY 1103 ATCTGTTGATACAGAAAAACAAACACATAAAGGCTGGCTGCAAGTGTGCTTCTTCTT 1162

Db 1574 ATCTGTTGATACAGAAAAACAAACACAAACATAAAGGTGTGGCTGCGAAGTGACTTCAATTC 1633
Qy 1163 GGAGCCCTGGACCTGTGGAGACCTAGCTCTGTGGAGGTGTGTTCTCCACACAAGTTTGATT 1222
Db 1634 GGAGCCCTGGACCTGTGGAGACCTAGCTCTGTGGAGGTGTGTTCTCCACACAAGTTTGATT 1693
Qy 1223 TCGAACTGCAGGATGTCTCCAGCGTGAATGAGGATGTCCTCTGACAACTGGGCTCCTCT 1282
Db 1694 TCGAACTGCAGGATGTCTCCAGCGTGAATGAGGATGTCCTCTGACAACTGGGCTCCTCT 1753
Qy 1283 GTAATATACAGCTCAAAAGGTTCAAGCCAAAGTATAAATCTTTTCAACAAGTCATTCCAGG 1342
Db 1754 GTAATATACAGCTCAAAAGGTTCAAGCCAAAGTATAAATCTTTTCAACAAGTCATTCCAGG 1813
Qy 1343 AGTACACAGCAGGAGAGACTCAGCAGTTTATTTGAGCTCTCATGAGCCAGAGAGGTGA 1402
Db 1814 AGTACACAGCAGGAGAGACTCAGCAGTTTATTTGAGCTCTCATGAGCCAGAGAGGTGA 1873
Qy 1403 CCAAGGGGAATGGTTACTTTCAGAAAATGGTTTCCATTTCCGAGATTACATCCACTTATA 1462
Db 1874 CCAAGGGGAATGGTTACTTTCAGAAAATGGTTTCCATTTCCGAGATTACATCCACTTATA 1933
Qy 1463 CGAGCTGCTCCGGTACACCTGTGGGTCACTGTGTGAAGCCACAGGGCTGTTATGAAGC 1522
Db 1934 CGAGCTGCTCCGGTACACCTGTGGGTCACTGTGTGAAGCCACAGGGCTGTTATGAAGC 1993
Qy 1523 ACCTCGCAGCAGTGTATCAACACAGGCTGCCCTTCTCGGACTTTCATCGCCCAAGAGGCTC 1582
Db 1994 ACCTCGCAGCAGTGTATCAACACAGGCTGCCCTTCTCGGACTTTCATCGCCCAAGAGGCTC 2053
Qy 1583 TCTGGAGACAGGAATCTTTGCAAAAGTGTGA AAAACACACACTTGACAGAGAATTTCTGAAG 1642
Db 2054 TCTGGAGACAGGAATCTTTGCAAAAGTGTGA AAAACACACACTTGACAGAGAATTTCTGAAG 2113
Qy 1643 CCATAAACATCAATTCCTTTCTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 1702
Db 2114 CCATAAACATCAATTCCTTTCTAGAGTGTGGCATCCATTTATATCAAGAGAGTACATCCA 2173
Qy 1703 AATCAGCCCTGAGCAAGAAATTTCAAGCTTCTTTCAAGGTAAAGCTTATATCAACT 1762
Db 2174 AATCAGCCCTGAGCAAGAAATTTCAAGCTTCTTTCAAGGTAAAGCTTATATCAACT 2233
Qy 1763 CAGGAACTCCCGATTAATTTGACTTCTTTGACATTTTCCCAATTTGCCAATTTGCAAGTG 1822
Db 2234 CAGGAACTCCCGATTAATTTGACTTCTTTGACATTTTCCCAATTTGCCAATTTGCAAGTG 2293
Qy 1823 CTCTGGACTTCATTAAGTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1882
Db 2294 CCCTGGACTTCATTAAGTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 2353
Qy 1883 CAGAAGACACAGTGGAAATCCATGGAAGAGGCCGCCAGAAACCTACATTTCCCGACAGGG 1942
Db 2354 CAGAAGACACAGTGGAAATCCATGGAAGAGGCCGCCAGAAACCTACATTTCCCGACAGGG 2413
Qy 1943 CTGTATCTTTGTTCTTCAACTGGAGCAGGAATTCAGGACTCTGGAGGTTCACACTCCGGG 2002
Db 2414 CTGTATCTTTGTTCTTCAACTGGAGCAGGAATTCAGGACTCTGGAGGTTCACACTCCGGG 2473
Qy 2003 ATTTTCAGCAAGTTGAATAAGCAAGATATACATATCTCTGGGAAAATATTTCAGCTCTGCCA 2062
Db 2474 ATTTTCAGCAAGTTGAATAAGCAAGATATACATATCTCTGGGAAAATATTTCAGCTCTGCCA 2533
Qy 2063 CAAGCCTCAGCCTCAATAAAGAGATGTGCTGTGTGGCTGGAAGCCTCAGTTTGTGTC 2122
Db 2534 CAAGCCTCAGCCTCAATAAAGAGATGTGCTGTGTGGCTGGAAGCCTCAGTTTGTGTC 2593
Qy 2123 TCAGCACTGTGAACAATTTATTTCTCATGTTGGAGAGCAGTCCCTCACCATAGAAG 2182
Db 2594 TCAGCACTGTGAACAATTTATTTCTCATGTTGGAGAGCAGTCCCTCACCATAGAAG 2653
Qy 2183 ATGAGGACACATCAGCTGTACAACTGAAACCTTGAAACCTTGAGTATTCAGCTACAGA 2242
Db 2654 ATGAGGACACATCAGCTGTACAAACCTTGAAACCTTGAGTATTCAGCTACAGA 2713

Qy 2243 ATCAA'GGCTGCCGGGTGCTGACTGACAGCTTTGGTAACTTGAAGAACCCTTCAAAAGC 2302
Db 2714 ATCAA'GGCTGCCGGGTGCTGACTGACAGCTTTGGTAACTTGAAGAACCCTTCAAAAGC 2773
Qy 2303 TCATA'ITGGATAAACATAAAGATGAATGAAGAAGATGCTATAAAACTAGCTGAAGGCCTGA 2362
Db 2774 TCATA'ITGGATAAACATAAAGATGAATGAAGAAGATGCTATAAAACTAGCTGAAGGCCTGA 2833
Qy 2363 AAAAC'ITGAAGAAGATGTGTTTATTTTCAATTTGACCCACTTCTCTGACATTTGAGAGGGAA 2422
Db 2834 AAAAC'ITGAAGAAGATGTGTTTATTTTCAATTTGACCCACTTCTCTGACATTTGAGAGGGAA 2893
Qy 2423 TGGAT'ACATAGTCAAGCTCTCTG'CAAGTGAACCTCTGACCTTGAAGAAATTCAAATTAG 2482
Db 2894 TGGAT'ACATAGTCAAGCTCTCTG'CAAGTGAACCTCTGACCTTGAAGAAATTCAAATTAG 2953
Qy 2483 TCTCC'IGCTGCTTGTCTGCAAAATGCAAGTGAATAATCTTACCTAGCTCAGAACTTTCACAAATTTGG 2542
Db 2954 TCTCC'IGCTGCTTGTCTGCAAAATGCAAGTGAATAATCTTACCTAGCTCAGAACTTTCACAAATTTGG 3013
Qy 2543 TCAAC'ITAGCATTCCTTGTATTTATCAGAAAATTAACCTGGAAAAAGATGGAATGAAGCTC 2602
Db 3014 TCAAC'ITAGCATTCCTTGTATTTATCAGAAAATTAACCTGGAAAAAGATGGAATGAAGCTC 3073
Qy 2603 TTTCA'GACTGATCGACAGGATGAACGTGTAGAACAGCTCACCGCACTGATGCTGCCCT 2662
Db 3074 TTTCA'GACTGATCGACAGGATGAACGTGTAGAACAGCTCACCGCACTGATGCTGCCCT 3133
Qy 2663 GGGCT'ITGAGCTGCAAGGCGAGCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTGCCAC 2722
Db 3134 GGGCT'ITGAGCTGCAAGGCGAGCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTGCCAC 3193
Qy 2723 AACTCG'CAAGCTTTGGTGTGAAAACTGGAGACTCACAGATACAGATTAAGATTTTAG 2782
Db 3194 AACTCG'CAAGCTTTGGTGTGAAAACTGGAGACTCACAGATACAGATTAAGATTTTAG 3253
Qy 2783 GTGCAT'TTTTGGAAAGAACCTCTGAAACACTTCCAGCAGTTTGAATTTGCGGGAATC 2842
Db 3254 GTGCAT'TTTTGGAAAGAACCTCTGAAACACTTCCAGCAGTTTGAATTTGCGGGAATC 3313
Qy 2843 GTGCA'GAGTGAATGGGTGCTTCCCTCATGGGTGATTTGAGAACTTTAAGCAATTAG 2902
Db 3314 GTGCA'GAGTGAATGGGTGCTTCCCTCATGGGTGATTTGAGAACTTTAAGCAATTAG 3373
Qy 2903 TGTTTT'ITGACTTTAGTACTAAGAAATTTCTACCTGATCCAGCAATTAGTCAGAAACTTA 2962
Db 3374 TGTTTT'ITGACTTTAGTACTAAGAAATTTCTACCTGATCCAGCAATTAGTCAGAAACTTA 3433
Qy 2963 GCCAAG'ITATCAAGTTAACTTTTCTGCAAGAGCTAGGCTTTGTTGGGTGCAATTTG 3022
Db 3434 GCCAAG'ITATCAAGTTAACTTTTCTGCAAGAGCTAGGCTTTGTTGGGTGCAATTTG 3493
Qy 3023 ATGATGA'IGATCTCAGTGTATTACAG 3049
Db 3494 ATGATGA'IGATCTCAGTGTATTACAG 3520

RESULT 25

US-09-841-739-12/:

; Sequence 12, Apillication US/09841739

; GENERAL INFORM:ION:

; APPLICANT: Ber'in, John

; TITLE OF INVEN:ION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH

; FILE REFERENCE 07334-329001

; CURRENT APPLIC/TION NUMBER: US/09/841,739

; CURRENT FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: US 09/697,089

; PRIOR FILING DATE: 2000-10-26

; PRIOR APPLICATION NUMBER: US 60/161,822

; PRIOR FILING DATE: 1998-10-27

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: SeqS EQ for Windows Version 4.0

; SEQ ID NO 12									
; LENGTH: 3615									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-09-841-739-12									
Query Match									
Best Local Similarity 85.7%; Score 2634; DB 32; Length 3615;									
Mismatches 2784; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
QY	263	GTCTTTTTCATCAGACATCAGAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT	322						
DB	2882	GTCTTTTTCATCAGACATCAGAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT	2823						
QY	323	TGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGGTGAAGATATGACATTATT	382						
DB	2822	TGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGGTGAAGATATGACATTATT	2763						
QY	383	TTAACTTGAAGAGCCTTTCAGAGAACCTTGTCTGTGGAGGAAGGACCACACCATCAC	442						
DB	2762	TTAACTTGAAGAGCCTTTCAGAGAACCTTGTCTGTGGAGGAAGGACCACACCATCAC	2703						
QY	443	GGGTGGAGCAGCTGACCCCTGAATGGCTCCTGCAGGCTCTTCAGAGCCCTGCATCAT	502						
DB	2702	GGGTGGAGCAGCTGACCCCTGAATGGCTCCTGCAGGCTCTTCAGAGCCCTGCATCAT	2643						
QY	503	AAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGCGCATTTGCCATGCTCTGGGG	562						
DB	2642	AAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAGCGCATTTGCCATGCTCTGGGG	2583						
QY	563	CGGGAAGTGCRAAGGCTCTGACCAAGTTCAAATTCGTCTTTCCTCCCTCAGCAGGG	622						
DB	2582	CGGGAAGTGCRAAGGCTCTGACCAAGTTCAAATTCGTCTTTCCTCCCTCAGCAGGG	2523						
QY	623	CCAGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGATATACCTGGCACAATCA	682						
DB	2522	CCAGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGATATACCTGGCACAATCA	2463						
QY	683	GGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGCGCAGAGGGTCTTTTCTCTCT	742						
DB	2462	GGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGCGCAGAGGGTCTTTTCTCTCT	2403						
QY	743	ATGGCTTACAATGAATTCAGGCCCCAGAACTGCCAGAAATCGAAGCCCTGATAAGGAAA	802						
DB	2402	ATGGCTTACAATGAATTCAGGCCCCAGAACTGCCAGAAATCGAAGCCCTGATAAGGAAA	2343						
QY	803	ACCACCGCTTCAGACATGGTCACTGTCACCACTACCACTGAGTCCCTGAGGCACATAC	862						
DB	2342	ACCACCGCTTCAGACATGGTCACTGTCACCACTACCACTGAGTCCCTGAGGCACATAC	2283						
QY	863	GGCAGTTTGGTGCCTTGAAGTGGGATATGACAGAAAGACGCGCCAGGCTC	922						
DB	2282	GGCAGTTTGGTGCCTTGAAGTGGGATATGACAGAAAGACGCGCCAGGCTC	2223						
QY	923	TCATCCGAGAAGTGTGATCAAGAGGCTTGTCTGAAGGCTTGTGTCTCCAAATTCAGAA	982						
DB	2222	TCATCCGAGAAGTGTGATCAAGAGGCTTGTCTGAAGGCTTGTGTCTCCAAATTCAGAA	2163						
QY	983	CCAGGTGCTTGAAGATCTCATGAAGACCCCTCTCTTGTGTGTCATCATCTGTGCAATCC	1042						
DB	2162	CCAGGTGCTTGAAGATCTCATGAAGACCCCTCTCTTGTGTGTCATCATCTGTGCAATCC	2103						
QY	1043	AGATGGGTGAAAGTGTGATCTCTCACACAAACACGCTGTTCACATACCTTCTATG	1102						
DB	2102	AGATGGGTGAAAGTGTGATCTCTCACACAAACACGCTGTTCACATACCTTCTATG	2043						
QY	1103	ATCTGTTGATACAGAAAAACAAACACATAAAGGCTGTGGCTGCAAGTGACTTTCATTC	1162						
DB	2042	ATCTGTTGATACAGAAAAACAAACACATAAAGGCTGTGGCTGCAAGTGACTTTCATTC	1983						
QY	1163	GGAGCCTGGACCACTGTGGAGACCTAGCTCTCGAGGGTGTGTCTCCCAAGTTTGATT	1222						
DB	1982	GGAGCCTGGACCACTGTGGAGACCTAGCTCTCGAGGGTGTGTCTCCCAAGTTTGATT	1923						

QY	1223	TCGAACTGCAGGATGTGTCAGCGTGAATGAGGATCTCTGCTGCAACACTGGGCTCTCT	1282						
DB	1922	TCGAACTGCAGGATGTGTCAGCGTGAATGAGGATCTCTGCTGCAACACTGGGCTCTCT	1863						
QY	1283	GTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAATTTCTTTCACAAAGTCAATCC	1342						
DB	1862	GTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAATTTCTTTCACAAAGTCAATCC	1803						
QY	1343	ACTACACACGAGGACGAACTCAGCAGTTTATTTGACGCTCTCATGAGCCAGAGGAGTGA	1402						
DB	1802	ACTACACACGAGGACGAACTCAGCAGTTTATTTGACGCTCTCATGAGCCAGAGGAGTGA	1743						
QY	1403	CCAAGGGGAATGGTTACTTTCGAGAAATGGTTTCCATTTTCGGACATTTACATCCAC	1462						
DB	1742	CCAAGGGGAATGGTTACTTTCGAGAAATGGTTTCCATTTTCGGACATTTACATCCAC	1683						
QY	1463	GCAGCCTGCTCGGTTACACCTGTGGGTCACTGTGTGAAGCCACCAGGCTGTATGAAGC	1522						
DB	1682	GCAGCCTGCTCGGTTACACCTGTGGGTCACTGTGTGAAGCCACCAGGCTGTATGAAGC	1623						
QY	1523	ACCTCGACAGTGTATCAACACGCGTCTCTCGGACTTTCCATCGCAAGAGGCCCTC	1582						
DB	1622	ACCTCGACAGTGTATCAACACGCGTCTCTCGGACTTTCCATCGCAAGAGGCCCTC	1563						
QY	1583	TCTGGAGACAGGAATCTTTTGCRAAGTGTGAAAAACACCCTGAGCAAGAAATTTCTG	1642						
DB	1562	TCTGGAGACAGGAATCTTTTGCRAAGTGTGAAAAACACCCTGAGCAAGAAATTTCTG	1503						
QY	1643	CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACAT	1702						
DB	1502	CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACAT	1443						
QY	1703	AATCAGCCCTGAGCCCAAGAAATTTTGAAGCTTTCTTTCAAGGTAAAGCTTATATAT	1762						
DB	1442	AATCAGCCCTGAGCCCAAGAAATTTTGAAGCTTTCTTTCAAGGTAAAGCTTATATAT	1383						
QY	1763	CAGGGAACATCCCCGATTACTTATTTGACTTCTTTGAACATTTTGCCTTGTGCAAG	1822						
DB	1382	CAGGGAACATCCCCGATTACTTATTTGACTTCTTTGAACATTTTGCCTTGTGCAAG	1323						
QY	1823	CTCTGAGCTTCAATTAACCTGGACTTTTATGGGGAGCTATGGCTTATGGGAAAAG	1882						
DB	1322	CTCTGAGCTTCAATTAACCTGGACTTTTATGGGGAGCTATGGCTTATGGGAAAAG	1363						
QY	1883	CAGAGACACAGTGGAAATCCACATGGAAGGCCCCAGAAACCTACATTTCCAGCAG	1942						
DB	1262	CAGAGACACAGTGGAAATCCACATGGAAGGCCCCAGAAACCTACATTTCCAGCAG	1203						
QY	1943	CTGTATCTTTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGTGGAGTCAACACT	2002						
DB	1202	CTGTATCTTTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGTGGAGTCAACACT	1143						
QY	2003	ATTTACAGAGTGAATAAGCAAGATATACATATCTGGGGAAAATATTTCAGCTCTG	2062						
DB	1142	ATTTACAGAGTGAATAAGCAAGATATACATATCTGGGGAAAATATTTCAGCTCTG	1083						
QY	2063	CAAGCCTCAGGCTGCAAAATAAGAGATGTCTGCTGCTGGAGCCCTCAGTTTGGT	2122						
DB	1082	CAAGCCTCAGGCTGCAAAATAAGAGATGTCTGCTGCTGGAGCCCTCAGTTTGGT	1023						
QY	2123	TCAGCACCTGTGAACATTTTCTCTCATGTGTGAAGCCAGTCCCTCCACCATAGA	2182						
DB	1022	TCAGCACCTGTGAACATTTTCTCTCATGTGTGAAGCCAGTCCCTCCACCATAGA	963						
QY	2183	ATGAGAGGCACATCACATCTGTAAACAACTGAAAACCTTGAGTATTATGACCTACA	2242						
DB	962	ATGAGAGGCACATCACATCTGTAAACAACTGAAAACCTTGAGTATTATGACCTACA	903						
QY	2243	ATCAACGGCTGCCGGTGGTCTGACTGACAGCTTGGGTGACTTTGAAGACCTTACA	2302						
DB	902	ATCAACGGCTGCCGGTGGTCTGACTGACAGCTTGGGTGACTTTGAAGACCTTACA	843						

QY 1081 AGCGTGTTCATACCTTCTATGATCTGTGTGATACAGAAAAACAAACATATAAGGT 1140
Db 4777 AGCGTGTTCATACCTTCTATGATCTGTGTGATACAGAAAAACAAACATATAAGGT 4836
QY 1141 GTGGCTGCAAGTGAAGTCTATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGT 1200
Db 4837 GTGGCTGCAAGTGAAGTCTATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGT 4896
QY 1201 GTGTTCTCCACAAAGTTGATTTGAACTGCAAGGATGTCTCCAGGCTGAATGAGGATGTC 1260
Db 4897 GTGTTCTCCACAAAGTTGATTTGAACTGCAAGGATGTCTCCAGGCTGAATGAGGATGTC 4956
QY 1261 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTCAAGCCAAAGTATAAA 1320
Db 4957 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTCAAGCCAAAGTATAAA 5016
QY 1321 TTCTTTTCAAAAGTCTATTCAGAGGTACACAGCAGGACGAAAGACTCAGCAGTTTATTGAGC 1380
Db 5017 TTCTTTTCAAAAGTCTATTCAGAGGTACACAGCAGGACGAAAGACTCAGCAGTTTATTGAGC 5076
QY 1381 TCTCATGAGCCAGAGGAGGTGACCAAGGGAATGGTTACTTGCAGAAAATGTTTCCATT 1440
Db 5077 TCTCATGAGCCAGAGGAGGTGACCAAGGGAATGGTTACTTGCAGAAAATGTTTCCATT 5136
QY 1441 TCGGACATTACATCCACTTATAGAGCCTGTCTCCGATACACCTGTGGGTCTATCTGTGAA 1500
Db 5137 TCGGACATTACATCCACTTATAGAGCCTGTCTCCGATACACCTGTGGGTCTATCTGTGAA 5196
QY 1501 GCCACAGGCTGTATGAAGCACTCGCAGCAGTGTATCAACACAGGCTGCTTCTCGGA 1560
Db 5197 GCCACAGGCTGTATGAAGCACTCGCAGCAGTGTATCAACACAGGCTGCTTCTCGGA 5256
QY 1561 CTTTCCATCGCAAGAGGCTCTCTGGAGACAGGAATCTTCAAGTGTGAAAACACC 1620
Db 5257 CTTTCCATCGCAAGAGGCTCTCTGGAGACAGGAATCTTCAAGTGTGAAAACACC 5316
QY 1621 ACTGAGCAAGAAATCTGAAAGCCATAACATCAATCTCTGTAGAGTGTGGCATCCAT 1680
Db 5317 ACTGAGCAAGAAATCTGAAAGCCATAACATCAATCTCTGTAGAGTGTGGCATCCAT 5376
QY 1681 TTATATCAAGAGGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAA 1740
Db 5377 TTATATCAAGAGGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTCAA 5436
QY 1741 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATTACTTATTTGACATCTTTGAA 1800
Db 5437 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATTACTTATTTGACATCTTTGAA 5496
QY 1801 CATTTGCCCAATGTGCAAGTCTCTGGACTTCAATTAAGTGGAGCTTTTATGGGGAGCT 1860
Db 5497 CATTTGCCCAATGTGCAAGTCTCTGGACTTCAATTAAGTGGAGCTTTTATGGGGAGCT 5556
QY 1861 ATGGCTTCATGGGAAAGGCTCGAAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1920
Db 5557 ATGGCTTCATGGGAAAGGCTCGAAGACACAGGTGGAATCCACATGGAAGAGGCCCA 5616
QY 1921 GAAACCTACATTCACAGAGGCTGTATCTTTGTTCTCACTGGAAGCAGGAATTCAGG 1980
Db 5617 GAAACCTACATTCACAGAGGCTGTATCTTTGTTCTCACTGGAAGCAGGAATTCAGG 5676
QY 1981 ACTCTGGAGGTACACACTCCGGGATTTCAAGAAAGTTGAATAAGCAAGATATCATATCTG 2040
Db 5677 ACTCTGGAGGTACACACTCCGGGATTTCAAGAAAGTTGAATAAGCAAGATATCATATCTG 5736
QY 2041 GGGAAATATTAGCTTCCCAAGAGCTCAGGCTGCAAAATTAAGAGATGTCTGGTGG 2100
Db 5737 GGGAAATATTAGCTTCCCAAGAGCTCAGGCTGCAAAATTAAGAGATGTCTGGTGG 5796
QY 2101 GCTGGAAGCTCAGTTTGTGCTCAGCAGCCTGTAAGAACATTTATCTCTCATGTGGAA 2160
Db 5797 GCTGGAAGCTCAGTTTGTGCTCAGCAGCCTGTAAGAACATTTATCTCTCATGTGGAA 5856
QY 2161 GCCAGTCCCTCACCATAGAGATGAGAGGCACATCATCTGTAAACAAACCTGAAAACC 2220

Db 5857 GCAGTCCCTCACCATAGAGATGAGAGGCACATCAGATCTGTACAAAACCTGAAAACC 5916
QY 2221 TTGAGTATTATGAGCTACAGAAATCAACGGCTGCCGGGT 2259
Db 5917 TTGAGTATTATGAGCTACAGAAATCAACGGCTGCCGGGT 5955
RESULT 27
US-09-557-676-917
; Sequence 917, Application US/09557676
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith
; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-136
; CURRENT APPLICATION NUMBER: US/09/557,676
; CURRENT FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 986
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 917
; LENGTH: 6012
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-676-917
Query Match 71.9%; Score 2208; DB 22; Length 6012;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2258; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAATTTCTATAAAGGACAATAGCCGAGCCCTTATTCAAAGAAATGGAAATGACTGTATA 60
Db 3697 ATGAATTTCTATAAAGGACAATAGCCGAGCCCTTATTCAAAGAAATGGAAATGACTGTATA 3756
QY 61 AAGCAAAATCAGAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGATTAACATC 120
Db 3757 AAGCAAAATCAGAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGATTAACATC 3816
QY 121 ATTTCGCTGGGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 180
Db 3817 ATTTCGCTGGGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 3876
QY 181 AAGGTTTCAGAGTCTCTGTAACCTCTTTCTTAATCCCTTTAAGAGTGGAACTATCCTCTA 240
Db 3877 AAGGTTTCAGAGTCTCTGTAACCTCTTTCTTAATCCCTTTAAGAGTGGAACTATCCTCTA 3936
QY 241 TTTCAGGACTTCAATGGCAAAAGTCTTTTTCATCAGACATCAGAAAGACACTTGGACAT 300
Db 3937 TTTCAGGACTTCAATGGCAAAAGTCTTTTTCATCAGACATCAGAAAGACACTTGGACAT 3996
QY 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACCTTTTATCCCTT 360
Db 3997 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACCTTTTATCCCTT 4056
QY 361 GGTGAAGATATTGACATTTATTTTAACTTGAAGCAACCTTCACAGAACTGTCTGTGG 420
Db 4057 GGTGAAGATATTGACATTTATTTTAACTTGAAGCAACCTTCACAGAACTGTCTGTGG 4116
QY 421 AGGAAGGACCAACACATCACCCTGGAGCAGCTGACCCCTGAATGGCCCTCTGCAAGCT 480
Db 4117 AGGAAGGACCAACACATCACCCTGGAGCAGCTGACCCCTGAATGGCCCTCTGCAAGCT 4176
QY 481 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGCAAGGCAAGTCCACTCTGCTGCAG 540
Db 4177 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGCAAGGCAAGTCCACTCTGCTGCAG 4236
QY 541 CGCATTTGCATCTCTGGGGCTCCGAAAGTGAAGGCTCTGACCAAGTCAAAATTCGTC 600
Db 4237 CGCATTTGCATCTCTGGGGCTCCGAAAGTGAAGGCTCTGACCAAGTCAAAATTCGTC 4296
QY 601 TTCCTTCCTCCGCTCAGCAGGCGCCAGGCTGAGCTTTTGAACCCCTCTGTGATCAACTC 660
Db 4297 TTCCTTCCTCCGCTCAGCAGGCGCCAGGCTGAGCTTTTGAACCCCTCTGTGATCAACTC 4356


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Qy 661 CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGG 720
Dy 4357 CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGG 4416
Qy 721 CAGAGGGTCTCTTTTCTCTTGTATGGGTACAAATGAATCAAGCCGCCAGAACTGCCCGGAA 780
Dy 4417 CAGAGGGTCTCTTTTCTCTTGTATGGGTACAAATGAATCAAGCCGCCAGAACTGCCCGGAA 4476
Qy 781 ATCAAGCCCTGATATAAGGAAGAACCCAGCGTTCAAGAACATGGTCACTGCTCAACCACTACC 840
Dy 4477 ATCAAGCCCTGATATAAGGAAGAACCCAGCGTTCAAGAACATGGTCACTGCTCAACCACTACC 4536
Qy 841 ACTGAGTGCCTGAGGCACATACGCACTTTGGTGGCTGCTGCTGAGGTGGGGGATG 900
Dy 4537 ACTGAGTGCCTGAGGCACATACGCACTTTGGTGGCTGCTGCTGAGGTGGGGGATG 4596
Qy 901 ACAGAAGACAGCCGCCAGGCTCTCATCCGAGAGTGTGTATCAAGGAGCTGCTGAGAGC 960
Dy 4597 ACAGAAGACAGCCGCCAGGCTCTCATCCGAGAGTGTGTATCAAGGAGCTGCTGAGAGC 4656
Qy 961 TTGTTGCTCCAAATTCAGAAATCAGAGTGTGTAGGAATTCATAGAACCCCTCTCTTT 1020
Dy 4657 TTGTTGCTCCAAATTCAGAAATCAGAGTGTGTAGGAATTCATAGAACCCCTCTCTTT 4716
Qy 1021 GTGTCATACCTGTGCAATCCAGATGGGTGAAAGTGTGAGTGTGCTGCTGAGAACCA 1080
Dy 4717 GTGTCATACCTGTGCAATCCAGATGGGTGAAAGTGTGAGTGTGCTGAGAACCA 4776
Qy 1081 ACCTGTGTCATACCTGTGATATCTGTGTATACAGAAAAACAAACAAATAAAGGT 1140
Dy 4777 ACCTGTGTCATACCTGTGATATCTGTGTATACAGAAAAACAAACAAATAAAGGT 4836
Qy 1141 GTGCTGCAAGTGTCTCATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGT 1200
Dy 4837 GTGCTGCAAGTGTCTCATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGT 4896
Qy 1201 GTGTTCTCCCAACAAGTTGATTTCCGAATCGAGGATGTCTCCAGCGTGAATGAGGATGC 1260
Dy 4897 GTGTTCTCCCAACAAGTTGATTTCCGAATCGAGGATGTCTCCAGCGTGAATGAGGATGC 4956
Qy 1261 CTGCTGCAACTGGCTCCTCTGTAATATACAGCTCAAGAGTTCAAGCCAAAGTATAAA 1320
Dy 4957 CTGCTGCAACTGGCTCCTCTGTAATATACAGCTCAAGAGTTCAAGCCAAAGTATAAA 5016
Qy 1321 TTCCTTCACAGTCAATCCAGGATACACAGCAGAGAGACATCAGCACTTATTCAGC 1380
Dy 5017 TTCCTTCACAGTCAATCCAGGATACACAGCAGAGAGACATCAGCACTTATTCAGC 5076
Qy 1381 TCTCATGAGCAGAGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAAATGGTTTCCATT 1440
Dy 5077 TCTCATGAGCAGAGAGGTGACCAAGGGGAATGGTTACTTGCAGAAAAATGGTTTCCATT 5136
Qy 1441 TCGGACATTAATCCACTTATPAGCAGCCTGCTCGGTACACCTGTGGGTCACTCTGGAA 1500
Dy 5137 TCGGACATTAATCCACTTATPAGCAGCCTGCTCGGTACACCTGTGGGTCACTCTGGAA 5196
Qy 1501 GCCACAGGGCTGTATGAAGCAGCTCGCAGCAGTGTATCAACAGCGCTGCTTCTCGGA 1560
Dy 5197 GCCACAGGGCTGTATGAAGCAGCTCGCAGCAGTGTATCAACAGCGCTGCTTCTCGGA 5256
Qy 1561 CTTTTCATTCGCAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1620
Dy 5257 CTTTTCATTCGCAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 5316
Qy 1621 ACTGAGCAAGAAATCTGAAGCCATTAACATCAATTCCTTGTGAGTGTGGCATCCAT 1680
Dy 5317 ACTGAGCAAGAAATCTGAAGCCATTAACATCAATTCCTTGTGAGTGTGGCATCCAT 5376
Qy 1681 TTATATCAAGAGTACATCAATCAAGCCCTGAGCCAGAAATTTGAAGCTTCTTTCAA 1740
Dy 5377 TTATATCAAGAGTACATCAATCAAGCCCTGAGCCAGAAATTTGAAGCTTCTTTCAA 5436
Qy 1741 GGTAAAAGCTTATATATCAACTCAGGGAACATCCCGGATTACTTATTTGACTTCTTTGAA 1800
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Dy 5437 GGTAAAGCTTATATATCAACTCAGGGAACATCCCGGATTACTTATTTGACTTCTTTGAA 5496
Qy 1801 CATTTTCCCAATTCGCAAGTGTCTCTGAGCTTCAATTAACCTGGAGCTTTTATGGGGAGCT 1860
Dy 5497 CATTTTCCCAATTCGCAAGTGTCTCTGAGCTTCAATTAACCTGGAGCTTTTATGGGGAGCT 5556
Qy 1861 ATGGCCTCATGGGAAAAGGCTGCAAGAGACACAGGTGGAATCCACATGGGAAGAGGCCCA 1920
Dy 5557 ATGGCCTCATGGGAAAAGGCTGCAAGAGACACAGGTGGAATCCACATGGGAAGAGGCCCA 5616
Qy 1921 GAAACCTACATTCACAGCAGGCTGTATCTTGTCTTCACTGGAAGCAGGAATTCAGG 1980
Dy 5617 GAAACCTACATTCACAGCAGGCTGTATCTTGTCTTCACTGGAAGCAGGAATTCAGG 5676
Qy 1981 ACTCTGAGGTCACTCTCGGGATTTTCAGCAAGTTGTAATAGCAAGATATACATATCTG 2040
Dy 5677 ACTCTGAGGTCACTCTCGGGATTTTCAGCAAGTTGTAATAGCAAGATATACATATCTG 5736
Qy 2041 GGAAPATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAAATAAAGAGATGTCTGGGTG 2100
Dy 5737 GGAAPATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAAATAAAGAGATGTCTGGGTG 5796
Qy 2101 GCTGGAAGCCTCAGTTTGTCTCTCAGCACCTGTGAAGAACATTTATCTCTCATGTTGAA 2160
Dy 5797 GCTGGAAGCCTCAGTTTGTCTCTCAGCACCTGTGAAGAACATTTATCTCTCATGTTGAA 5856
Qy 2161 GCCAGTCCCTCAACATAGAGATGAGAGCAGACATCATCTGTAAACAAACCTGAAAAAC 2220
Dy 5857 GCCAGTCCCTCAACATAGAGATGAGAGCAGACATCATCTGTAAACAAACCTGAAAAAC 5916
Qy 2221 TTGAGTATTATGACCTTACAGAAATCAACGGCTGCCGGT 2259
Dy 5917 TTGAGTATTATGACCTTACAGAAATCAACGGCTGCCGGT 5955

RESULT 28
US-10-042-938-91
: Sequence 911, application US/10042938
: GENERAL INFORMATION:
: APPLICANT: Rohison, Keith
: TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs
: FILE REFERENCE: 5800-136
: CURRENT APPLICATION NUMBER: US/10/042,938
: CURRENT FILING DATE: 2002-01-09
: PRIOR APPLICATION NUMBER: 09/557,676
: PRIOR FILING DATE: 2000-APR-25
: NUMBER OF SEQ ID NOS: 986
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 911
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-042-938-911

Query Match 71.9%; Score 2208; DB 38; Length 6012;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2258; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAATTCATAAAGGACAATAGCCGAGCCCTTATTCAAAAGATGGGAATGACTGTTATA 60
Dy 3697 ATGAATTCATAAAGGACAATAGCCGAGCCCTTATTCAAAAGATGGGAATGACTGTTATA 3756
Qy 61 AACCAAAACACAGATGACCTATTGTATGGAATGCTCTGATCGCGAGAGTAACATC 120
Dy 3757 AACCAAAACACAGATGACCTATTGTATGGAATGCTCTGATCGCGAGAGTAACATC 3816
Qy 121 ATTTGCTTCGAGAGAGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGA 180
Dy 3817 ATTTGCTTCGAGAGAGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGA 3876
Qy 181 AAGGGTTAGAGTCTCTAAACCTCTTTCTTAAATCCCTTAAAGGAGTGAACATCTCTCTA 240
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Db 3877 AAGGGTTCAGAGTCCCTGTAACCTCTTTCTTAATCCCTTAAGGAGTGGAACTATCCTCTA 3936
Qy 241 TTTCAGGACTCAATGGACAAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGACGAT 300
Db 3937 TTTCAGGACTCAATGGACAAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGACGAT 3996
Qy 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTTT 360
Db 3997 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCTTT 4056
Qy 361 GGTGAAGATATTCAGATATTTTAACTTGAAGACCTTCCACAGAACCTTCTCTGTGG 420
Db 4057 GGTGAAGATATTCAGATATTTTAACTTGAAGACCTTCCACAGAACCTTCTCTGTGG 4116
Qy 421 AGGAAGGACCAACACATCACCCTGGGAGCAGCTGACCCTGAATGGCTCTCTGAGGCT 480
Db 4117 AGGAAGGACCAACACATCACCCTGGGAGCAGCTGACCCTGAATGGCTCTCTGAGGCT 4176
Qy 481 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGTGCGAG 540
Db 4177 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGTGCGAG 4236
Qy 541 CGCATTTGCCATCTCTGGGGCTCCGGAAGTGCAGAGCTCTGACCAAGTTCAAAATTCGTC 600
Db 4237 CGCATTTGCCATCTCTGGGGCTCCGGAAGTGCAGAGCTCTGACCAAGTTCAAAATTCGTC 4296
Qy 601 TTCTTCTCCCTCTCAGCAGGGCCAGGGTGGAGCTTTTGAACCCCTCTGTGATCAACTC 660
Db 4297 TTCTTCTCCCTCTCAGCAGGGCCAGGGTGGAGCTTTTGAACCCCTCTGTGATCAACTC 4356
Qy 661 CTGGATATACCTGGCACATCAGGAAGCAGACATTCATGGCCATCTGCTGAAGCTGGG 720
Db 4357 CTGGATATACCTGGCACATCAGGAAGCAGACATTCATGGCCATCTGCTGAAGCTGGG 4416
Qy 721 CAGAGGTTCTTTTCTTCTTCTGATGGCTACAAATGAATCAAGCCCGAGAACTGCCAGAA 780
Db 4417 CAGAGGTTCTTTTCTTCTTCTGATGGCTACAAATGAATCAAGCCCGAGAACTGCCAGAA 4476
Qy 781 ATCGAAGCCCTCATGAAGAAACACCGCTTCAAGAACATGGTATCGTCAACCTACC 840
Db 4477 ATCGAAGCCCTCATGAAGAAACACCGCTTCAAGAACATGGTATCGTCAACCTACC 4536
Qy 841 ACTGAGTGCTCAGGCACATCAGGCAGATTTGGTGCCCTGACTGCTGAGGTGGGGATATG 900
Db 4537 ACTGAGTGCTCAGGCACATCAGGCAGATTTGGTGCCCTGACTGCTGAGGTGGGGATATG 4596
Qy 901 ACAGAAACAGCCCGCAGGCTCTATCCGAGAAAGTGTGATCAAGAGGTTGCTGAAGGC 960
Db 4597 ACAGAAACAGCCCGCAGGCTCTATCCGAGAAAGTGTGATCAAGAGGTTGCTGAAGGC 4656
Qy 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGCCCTCTCTTT 1020
Db 4657 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGCCCTCTCTTT 4716
Qy 1021 GTGGTCATCAGTGTGCAATCCAGATGGGTGAAAGTGTGAGTTCCTCTCACACAAACA 1080
Db 4717 GTGGTCATCAGTGTGCAATCCAGATGGGTGAAAGTGTGAGTTCCTCTCACACAAACA 4776
Qy 1081 AGCTGTGCCATACCTTCTATGATCTGTGATACAGAAACAAACACAAACATAAAGT 1140
Db 4777 AGCTGTGCCATACCTTCTATGATCTGTGATACAGAAACAAACACAAACATAAAGT 4836
Qy 1141 GTGGTCGAGGTGACTTCAATCCGAGCCTGGACCTGAGGACCTAGCTCTGGAGGT 1200
Db 4837 GTGGTCGAGGTGACTTCAATCCGAGCCTGGACCTGAGGACCTAGCTCTGGAGGT 4896
Qy 1201 GTGTTCTCCCAAGTTTGAATTCGAACCTGCAAGGATGTCTCCAGCGTGAATGAGGATGTC 1260
Db 4897 GTGTTCTCCCAAGTTTGAATTCGAACCTGCAAGGATGTCTCCAGCGTGAATGAGGATGTC 4956
Qy 1261 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAGTTCAAAGCCAAAGTATAA 1320
Db 4957 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAGTTCAAAGCCAAAGTATAA 5016

Qy 1321 TTCTTTCAAGTCAATCCAGGAGTACACAGCAGGACGAAGACTCAGCAGTTTATTGAGC 1380
Db 5017 TTCTTTCAAGTCAATCCAGGAGTACACAGCAGGACGAAGACTCAGCAGTTTATTGAGC 5076
Qy 1381 TCTCATGAGCCACAGAGGAGTGAACCAAGGGAATGTTACTTCAGAAAAATGTTTCCATT 1440
Db 5077 TCTCATGAGCCACAGAGGAGTGAACCAAGGGAATGTTACTTCAGAAAAATGTTTCCATT 5136
Qy 1441 TCGGACATTTACATCCATTTATAGCAGCCTGCTCCGGTACACCTGTGGGTCTCTGTGGAA 1500
Db 5137 TCGGACATTTACATCCATTTATAGCAGCCTGCTCCGGTACACCTGTGGGTCTCTGTGGAA 5196
Qy 1501 GCCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACAGGGCTGCTCTCGGA 1560
Db 5197 GCCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACAGGGCTGCTCTCGGA 5256
Qy 1561 CTTTCCATCGCCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1620
Db 5257 CTTTCCATCGCCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 5316
Qy 1621 ACTGAGCAAGAAATTTCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680
Db 5317 ACTGAGCAAGAAATTTCTGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 5376
Qy 1681 TTATATCAAGAGTACATCCAAATCAGCCCTGAGCCAGGAATTTCAAGCTTTCTTTCAA 1740
Db 5377 TTATATCAAGAGTACATCCAAATCAGCCCTGAGCCAGGAATTTGAAGCTTTCTTTCAA 5436
Qy 1741 GGTAAAGCTTATATCAACTCAGGAAACATCCCGGATTACTTATTTGACTTTCTTTGAA 1800
Db 5437 GGTAAAGCTTATATCAACTCAGGAAACATCCCGGATTACTTATTTGACTTTCTTTGAA 5496
Qy 1801 CATTTGCCCAATTTGCAAGTCTCTGGACTTCAATTAACACTGGACTTTTATGGGGAGCT 1860
Db 5497 CATTTGCCCAATTTGCAAGTCTCTGGACTTCAATTAACACTGGACTTTTATGGGGAGCT 5556
Qy 1861 ATGGCTTTCATGGAAGAGGCTGCAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1920
Db 5557 ATGGCTTTCATGGAAGAGGCTGCAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCA 5616
Qy 1921 GAAACTCATTTCCAGCAGGCTGTATCTTTTCTTCAACTGGAAGCAGGAATTCAGG 1980
Db 5617 GAAACTCATTTCCAGCAGGCTGTATCTTTTCTTCAACTGGAAGCAGGAATTCAGG 5676
Qy 1981 ACTCTGGAGGTCACTCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCAGATATCTG 2040
Db 5677 ACTCTGGAGGTCACTCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCAGATATCTG 5736
Qy 2041 GGGAAATATTCAGCTCTGCCACAAGCTTCAGGCTGCAAAATAAGAGATGTCTGGTGTG 2100
Db 5737 GGGAAATATTCAGCTCTGCCACAAGCTTCAGGCTGCAAAATAAGAGATGTCTGGTGTG 5796
Qy 2101 GCTGGAAGCCTCAGTTTGGTCTCAGCAGCCTGTAAGAATTTATTTCTCTATGTTGGAA 2160
Db 5797 GCTGGAAGCCTCAGTTTGGTCTCAGCAGCCTGTAAGAATTTATTTCTCTATGTTGGAA 5856
Qy 2161 GCCAGTCCCTCACCATAGAAGATGAGAGGCACATCAGATCTGTAACAACCTGAAAAAC 2220
Db 5857 GCCAGTCCCTCACCATAGAAGATGAGAGGCACATCAGATCTGTAACAACCTGAAAAAC 5916
Qy 2221 TTGAGTATTCATGACCTACAGAAATCAACGGCTGCCGGT 2259
Db 5917 TTGAGTATTCATGACCTACAGAAATCAACGGCTGCCGGT 5955

RESULT 29
US-10-042-938-917
; Sequence 917, Application US/10042938
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith
; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-136

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; CURRENT APPLICATION NUMBER: US/10/042,938
; CURRENT FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: 09/557,676
; PRIOR FILING DATE: 2000-APR-25
; NUMBER OF SEQ ID NOS: 986
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 917
; LENGTH: 6012
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-042-938-917

Query Match          71.9%; Score 2208; DB 38; Length 6012;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2258; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGACATAGCCGAGCCCTTATTCAAAAGATGGGAATGACTGTTATA 60
DB 3697 ATGAATTTTCATAAAGGACATAGCCGAGCCCTTATTCAAAAGATGGGAATGACTGTTATA 3756

QY 61 AAGCAAAATCAGATGACCTATTTGTATGGAATGTTCTGAATCGCGAAGATAAACATC 120
DB 3757 AAGCAAAATCAGATGACCTATTTGTATGGAATGTTCTGAATCGCGAAGATAAACATC 3816

QY 121 ATTTGCTGCGAAGAGTGGAGAGGATGCTGCTAGAGGGATCATTCACATGATTTTGA 180
DB 3817 ATTTGCTGCGAAGAGTGGAGAGGATGCTGCTAGAGGGATCATTCACATGATTTTGA 3876

QY 181 AAGGGTTTCAGAGTCCCTGTAACTCTTCTTTAAATPCCCTTAAAGGAGTGGAACTATCCCTA 240
DB 3877 AAGGGTTTCAGAGTCCCTGTAACTCTTCTTTAAATPCCCTTAAAGGAGTGGAACTATCCCTA 3936

QY 241 TTTTCAGGACTTGAATGACAAAGTCTTTTTCATCAGACATCAGAAGGAGACTTTGAGGAT 300
DB 3937 TTTTCAGGACTTGAATGACAAAGTCTTTTTCATCAGACATCAGAAGGAGACTTTGAGGAT 3996

QY 301 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACTTTTATCCCTT 360
DB 3997 TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTCTGAACTTTTATCCCTT 4056

QY 361 GGTCAAGATATGACATATTTTAACTTGAAGACCTTCACAGAACCTGCTCTGG 420
DB 4057 GGTCAAGATATGACATATTTTAACTTGAAGACCTTCACAGAACCTGCTCTGG 4116

QY 421 AGAAGACCAACACATACCCGCTGGAGCAGCTGACCTGAAATGGCTCTCTGAGGCT 480
DB 4117 AGAAGACCAACACATACCCGCTGGAGCAGCTGACCTGAAATGGCTCTCTGAGGCT 4176

QY 481 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAAGGCAAGTCCACTCTGCTCGAG 540
DB 4177 CTTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAAGGCAAGTCCACTCTGCTCGAG 4236

QY 541 CGCATTCGCCATGCTCTGGGCTCCGGAAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTC 600
DB 4237 CGCATTCGCCATGCTCTGGGCTCCGGAAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTC 4296

QY 601 TTCTTCCTCCGCTCTCAGCAGGGCCAGGGTGGACTTTTGAAGCCCTCTGTGATCAACTC 660
DB 4297 TTCTTCCTCCGCTCTCAGCAGGGCCAGGGTGGACTTTTGAAGCCCTCTGTGATCAACTC 4356

QY 661 CTGATATACCTGGCAACATCAGGAAGCAGACATTTACGTCATGCTGTAAGCTCGG 720
DB 4357 CTGATATACCTGGCAACATCAGGAAGCAGACATTTACGTCATGCTGTAAGCTCGG 4416

QY 721 CAGAGGCTCTTTTCCCTCTGTATGGCTACAATGAATCAAGCCCAAGACTGCCAGAA 780
DB 4417 CAGAGGCTCTTTTCCCTCTGTATGGCTACAATGAATCAAGCCCAAGACTGCCAGAA 4476

QY 781 ATCGAAGCCCTGTAAAGGAACACCGCTTCAAGAAATGTCATCGTCACACTACC 840
DB 4477 ATCGAAGCCCTGTAAAGGAACACCGCTTCAAGAAATGTCATCGTCACACTACC 4536

QY 841 ACTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATG 900
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||||| 4537 ACTGAGTGCCTGAGGCACATACCGCAGTTTGGTGCCCTGACTGCTGAGGTGGGGGATATG 4596
QY 901 ACAGAA:JACAGCGCCCGAGGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGTCTGAAGGC 960
DB 4597 ACAGAA:JACAGCGCCCGAGGCTCTCATCCGAGAAGTGTGTATCAAGGAGCTTGTCTGAAGGC 4656
QY 961 TTGTTG:TCCAAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020
DB 4657 TTGTTG:TCCAAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 4716
QY 1021 GTGCTC:ATCACTTGTGCAATCCAGATGGGTGAAGTGAAGTGTCCACTCTCACACACAACA 1080
DB 4717 GTGCTC:ATCACTTGTGCAATCCAGATGGGTGAAGTGAAGTGTCCACTCTCACACACAACA 4776
QY 1081 ACCTG:TTCCATACCTTCTATGATCTGTTGATACAGAAAAACAACAACAATAAAGGT 1140
DB 4777 ACCTG:TTCCATACCTTCTATGATCTGTTGATACAGAAAAACAACAACAATAAAGGT 4836
QY 1141 GTGCTC:CAAGTGACCTTCATTCGGAGCTCGACCACTGTGGAGACCTAGCTCTGGAGGT 1200
DB 4837 GTGCTC:CAAGTGACCTTCATTCGGAGCTCGACCACTGTGGAGACCTAGCTCTGGAGGT 4896
QY 1201 GTGCTC:CCACAAAGTTTGATTTGAACTCGAAGTGTGCCAGTGTCCAGCTGGAATGAGGATGTC 1260
DB 4897 GTGCTC:CCACAAAGTTTGATTTGAACTCGAAGTGTGCCAGTGTCCAGCTGGAATGAGGATGTC 4956
QY 1261 CTGCTG:CAACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTTCAAGCCAAAGTATATA 1320
DB 4957 CTGCTG:CAACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTTCAAGCCAAAGTATATA 5016
QY 1321 TTTCTTTCACAAGTCAATTCAGAGGAGTACACAGCAGGAGAACTCAGCAGTTTATTGACG 1380
DB 5017 TTTCTTTCACAAGTCAATTCAGAGGAGTACACAGCAGGAGAACTCAGCAGTTTATTGACG 5076
QY 1381 TCTCATCAGCCAGAGGAGTGACCAAGGGAATGGTTACTTGCAGAAAAATGGTTTCCATT 1440
DB 5077 TCTCATCAGCCAGAGGAGTGACCAAGGGAATGGTTACTTGCAGAAAAATGGTTTCCATT 5136
QY 1441 TCGGACA:TTACATCCACTTATAGCAGCTCTCCGGTACACCTCTGGTCTATCTGTGGAA 1500
DB 5137 TCGGACA:TTACATCCACTTATAGCAGCTCTCCGGTACACCTCTGGTCTATCTGTGGAA 5196
QY 1501 GCCACCA:GGCTGTTATGAAGACCTCGCAGCAGTGTATCAACAGGCTGCCCTCTCGGA 1560
DB 5197 GCCACCA:GGCTGTTATGAAGACCTCGCAGCAGTGTATCAACAGGCTGCCCTCTCGGA 5256
QY 1561 CTTTCCA:CGCCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACCC 1620
DB 5257 CTTTCCA:CGCCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACCC 5316
QY 1621 ACTGAGC:AGAAAATTCGTGAAGGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680
DB 5317 ACTGAGC:AGAAAATTCGTGAAGGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 5376
QY 1681 TTATATC:JAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAA 1740
DB 5377 TTATATC:JAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAA 5436
QY 1741 GGTAAAA:CTTATATATCAACTCAGGGAACATCCCGGATTTATTTGACTTCTTTGAA 1800
DB 5437 GGTAAAA:CTTATATATCAACTCAGGGAACATCCCGGATTTATTTGACTTCTTTGAA 5496
QY 1801 CATTTGC:CAATTTGCAAGTGTCTGGACTTCATTTAACTGGACTTTTATGGGGAGCT 1860
DB 5497 CATTTGC:CAATTTGCAAGTGTCTGGACTTCATTTAACTGGACTTTTATGGGGAGCT 5556
QY 1861 ATGGCTTC:ATGGGAAAAGGCTGCAGAAAGACACAGGTGGATCCACATGGGAAGAGGCCCA 1920
DB 5557 ATGGCTTC:ATGGGAAAAGGCTGCAGAAAGACACAGGTGGATCCACATGGGAAGAGGCCCA 5616
QY 1921 GAAACCTTA:CATTCGCCAGCAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGG 1980
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Db 5617 GAAACCTACATCCAGCAGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGG 5676
Qy 1981 ACTCTGGAGGTCACACTCGGGGATTTACAGAGTTTGAATAAGCAAGATATCATATCTG 2040
Db 5677 ACTCTGGAGGTCACACTCGGGGATTTACAGAGTTTGAATAAGCAAGATATCATATCTG 5736
Qy 2041 GGGAAATATTCAGCTCTGCCACAAAGCCTCAGGCTGCAAAATAAAGAGATGTCTGGTGTG 2100
Db 5737 GGGAAATATTCAGCTCTGCCACAAAGCCTCAGGCTGCAAAATAAAGAGATGTCTGGTGTG 5796
Qy 2101 GCTGGAAGCCTCAGTTTGTCTCAGCACCTCTAAGAACATTTATTTCTCTATGCTGGAA 2160
Db 5797 GCTGGAAGCCTCAGTTTGTCTCAGCACCTCTAAGAACATTTATTTCTCTATGCTGGAA 5856
Qy 2161 GCCAGTCCCTCACCATAGAGATGAGAGGCACATCATCTGTACAAACCTGAAACC 2220
Db 5857 GCCAGTCCCTCACCATAGAGATGAGAGGCACATCATCTGTACAAACCTGAAACC 5916
Qy 2221 TTGAGTATTCATGACCTACAGAAATCAAGGCTGCCGGGT 2259
Db 5917 TTGAGTATTCATGACCTACAGAAATCAAGGCTGCCGGGT 5955

RESULT 30

US-09-578-789-15
; Sequence 15, Application us/09578789
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Frederick Plo
; APPLICANT: Adam Godzik
; TITLE OF INVENTION: Novel Card Polypeptides
; FILE REFERENCE: P-LJ 4141
; CURRENT APPLICATION NUMBER: US/09/578,789
; CURRENT FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2343
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2340)
US-09-578-789-15

Query Match 71.8%; Score 2207; DB 22; Length 2343;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TGAATTTCAATAAGGACAAATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTATAA 61
Db 29 TGAATTTCAATAAGGACAAATAGCCGAGCCCTTATTCAAGAAATGGGAATGACTGTATAA 88
Qy 62 AGCAATCACAGATGACCTATTTGTATGAATGTTCTGAATCGCGAAGATTAACATCA 121
Db 89 AGCAATCACAGATGACCTATTTGTATGAATGTTCTGAATCGCGAAGATTAACATCA 148
Qy 122 TTTGCTGGAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAATA 181
Db 149 TTTGCTGGAGAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAATA 208
Qy 182 AGGGTTACAGTCTCTTAACCTCTTTCTAAATCCCTTAAGAGTGGAACTATCCTCTAT 241
Db 209 AGGGTTACAGTCTCTTAACCTCTTTCTAAATCCCTTAAGAGTGGAACTATCCTCTAT 268
Qy 242 TTCAGGACTTGAATGGACAAAGTCTTTTTCATFCAGACATCAGAAGGAGACTTTGGAGATT 301
Db 269 TTCAGGACTTGAATGGACAAAGTCTTTTTCATFCAGACATCAGAAGGAGACTTTGGAGATT 328
Qy 302 TGGCTCAGGATTTAAGGACTGTACCATACCCATCTTTCTGAACTTTTATCCCTTTG 361
Db 329 TGGCTCAGGATTTAAGGACTGTACCATACCCATCTTTCTGAACTTTTATCCCTTTG 388

Qy 362 GTGAAGATATTGACATATTATTTTAACTTGAAGACACCTTTCACAGAACTCTCTGTGTA 421
Db 369 GTGAAGATATTGACATATTATTTTAACTTGAAGACACCTTTCACAGAACTCTCTGTGTA 448
Qy 422 GGAAGGACCAACACCATCACCCGCTGGAGCAGCTGACCCCTGAATGGCCCTCTCTGAGGCTC 481
Db 449 GGAAGGACCAACACCATCACCCGCTGGAGCAGCTGACCCCTGAATGGCCCTCTCTGAGGCTC 508
Qy 482 TTCAGAGCCCTTGCATCATTTGAAGGGATCTGGCAAGGCAAGTCCACTCTCTGCTGACG 541
Db 509 TTCAGAGCCCTTGCATCATTTGAAGGGATCTGGCAAGGCAAGTCCACTCTCTGCTGACG 568
Qy 542 GCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGCTCTGACCAAGTTTCAAAATTCGTCT 601
Db 569 GCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGCTCTGACCAAGTTTCAAAATTCGTCT 628
Qy 602 TCTTCTCCGCTCTAGCAGGCCCCAGGGTGGACTTTTGAACCCCTCTGTGTATCAACTTCC 661
Db 629 TCTTCTCCGCTCTAGCAGGCCCCAGGGTGGACTTTTGAACCCCTCTGTGTATCAACTTCC 688
Qy 662 TGGATATACCTGGCACAAATCAGGAAGCAGACATTTATGGCCATGCTGTGAAGCTGCGGC 721
Db 689 TGGATATACCTGGCACAAATCAGGAAGCAGACATTTATGGCCATGCTGTGAAGCTGCGGC 748
Qy 722 AGAGGTTCTTTTCTTCTTGTATGCTACAATGAATTTCAAGCCCCAGAACTGCCCAGAAA 781
Db 749 AGAGGTTCTTTTCTTGTATGCTACAATGAATTTCAAGCCCCAGAACTGCCCAGAAA 808
Qy 782 TCGAAGCCCTGATAAAGGAAACACCCGCTTCAAGAACATGCTCATCTGCTACCACTATCA 841
Db 809 TCGAAGCCCTGATAAAGGAAACACCCGCTTCAAGAACATGCTCATCTGCTACCACTATCA 868
Qy 842 CTGAGTGGCTGAGGACATACCGGAGTTTGGTGCCTGACTGCTGAGTGGGGGATATGA 901
Db 869 CTGAGTGGCTGAGGACATACCGGAGTTTGGTGCCTGACTGCTGAGTGGGGGATATGA 928
Qy 902 CAGAAGACAGCCGCCAGGCTCTCATCCGAGAACTGCTGATCAAGAGCTTGTCTGAAGGCT 961
Db 929 CAGAAGACAGCCGCCAGGCTCTCATCCGAGAACTGCTGATCAAGAGCTTGTCTGAAGGCT 988
Qy 962 TGTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGAACTCATGAAGACCCCTCTCTTTTG 1021
Db 989 TGTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGAACTCATGAAGACCCCTCTCTTTTG 1048
Qy 1022 TGGTCACTACTTGTGCAATCCAGATGGGTGAAGTGAGTTCCACTCTCACACACAAACA 1081
Db 1049 TGGTCACTACTTGTGCAATCCAGATGGGTGAAGTGAGTTCCACTCTCACACACAAACA 1108
Qy 1082 CGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACAAACATAAGGTG 1141
Db 1109 CGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACAAACATAAGGTG 1168
Qy 1142 TGGCTGCAAGTCACTTTCATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGTG 1201
Db 1169 TGGCTGCAAGTCACTTTCATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGTG 1228
Qy 1202 TGGTCTCCCAAGTTTGTATTTTGAAGTGCAGAGTGTGTCAGCGTGAATGAGGATGTC 1261
Db 1229 TGGTCTCCCAAGTTTGTATTTTGAAGTGCAGAGTGTGTCAGCGTGAATGAGGATGTC 1288
Qy 1262 TGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATAAT 1321
Db 1289 TGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATAAT 1348
Qy 1322 TCTTTTCAAGTTCATTCAGGAGTACAGCAGGAGAGACTCAGAGCTTTTATGAGCT 1381
Db 1349 TCTTTTCAAGTTCATTCAGGAGTACAGCAGGAGAGACTCAGAGCTTTTATGAGCT 1408
Qy 1382 CTCATGAGCCAGAGGAGTACCAAGGGAAATGGTTACTTGCAGAAATGGTTTCCATTT 1441
Db 1409 CTCATGAGCCAGAGGAGTACCAAGGGAAATGGTTACTTGCAGAAATGGTTTCCATTT 1468
Qy 1442 CGGACATTATCCACTTATAGCAGCTCTCCGGTACACCTGTGGGTCTATCTGTGGAAG 1501

```
Db 1469 CGGACATTACATCCATATAGACGCTGCTCCGGTACACTGTGGGTCACTGTGGAAG 1528
Qy 1502 CCACAGGGCTGTATGAAGACCTCGCAGAGTGTATCAACAGCGTGCTTCTCGGAC 1561
Db 1529 CCACAGGGCTGTATGAAGACCTCGCAGAGTGTATCAACAGCGTGCTTCTCGGAC 1588
Qy 1562 TTTCCATCGCCAGAGGCTCTCTGAGACAGGAATCTTTGCAAGTGTGAAACACCA 1621
Db 1589 TTTCCATCGCCAGAGGCTCTCTGAGACAGGAATCTTTGCAAGTGTGAAACACCA 1648
Qy 1622 CTGAGCAAGAAATCTGAAGCCATAAATCAATCTCTTTGTAGAGTGTGGCATCAT 1681
Db 1649 CTGAGCAAGAAATCTGAAGCCATAAATCAATCTCTTTGTAGAGTGTGGCATCAT 1708
Qy 1682 TATATCAAGAGATACATCAAAATCAGCCTGAGCCAGATTTGAAGCTTCTTTCAAG 1741
Db 1709 TATATCAAGAGATACATCAAAATCAGCCTGAGCCAGATTTGAAGCTTCTTTCAAG 1768
Qy 1742 GTAAAGCTTATATCAACTCAGGGAACATCCCGATTTACTTATTTGACTTCTTTGAAC 1801
Db 1769 GTAAAGCTTATATCAACTCAGGGAACATCCCGATTTACTTATTTGACTTCTTTGAAC 1828
Qy 1802 ATTTGCCCAATTTGCAAGTCTCTGAGCTTCATTAAGTGGAGTCTTTATGGGGAGCTA 1861
Db 1829 ATTTGCCCAATTTGCAAGTCTCTGAGCTTCATTAAGTGGAGTCTTTATGGGGAGCTA 1888
Qy 1862 TGGCTTCATGGGAAAGGCTGCAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAG 1921
Db 1889 TGGCTTCATGGGAAAGGCTGCAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAG 1948
Qy 1922 AAACCTACATTCACAGGAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGA 1981
Db 1949 AAACCTACATTCACAGGAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGA 2008
Qy 1982 CTCTGGAGGTCACACTCCGGGATTTACAGCAAGTTGAAATAGCAGATATCACATATCTGG 2041
Db 2009 CTCTGGAGGTCACACTCCGGGATTTACAGCAAGTTGAAATAGCAGATATCACATATCTGG 2068
Qy 2042 GGAATATTCAGCTCTGCCACAGCCTCAGGCTGCAAAATAGAGATGTCTGTCTGG 2101
Db 2069 GGAATATTCAGCTCTGCCACAGCCTCAGGCTGCAAAATAGAGATGTCTGTCTGG 2128
Qy 2102 CTGGAAGCCTCAGTTGGTCTCAGACCTGTAGAACATTTATCTCTATGTTGGAAG 2161
Db 2129 CTGGAAGCCTCAGTTGGTCTCAGACCTGTAGAACATTTATCTCTATGTTGGAAG 2188
Qy 2162 CCAGTCCCTCACCATAGAGATGAGAGCAGCATCATCTGTAAACAACTGAAACCT 2221
Db 2189 CCAGTCCCTCACCATAGAGATGAGAGCAGCATCATCTGTAAACAACTGAAACCT 2248
Qy 2222 TGAGTATTCAGCTCAGAAATCAACGGCTGCGGGT 2259
Db 2249 TGAGTATTCAGCTCAGAAATCAACGGCTGCGGGT 2286

RESULT 31
US-09-579-240-15
; Sequence 15, Application US/09579240
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Frederick Pio
; APPLICANT: Adam Godzik
; TITLE OF INVENTION: Novel Card-Domain Containing
; FILE REFERENCE: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; CURRENT APPLICATION NUMBER: US/09/579,240
; CURRENT FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2343
; TYPE: DNA
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; ORGANISM: H. mo Sapien
; FEATURE:
; NAME/KEY: CUS
; LOCATION: ( : )...(2340)
US-09-579-240-15

Query Match 71.8%; Score 2207; DB 22; Length 2343;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAATTCATATAAGGACAATAGCGAGCCCTTATTCAAAAGATGGGAATGACTCTTTAA 61
Db 29 TGAATTCATATAAGGACAATAGCGAGCCCTTATTCAAAAGATGGGAATGACTCTTTAA 88
Qy 62 AGCAATPCACAGATGACTATTTCTATGGAATGTTCTGAATCGGAGAGTAACATCA 121
Db 89 AGCAATPCACAGATGACTATTTCTATGGAATGTTCTGAATCGGAGAGTAACATCA 148
Qy 122 TTTGCTTCGAGAGAGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTGAAA 181
Db 149 TTTGCTTCGAGAGAGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTGAAA 208
Qy 182 AGGTTTJAGAGTCTGTAACTCTTTCTTAAATCCCTTAAAGAGTGGAACTATCTCTAT 241
Db 209 AGGTTTJAGAGTCTGTAACTCTTTCTTAAATCCCTTAAAGAGTGGAACTATCTCTAT 268
Qy 242 TTCAGGACTTGAATGGAACAAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGACGAT 301
Db 269 TTCAGGACTTGAATGGAACAAAGTCTTTTTCATCAGACATCAGAGGAGACTTGGACGAT 328
Qy 302 TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTG 361
Db 329 TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTG 388
Qy 362 GTGAAGTATTGACATTTATTTTAACTTGAAGACACCTTTCACAGAACCTGTCTGTGA 421
Db 389 GTGAAGTATTGACATTTATTTTAACTTGAAGACACCTTTCACAGAACCTGTCTGTGA 448
Qy 422 GGAAGTCCACACCTACCGGCTGGAGCAGCTGACCTGATGGCTCTCTCGAGCTC 481
Db 449 GGAAGTCCACACCTACCGGCTGGAGCAGCTGACCTGATGGCTCTCTCGAGCTC 508
Qy 482 TTCAGACCCCTGCATCTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGAGC 541
Db 509 TTCAGACCCCTGCATCTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGAGC 568
Qy 542 GCATTCATGCTCTGGGGCTCCGGAAGTGGCAAGGCTCTGACCAAGTTCAAATTCGTCT 601
Db 569 GCATTCATGCTCTGGGGCTCCGGAAGTGGCAAGGCTCTGACCAAGTTCAAATTCGTCT 628
Qy 602 TCTTCCCTCCTCAGCAGGCGCCAGGGTGGACTTTTGTAAACCCCTCTGTGATCAACTCC 661
Db 629 TCTTCCCTCCTCAGCAGGCGCCAGGGTGGACTTTTGTAAACCCCTCTGTGATCAACTCC 688
Qy 662 TGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGGCATGCTGCTGAAAGTGGGC 721
Db 689 TGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGGCATGCTGCTGAAAGTGGGC 748
Qy 722 AGAGGGTCTTTTCTCTTGTGATGGCTTCAATGAATTCAGGCCCGCAAGTTCGCCAGAAA 781
Db 749 AGAGGGTCTTTTCTCTTGTGATGGCTTCAATGAATTCAGGCCCGCAAGTTCGCCAGAAA 808
Qy 782 TCGAAGCTCTGATAAGGAAACACCCGCTTCAAGAACATGGTCTGTCACCACTACCA 841
Db 809 TCGAAGCTCTGATAAGGAAACACCCGCTTCAAGAACATGGTCTGTCACCACTACCA 868
Qy 842 CTGAGTCTCTGAGGACATACCGCAGTTTGTGCCCTGACTGCTGAGTGGGGATATGA 901
Db 869 CTGAGTCTCTGAGGACATACCGCAGTTTGTGCCCTGACTGCTGAGTGGGGATATGA 928
Qy 902 CAGAAGATACGCGCAGGCTCTCATCGGAGAAAGTGTGATCAAGGAGCTTGTCTGAAGCT 961
Db 929 CAGAAGATACGCGCAGGCTCTCATCCGAGAAAGTGTGATCAAGGAGCTTGTCTGAAGCT 988
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QY 962 TGTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTG 1021
Db TGTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTG 1048
QY 1022 TGTGCTACACTTGTGCAATCCAGATGGGTGAAAGTGGATGCTTCCACTCTCACACACAAACAA 1081
Db TGTGCTACACTTGTGCAATCCAGATGGGTGAAAGTGGATGCTTCCACTCTCACACACAAACAA 1108
QY 1082 CGCTGTCCATACCTTCTATGATCTGTTGATACAGAAAAACAACACAAACATAAAGGTG 1141
Db CGCTGTCCATACCTTCTATGATCTGTTGATACAGAAAAACAACACAAACATAAAGGTG 1168
QY 1142 TGGCTGCAAGTGACTTCATTTCGGAGCCTGGACCACCTGTGGAGACCTAGCTCTGGAGGTG 1201
Db TGGCTGCAAGTGACTTCATTTCGGAGCCTGGACCACCTGTGGAGACCTAGCTCTGGAGGTG 1228
QY 1202 TGTCTCCCAAGTTTGATTTTCCAACTGCAGGATGTCCTCAGCGTGAATGAGGATGCC 1261
Db TGTCTCCCAAGTTTGATTTTCCAACTGCAGGATGTCCTCAGCGTGAATGAGGATGCC 1288
QY 1262 TGGTGACAACCTGGGCTCCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATTAAT 1321
Db TGGTGACAACCTGGGCTCCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATTAAT 1348
QY 1322 TCTTTTCAAAAGTCAATCCAGGAGTACACAGCAGCAAGAACTCAGCAGTCTTATTGACGT 1381
Db TCTTTTCAAAAGTCAATCCAGGAGTACACAGCAGCAAGAACTCAGCAGTCTTATTGACGT 1408
QY 1349 TCYTTCACAGTCATCCAGGAGTACACAGCAGCAAGAACTCAGCAGTCTTATTGACGT 1408
QY 1382 CTCATGAGCCAGAGGAGGTGACCAAGGGGAATGTTTACTTTCGAAAAATGTTTCCATTT 1441
Db CTCATGAGCCAGAGGAGGTGACCAAGGGGAATGTTTACTTTCGAAAAATGTTTCCATTT 1468
QY 1442 CGGACATTACATCCACTTATAGAGCCTGCTCCGGTACACCTGTGGGTATCTGTGGAAG 1501
Db CGGACATTACATCCACTTATAGAGCCTGCTCCGGTACACCTGTGGGTATCTGTGGAAG 1528
QY 1502 CCACGAGGCTGTATGAAGCCTCGCAGCAGTGTATCAACAGCGCTGCTTCTCGGAC 1561
Db CCACGAGGCTGTATGAAGCCTCGCAGCAGTGTATCAACAGCGCTGCTTCTCGGAC 1588
QY 1562 TTTCCATCGCCAAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCA 1621
Db TTTCCATCGCCAAAGAGCCCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCA 1648
QY 1622 CTGAGCAAGAAATCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCCATT 1681
Db CTGAGCAAGAAATCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCCATT 1708
QY 1682 TATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTTCAAG 1741
Db TATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTTTCAAG 1768
QY 1742 GTAAAGCTTATATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTTGAAC 1801
Db GTAAAGCTTATATATCAACTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTTGAAC 1828
QY 1802 ATTTGCCCAATTTGCAAGTGTCTTGAGCTTTCATTAACCTGGACTTTTATGGGGAGCTA 1861
Db ATTTGCCCAATTTGCAAGTGTCTTGAGCTTTCATTAACCTGGACTTTTATGGGGAGCTA 1888
QY 1862 TGGCTTCATGGAAAGGCTGCGAAGACACACAGGTGGAATCCACATGGAAGAGCCCCAG 1921
Db TGGCTTCATGGAAAGGCTGCGAAGACACACAGGTGGAATCCACATGGAAGAGCCCCAG 1948
QY 1922 AAAGCTACATTTCCAGCAGGCTGTATCTTTTGTCTTCAACTGGAAGCAGGAATTCAGGA 1981
Db AAAGCTACATTTCCAGCAGGCTGTATCTTTTGTCTTCAACTGGAAGCAGGAATTCAGGA 2008
QY 1982 CTCGGAGGTACACTCCGGGATTTACGCAAGTTTGAATAAGCAAGATATCACATATCTGG 2041
Db CTCGGAGGTACACTCCGGGATTTACGCAAGTTTGAATAAGCAAGATATCACATATCTGG 2068

QY 2042 GGAATAATTCAGCTCGCCACAAGCCTCAGGCTGCAAAATAAGAGATGTCTGGTGTGG 2101
Db GGAATAATTCAGCTCGCCACAAGCCTCAGGCTGCAAAATAAGAGATGTCTGGTGTGG 2128
QY 2102 CTGGAAGCCTCAGTTTGGTCTCTCAGCACCTGTGAAGACATTTATTTCTCATGTTGGAAG 2161
Db CTGGAAGCCTCAGTTTGGTCTCTCAGCACCTGTGAAGACATTTATTTCTCATGTTGGAAG 2188
QY 2162 CCAGTCCCTTCACATAGAAGATGAGAGGCACATCATCTGTAACAAACCTGAAAAACCT 2221
Db CCAGTCCCTTCACATAGAAGATGAGAGGCACATCATCTGTAACAAACCTGAAAAACCT 2248
QY 2222 TGAGTATTCATGACCTACAGAATCAACGGCTGCCGGT 2259
Db TGAGTATTCATGACCTACAGAATCAACGGCTGCCGGT 2286
RESULT 32
US-09-578-789-17
; Sequence 17, Application US/09578789
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Frederick Plo
; APPLICANT: Adam Godzik
; TITLE OF INVENTION: Novel Card Polypeptides
; FILE REFERENCE: P-LJ 4141
; CURRENT APPLICATION NUMBER: US/09/578,789
; CURRENT FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 2415
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2412)
US-09-578-789-17
Query Match 71.8%; Score 2205; DB 22; Length 2415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2255; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TGAATTTTCATAAAGGACAATAGCGAGCCCTTATTCAAAGAATGGGAATGACTCTTATAA 61
Db 29 TGAATTTTCATAAAGGACAATAGCGAGCCCTTATTCAAAGAATGGGAATGACTCTTATAA 88
QY 62 AGCAAAATCACAGATGACCTATTGTTGATGGAATGTTCTGAATCGCGAAGAAAGTAACATCA 121
Db 89 AGCAAAATCACAGATGACCTATTGTTGATGGAATGTTCTGAATCGCGAAGAAAGTAACATCA 148
QY 122 TTTGCTCGAGAGAGGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGAATA 181
Db 149 TTTGCTCGAGAGAGGTGGAGCAGGATGCTGCTAGAGGATCATTCACATGATTTTGAATA 208
QY 182 AGGTTTCAGAGTCTCTGTAACCTCTTTCTTAAATCCCTTAAAGGAGTGAATCTCTAT 241
Db 209 AGGTTTCAGAGTCTCTGTAACCTCTTTCTTAAATCCCTTAAAGGAGTGAATCTCTAT 268
QY 242 TTCAAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAGGAGATTTGAGCAGTT 301
Db 269 TTCAAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAGGAGATTTGAGCAGTT 328
QY 302 TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCCCTG 361
Db 329 TGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACCTTTTATCCCCCTG 388
QY 362 GTGAAGATATGACATATTTTAACTTGAAGACCTTTCACAGACCTGTCTCTGTGGA 421
Db 389 GTGAAGATATGACATATTTTAACTTGAAGACCTTTCACAGACCTGTCTCTGTGGA 448
QY 422 GGAAGGACCAACCAATCAGCGCTGAGGAGCTGACCCCTGAATGGCTCTCTGAGGCTC 481

Db 449 GGAAGGACCAACACCAATCACCGCTGGAGCAGCTGACCTGAATGGCTCTCTGAGGCTC 508
QY 482 TTCAGAGCCCTGATCATTTGAAGGGAATCTGCAAGGCAAGTCCACTCTGCTGAGC 541
Db 509 TTCAGAGCCCTGATCATTTGAAGGGAATCTGCAAGGCAAGTCCACTCTGCTGAGC 568
QY 542 GCATTGCCATCTCTGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAAATTCGTCT 601
Db 569 GCATTGCCATCTCTGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAAATTCGTCT 628
QY 602 TCTTCCCTCCGCTCAGCAGGGCCAGGGTGGACTTTTGTGAAACCTCTGTGATCAACTCC 661
Db 629 TCTTCCCTCCGCTCAGCAGGGCCAGGGTGGACTTTTGTGAAACCTCTGTGATCAACTCC 688
QY 662 TGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGGC 721
Db 689 TGGATATACCTGGCACAAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGGGC 748
QY 722 AGAGGGTTCCTTCTTCTGATGGCTACAAATGAATTCGAAGCCCAAGAACTGCCCAAGAA 781
Db 749 AGAGGGTTCCTTCTTCTGATGGCTACAAATGAATTCGAAGCCCAAGAACTGCCCAAGAA 808
QY 782 TCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGGTTCATCGTCAACCACTACCA 841
Db 809 TCGAAGCCCTGATAAAGGAAACACCGCTTCAAGAACATGGTTCATCGTCAACCACTACCA 868
QY 842 CTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATGA 901
Db 869 CTGAGTGCCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATGA 928
QY 902 CAGAAGACAGCGCCAGGCTCTCATCCGAGAAGTCTGATCAAGGAGCTTCTGAGAGCT 961
Db 929 CAGAAGACAGCGCCAGGCTCTCATCCGAGAAGTCTGATCAAGGAGCTTCTGAGAGCT 988
QY 962 TGTGCTCCAAATTCAGAAATCAGAGTCTGAGGAATCTCATGAAGACCCCTCTCTTG 1021
Db 989 TGTGCTCCAAATTCAGAAATCAGAGTCTGAGGAATCTCATGAAGACCCCTCTCTTG 1048
QY 1022 TGTGCTCACTGTCGAATCCAGATGGGTGAAGTGGTCCACTCTCACACAAACAA 1081
Db 1049 TGTGCTCACTGTCGAATCCAGATGGGTGAAGTGGTCCACTCTCACACAAACAA 1108
QY 1082 CGCTGTTCATACCTCTATGATCTGTTGATACAGAAAACAAACAAACATAAAGGTG 1141
Db 1109 CGCTGTTCATACCTCTATGATCTGTTGATACAGAAAACAAACAAACATAAAGGTG 1168
QY 1142 TGGCTCCAAAGTCACTTCGAGCCTGGACCCTGTGGAGACCTAGCTCTGGAGGGTG 1201
Db 1169 TGGCTCCAAAGTCACTTCATTCGAGCCTGGACCCTGTGGAGACCTAGCTCTGGAGGGTG 1228
QY 1202 TGTCTCCCAAGTTTGATTTCCGAAGTCCAGGATGTGTCCAGCGTGAATGAGGATGTC 1261
Db 1229 TGTCTCCCAAGTTTGATTTCCGAAGTCCAGGATGTGTCCAGCGTGAATGAGGATGTC 1288
QY 1262 TGCTGACAACTGGGCTCTCTCTGATAATATACAGCTCAAGGTTCAAGCCAAAGTATAAT 1321
Db 1289 TGCTGACAACTGGGCTCTCTCTGATAATATACAGCTCAAGGTTCAAGCCAAAGTATAAT 1348
QY 1322 TCTTTTCAAGTCACTTCAGAGGATACAGCAGGAGGAGACTCAGCAGTTTATTCAGCT 1381
Db 1349 TCTTTTCAAGTCACTTCAGAGGATACAGCAGGAGGAGACTCAGCAGTTTATTCAGCT 1408
QY 1382 CTCATGAGCCAGAGGTCACCAAGGGAATGGTTACTTCGAGAAATGGTTTCCATT 1441
Db 1409 CTCATGAGCCAGAGGTCACCAAGGGAATGGTTACTTCGAGAAATGGTTTCCATT 1468
QY 1442 CGGACATTACCTCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTCACTGTGGAG 1501
Db 1469 CGGACATTACCTCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTCACTGTGGAG 1528
QY 1502 CCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGAC 1561
Db 1529 CCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGGAC 1588

RESULT 33
US-09-579-240-17
; Sequence 17, Application US/09579240
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Frederick Pio
; APPLICANT: Adam Godzik
; TITLE OF INVENTION: Novel Card-Domain Containing
; FILE REFERENCE: P-LJ 4211
; CURRENT APPLICATION NUMBER: US/09/579,240
; CURRENT FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 2415
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (2412)
US-09-579-240-17

QY 1562 TTTCATCTGCGCAAGAGCGCTCTCTGGAGCAGGAATCTTTGCAAGTGTGAAAAACACCA 1621
Db 1589 TTTCATCTGCGCAAGAGCGCTCTCTGGAGCAGGAATCTTTGCAAGTGTGAAAAACACCA 1648
QY 1622 CTGAACCAAGAAATCTCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCCATT 1681
Db 1649 CTGAACCAAGAAATCTCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCCATT 1708
QY 1682 TATAACAAGAGATACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTCTTCAAG 1741
Db 1709 TATAACAAGAGATACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTCTCTTCAAG 1768
QY 1742 GTAAAAGCTTATATCAACTCAGGGAACATCCCGGATTAATTTGAGCTTCTTGAAC 1801
Db 1769 GTAAAAGCTTATATCAACTCAGGGAACATCCCGGATTAATTTGAGCTTCTTGAAC 1828
QY 1802 ATTTCGCAATTCGCAAGTCTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTA 1861
Db 1829 ATTTCGCAATTCGCAAGTCTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTA 1888
QY 1862 TGGCTTCATGGGAAAGGCTGCAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAG 1921
Db 1889 TGGCTTCATGGGAAAGGCTGCAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAG 1948
QY 1922 AAACCTACATTCACAGAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGA 1981
Db 1949 AAACCTACATTCACAGAGGCTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGA 2008
QY 1982 CTCTGAGGTCACTCCGGGATTTTCAGCAAGTTCGAATGAAGCAAGATATCACATATCTGG 2041
Db 2009 CTCTGAGGTCACTCCGGGATTTTCAGCAAGTTCGAATGAAGCAAGATATCACATATCTGG 2068
QY 2042 GGAATAATTCAGCTCTGCAACAGCTCAGGCTGCAAAATAAAGAGATGTGCTGGTGTG 2101
Db 2069 GGAATAATTCAGCTCTGCAACAGCTCAGGCTGCAAAATAAAGAGATGTGCTGGTGTG 2128
QY 2102 CTGGAAACCTCAGTTTGGTCTCAGCACCTGTAAAGCAATTTATCTCTCATGTGTGAAG 2161
Db 2129 CTGGAAACCTCAGTTTGGTCTCAGCACCTGTAAAGCAATTTATCTCTCATGTGTGAAG 2188
QY 2162 CCAGCTCCCTCACCATAGAAGATGAGGACACATCATCTGTACAAACCTGAAACCT 2221
Db 2189 CCAGCTCCCTCACCATAGAAGATGAGGACACATCATCTGTACAAACCTGAAACCT 2248
QY 2222 TCAGTAATTCATGACCTACAGAAATCAACGCTGCCGG 2257
Db 2249 TCAGTAATTCATGACCTACAGAAATCAACGCTGCCGG 2284

Db 2129 CTGGAAGCCCTAGTTGGTCCCTCAGCAGACCTGTGAAGAACATTTATCTCTCATGGTGAAG 2188
QY 2162 CCAGTCCCTCACCATAGAGATGAGAGGACATCATCATCTGTAACAAACCTGAAACCT 2221
Db 2189 CCAGTCCCTCACCATAGAGATGAGAGGACATCATCATCTGTAACAAACCTGAAACCT 2248
QY 2222 TGAGTATTCATGACCTACAGAATCAACGGCTGCGCG 2257
Db 2249 TGAGTATTCATGACCTACAGAATCAACGGCTGCGCG 2284
RESULT 34
US-09-577-408-3077
; Sequence 3077, Application US/09577408
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/577,408
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 8502
; SOFTWARE: PL_GCT_genes Version 1.0
; SEQ ID NO 3077
; LENGTH: 3018
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (682)...(2040)
; OTHER INFORMATION: similar to g13688110 in the genepept database release 115,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-577-408-3077
Query Match 71.8%; Score 2205; DB 22; Length 3018;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2255; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TGAATTTCAATAGGACAATAGCGAGCCCTATTCAAGAAATGGGAATGACTGTTATAA 61
Db 236 TGAATTTCAATAGGACAATAGCGAGCCCTATTCAAGAAATGGGAATGACTGTTATAA 295
QY 62 AGCAATCAGATGACCTATTTGTATGGAATGTTCTGAATCGGAAGAAGTAAACATCA 121
Db 296 AGCAATCAGATGACCTATTTGTATGGAATGTTCTGAATCGGAAGAAGTAAACATCA 355
QY 122 TTGCTCGGAGAGGTGGAGAGATGCTGCTAGAGGGATCATTCACATGATTTGAAAA 181
Db 356 TTGCTCGGAGAGGTGGAGAGATGCTGCTAGAGGGATCATTCACATGATTTGAAAA 415
QY 182 AGGTTTCAGAGTCTGTAACTCTTTCTTAAATCCCTTAAGAGAGTGGAACTATCCCTCTAT 241
Db 416 AGGTTTCAGAGTCTGTAACTCTTTCTTAAATCCCTTAAGAGAGTGGAACTATCCCTCTAT 475
QY 242 TTCAGGACTTGAATGGACAAAGCTTTTTCATCAGACATCAGAGGAGACTTGGACGATT 301
Db 476 TTCAGGACTTGAATGGACAAAGCTTTTTCATCAGACATCAGAGGAGACTTGGACGATT 535
QY 302 TGGCTCAGGATTTAAAGGACTTGTACCATACCCATCTTTTCTGAATTTTATCCCTTG 361
Db 536 TGGCTCAGGATTTAAAGGACTTGTACCATACCCATCTTTTCTGAATTTTATCCCTTG 595
QY 362 GTGAGATATGACATTTATTTAACTTGAAGACCTTTCACAGAACCTGCTGTGGGA 421
Db 596 GTGAGATATGACATTTATTTAACTTGAAGACCTTTCACAGAACCTGCTGTGGGA 655
QY 422 GGAAGGACCAACCATCACCGGTGGAGCAGCTGACCCCTGAATGGCCCTCCTGCAGGCTC 481
Db 656 GGAAGGACCAACCATCACCGGTGGAGCAGCTGACCCCTGAATGGCCCTCCTGCAGGCTC 715

QY 482 TTCAAGTCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACATCTCTGCTGCAGC 541
Db 716 TTCAAGTCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACATCTCTGCTGCAGC 775
QY 542 GCATTTCATATGCTCTGGGGTCCGGAAGTGCAGAGGCTCTGACCAAGTTCAAAATTCGTCT 601
Db 776 GCATTTCATATGCTCTGGGGTCCGGAAGTGCAGAGGCTCTGACCAAGTTCAAAATTCGTCT 835
QY 602 TCTTTCCTCCGCTCTCAGCAGGGCCAGGGTGGACTTTTGAAGCCCTCTGTGATCAACTCC 661
Db 836 TCTTTCCTCCGCTCTCAGCAGGGCCAGGGTGGACTTTTGAAGCCCTCTGTGATCAACTCC 895
QY 662 TGGATATACCTGCGACAAATCAGGAAGCAGACATTCATGGCCATGCTCTGAAGTGGGG 721
Db 896 TGGATATACCTGCGACAAATCAGGAAGCAGACATTCATGGCCATGCTCTGAAGTGGGG 955
QY 722 AGAGGGTCTCTTTCCTCTTGAATGGCTACAAATGAATCAAGCCCAAGAACTGCCAGAAA 781
Db 956 AGAGGGTCTCTTTCCTCTTGAATGGCTACAAATGAATCAAGCCCAAGAACTGCCAGAAA 1015
QY 782 TCGAAGTCTCTGATTAAGGAAACACCGCTTCAAGAAACATGGTCATGTCACCACTACCA 841
Db 1016 TCGAAGTCTCTGATTAAGGAAACACCGCTTCAAGAAACATGGTCATGTCACCACTACCA 1075
QY 842 CTGAGTCTCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATGA 901
Db 1076 CTGAGTCTCTGAGGCACATACGGCAGTTTGGTGCCTGACTGCTGAGGTGGGGATATGA 1135
QY 902 CAGAAGTCAAGCGCCAGGGCTCTCATCCGGAAGTGTGATCAAGGAGCTTGTCTGAAGGCT 961
Db 1136 CAGAAGTCAAGCGCCAGGGCTCTCATCCGGAAGTGTGATCAAGGAGCTTGTCTGAAGGCT 1195
QY 962 TGTGTCCTCAAAATTCAGAAATCCAGGTGCTTGAAGGAACTCTCATGAAGACCCCTCTCTTTG 1021
Db 1196 TGTGTCCTCAAAATTCAGAAATCCAGGTGCTTGAAGGAACTCTCATGAAGACCCCTCTCTTTG 1255
QY 1022 TGTGTCCTCAAAATTCAGAAATCCAGGTGCTTGAAGGAACTCTCATGAAGGAACTTGTCTGAAGGCT 1081
Db 1256 TGTGTCCTCAAAATTCAGAAATCCAGGTGCTTGAAGGAACTCTCATGAAGGAACTTGTCTGAAGGCT 1315
QY 1082 CGCTGTCTCAATACCTCTATGATCTGTGATACAGAAACAAACACAAACATATAAGGTG 1141
Db 1316 CGCTGTCTCAATACCTCTATGATCTGTGATACAGAAACAAACACAAACATATAAGGTG 1375
QY 1142 TGGCTGTCAAGTGAATTCATTCGGAGCCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTG 1201
Db 1376 TGGCTGTCAAGTGAATTCATTCGGAGCCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTG 1435
QY 1202 TGTGTCCTCAAAAGTTGATTTCAAGCTGCAGAGTGTCTCCAGCGTGAATGAGATGCTC 1261
Db 1436 TGTGTCCTCAAAAGTTGATTTCAAGCTGCAGAGTGTCTCCAGCGTGAATGAGATGCTC 1495
QY 1262 TGTGTCCTCAAAAGTTGATTTCAAGCTGCAGAGTGTCTCCAGCGTGAATGAGATGCTC 1321
Db 1496 TGTGTCCTCAAAAGTTGATTTCAAGCTGCAGAGTGTCTCCAGCGTGAATGAGATGCTC 1555
QY 1322 TCTTTTCCTCAAGTGAATTCAGAGGATACACAGCAGGACCAAGACTCAGCAGTTTATTTGACGT 1381
Db 1556 TCTTTTCCTCAAGTGAATTCAGAGGATACACAGCAGGACCAAGACTCAGCAGTTTATTTGACGT 1615
QY 1382 CTCTATGCGCAGAGGAGTGAACCAAGGGGAATGTTTACTTTCAGAAATGTTTCCATTT 1441
Db 1616 CTCTATGCGCAGAGGAGTGAACCAAGGGGAATGTTTACTTTCAGAAATGTTTCCATTT 1675
QY 1442 CGGACATATACATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTGCTATCTGTGGAAG 1501
Db 1676 CGGACATATACATCCACTTATAGCAGCTGCTCCGGTACACCTGTGGGTGCTATCTGTGGAAG 1735
QY 1502 CCACCAAGTCTGTTATGAAGCAGCTCGCAGCAGTGTATCAACAGGCTGCTCTTCGCGAC 1561
Db 1736 CCACCAAGTCTGTTATGAAGCAGCTCGCAGCAGTGTATCAACAGGCTGCTCTTCGCGAC 1795

QY 1562 TTTCCATCGCCAGAGGCGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCA 1621
Db 1796 TTTCCATCGCCAGAGGCGCTCTCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCA 1855
QY 1622 CTGAGCAAGAAATCTGAAAGCCATAACACATCAATTCCTTTGTAGAGTGTGGCATCCCAT 1681
Db 1856 CTGAGCAAGAAATCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCCCAT 1915
QY 1682 TATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAG 1741
Db 1916 TATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAG 1975
QY 1742 GTAAAGCTTATATATCAACTCAGGGAACATCCCCGATTAATTTGACTTCTTTTGAAC 1801
Db 1976 GTAAAGCTTATATATCAACTCAGGGAACATCCCCGATTAATTTGACTTCTTTTGAAC 2035
QY 1802 ATTTGCCCAATTTGTCAAGTGTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTA 1861
Db 2036 ATTTGCCCAATTTGTCAAGTGTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCTA 2095
QY 1862 TGGCTTCATGGGAAAGGCTGCAGAAAGACACAGGTGGAAATCCACATGGAAGAGGCCCCAG 1921
Db 2096 TGGCTTCATGGGAAAGGCTGCAGAAAGACACAGGTGGAAATCCACATGGAAGAGGCCCCAG 2155
QY 1922 AAACCTACATTTCCACAGAGGCGTGTATCTTTGCTTCAACTGGAAGCAGGAATTCAGGA 1981
Db 2156 AAACCTACATTTCCACAGAGGCGTGTATCTTTGCTTCAACTGGAAGCAGGAATTCAGGA 2215
QY 1982 CTCGTGAGGTACACCTCCGGGATTCAGCAAGTTGCAATGAAGCAAGATATCATATCTGG 2041
Db 2216 CTCGTGAGGTACACCTCCGGGATTCAGCAAGTTGCAATGAAGCAAGATATCATATCTGG 2275
QY 2042 GAAAAATATTGAGCTCTGCCACAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGTGTGG 2101
Db 2276 GAAAAATATTGAGCTCTGCCACAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGTGTGG 2335
QY 2102 CTGGAAGCCTCAGTTTGGTCTCAGCACCTGTGAAGAACATTTATTTCTCATGTGTGAAG 2161
Db 2336 CTGGAAGCCTCAGTTTGGTCTCAGCACCTGTGAAGAACATTTATTTCTCATGTGTGAAG 2395
QY 2162 CCAGTCCCTCACCATAGAAGTGAAGGCACATCAGATCTGTACAAACCTGAAAACT 2221
Db 2396 CCAGTCCCTCACCATAGAAGTGAAGGCACATCAGATCTGTACAAACCTGAAAACT 2455
QY 2222 TGAGTATTTCATGACCTACAGAAATCAACGGCTGCCGG 2257
Db 2456 TGAGTATTTCATGACCTACAGAAATCAACGGCTGCCGG 2491

RESULT 35
PCT-US01-07143-22
; Sequence 22, Application PC/TUS0107143
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM p.l.c.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: PCT/US01/07143
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 2215
; TYPE: DNA
; ORGANISM: Homo sapiens

PCT-US01-07143-22
Query Match 67.1%; Score 2062; DB 1; Length 2215;
Best Local Similarity 99.9%; Pred No. 0;
Matches 2212; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 43 ATGGGAATGACTGTTTATAAAGCAAAATCACAGATGACCTATTTGTATGGAAATTTCTTGAAT 102
Db 1 ATGGGAATGACTGTTTATAAAGCAAAATCACAGATGACCTATTTGTATGGAAATTTCTTGAAT 60
QY 103 CCCGAAGAAGTAAACATCATTTTGCTGCGAGAAGGTGGAGCAGAGATGCTCTAGAGGGATC 162
Db 61 CGCGAAGAAGTAAACATCATTTTGCTGCGAGAAGGTGGAGCAGAGATGCTCTAGAGGGATC 120
QY 163 ATTCACATGATTTTCAAAAAGGTTTCAGAGTCTCTGTAACTCTTTCTTTAAATCCCTTAAAG 222
Db 121 ATTCACATGATTTTCAAAAAGGTTTCAGAGTCTCTGTAACTCTTTCTTTAAATCCCTTAAAG 180
QY 223 GAGTGGAACTATPCCTCTATTTTCAGGACTTTGAATGACAAAGTCTTTTTCATCAGACATCA 282
Db 181 GAGTGGAACTATPCCTCTATTTTCAGGACTTTGAATGACAAAGTCTTTTTCATCAGACATCA 240
QY 283 GAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTT 342
Db 241 GAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTT 300
QY 343 CTGAACTTTTATCCCTCTGGTGAAGATATTGACATTTATTTTAACTTTGAAAAGCACCCTTC 402
Db 301 CTGAACTTTTATCCCTCTGGTGAAGATATTGACATTTATTTTAACTTTGAAAAGCACCCTTC 360
QY 403 ACAGAACCTGTCTGTGGAGGAAGCAACACCATCATCCCGCTGGAGCAGCTGACCCTG 462
Db 361 ACAGAACCTGTCTGTGGAGGAAGCAACACCATCATCCCGCTGGAGCAGCTGACCCTG 420
QY 463 AATGCCCTCTCGCAGGCTCTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGC 522
Db 421 AATGCCCTCTCGCAGGCTCTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGC 480
QY 523 AAGTCCACTCTGCTCAGCGCATTTGCCATGTCTCGGGCTCCGGAAGTGCAGAGCTCTG 582
Db 481 AAGTCCACTCTGCTCAGCGGAATTTGCCATGTCTCGGGCTCCGGAAGTGCAGAGCTCTG 540
QY 583 ACCAAGTTCAAATTCGTCTCTTCCTCCGTCTCAGCAGGGCCCAAGGGTGGACTTTTGA 642
Db 541 ACCAAGTTCAAATTCGTCTCTTCCTCCGTCTCAGCAGGGCCCAAGGGTGGACTTTTGA 600
QY 643 ACCCTCTGTGATCAACTCTCTGGATATACCTGGCAAAATCAGGAAGCAGACATTCATGGCC 702
Db 601 ACCCTCTGTGATCAACTCTCTGGATATACCTGGCAAAATCAGGAAGCAGACATTCATGGCC 660
QY 703 ATGCTGCTGAAGCTGCGCAGAGGCTTCTTTTCTTCTTGATGGCTACAAATGAATTCAG 762
Db 661 ATGCTGCTGAAGCTGCGCAGAGGCTTCTTTTCTTCTTGATGGCTACAAATGAATTCAG 720
QY 763 CCCCAGAACTGCCAGAAATCGAAGCCCTGTATAAGGAAAAACCCGCTTCAAGAACATG 822
Db 721 CCCCAGAACTGCCAGAAATCGAAGCCCTGTATAAGGAAAAACCCGCTTCAAGAACATG 780
QY 823 GTCATCGTCCACCCTACCACTACCACTGAGTGCCTGAGGCACATACGGCAGTTTGGTCCCTGACT 882
Db 781 GTCATCGTCCACCCTACCACTACCACTGAGTGCCTGAGGCACATACGGCAGTTTGGTCCCTGACT 840
QY 883 GCTGAGGTGGGGATATGACAGAAGACAGCGCCAGGCTCTCATCCGAGAAGTGTGTATC 942
Db 841 GCTGAGGTGGGGATATGACAGAAGACAGCGCCAGGCTCTCATCCGAGAAGTGTGTATC 900
QY 943 AAGGAGCTTGTGTAAGGCTTGTGTCTCCAAATTCAGAAATCCAGGTGCTTGAAGGAATCTC 1002
Db 901 AAGGAGCTTGTGTAAGGCTTGTGTCTCCAAATTCAGAAATCCAGGTGCTTGAAGGAATCTC 960
QY 1003 ATGAAGACCCCTCTCTTTGTGTGTCATCAGTGTGCAATCCAGATGGGTGAAAGTGTG 1062
Db 961 ATGAAGACCCCTCTCTTTGTGTGTCATCAGTGTGCAATCCAGATGGGTGAAAGTGTG 1020

QY 1063 CACTCTCACACAAACAGCGTGTCCATACCTTCTATGATCTGTGTATACAGAAAAC 1122
Db CACTCTCACACAAACAGCGTGTCCATACCTTCTATGATCTGTGTATACAGAAAAC 1080
QY 1123 AAACACAAACATAAAGGTGTGGTGCAGGTGACTTCAATCGGAGCCCTGGACCACTGTGGA 1182
Db AAACACAAACATAAAGGTGTGGTGCAGGTGACTTCAATCGGAGCCCTGGACCACTGTGGA 1140
QY 1183 GACTAGCTCTGGAGGTGTGTCTCCCAACAGTGTGATTTCGAACCTGCAGGATGTGTCC 1242
Db GACTAGCTCTGGAGGTGTGTCTCCCAACAGTGTGATTTCGAACCTGCAGGATGTGTCC 1200
QY 1243 AGCGTGAATCAGATCTCCCTGCTGACAACTCGGCTCTCTGTAATATACAGCTCAAGG 1302
Db AGCGTGAATCAGATCTCCCTGCTGACAACTCGGCTCTCTGTAATATACAGCTCAAGG 1260
QY 1303 TTCAAGCCAAAGTATTAATTTCTTTCACAACTCAATCCAGGAGTACACAGCAGGACGAAGA 1362
Db TTCAAGCCAAAGTATTAATTTCTTTCACAACTCAATCCAGGAGTACACAGCAGGACGAAGA 1320
QY 1363 CTCAGCAGTTTATGAGCTCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGTTACTTG 1422
Db CTCAGCAGTTTATGAGCTCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGTTACTTG 1380
QY 1423 CAGAAATGTTTCCATTTTCGGACATFACATCCACTTATAGCAGCCCTGCTCCCGGTACACC 1482
Db CAGAAATGTTTCCATTTTCGGACATFACATCCACTTATAGCAGCCCTGCTCCCGGTACACC 1440
QY 1483 TGTGGGTCACTCTGGAAGCCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAA 1542
Db TGTGGGTCACTCTGGAAGCCACAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAA 1500
QY 1543 CAGGCTGCTCTCTCGGACATTTCCATCGCCCAAGGCTCTCTGGACAGGATCTTTG 1602
Db CAGGCTGCTCTCTCGGACATTTCCATCGCCCAAGGCTCTCTGGACAGGATCTTTG 1560
QY 1603 CAAAGTGTGAAGAACACCTGAGCAGCAAAATCTGAAAGCCATACATCAATCTCTT 1662
Db CAAAGTGTGAAGAACACCTGAGCAGCAAAATCTGAAAGCCATACATCAATCTCTT 1620
QY 1663 GTAGAGTGGCATCCATTTATATCAAGAGTACATCCAAATCAGCCCTGAGCCCAAGAA 1722
Db GTAGAGTGGCATCCATTTATATCAAGAGTACATCCAAATCAGCCCTGAGCCCAAGAA 1680
QY 1723 TTTGAAGCTTTCTTCAAGTAAAGCTTATATCAACTCAGGGAACATCCCGGATTC 1782
Db TTTGAAGCTTTCTTCAAGTAAAGCTTATATCAACTCAGGGAACATCCCGGATTC 1740
QY 1783 TTATTTGACTTCTTTGAACATTTGCCAATTTGTGCAAGTCTCTGGACTTTCATTAACATG 1842
Db TTATTTGACTTCTTTGAACATTTGCCAATTTGTGCAAGTCTCTGGACTTTCATTAACATG 1800
QY 1843 GACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTGCAGAAACAGAGTGGGAATC 1902
Db GACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTGCAGAAACAGAGTGGGAATC 1860
QY 1903 CACATGAAGAGCCCCAGAAACCTACATTCAGAGGCTGTATCTTTGTTCTTCAAC 1962
Db CACATGAAGAGCCCCAGAAACCTACATTCAGAGGCTGTATCTTTGTTCTTCAAC 1920
QY 1963 TGGAGCAGAAATTCAGGACTCTGGAGTCACTCCGGAATTCAGCAAGTTGAATAAG 2022
Db TGGAGCAGAAATTCAGGACTCTGGAGTCACTCCGGAATTCAGCAAGTTGAATAAG 1980
QY 2023 CAGATATACATATCTGGGGAATAATTCAGCTCTGCGCAAGCCCTCAGGCTGCAAAATA 2082
Db CAGATATACATATCTGGGGAATAATTCAGCTCTGCGCAAGCCCTCAGGCTGCAAAATA 2040
QY 2083 AAGAGATGTCTGTGTGGTGGAAAGCCCTCAGTTTGTCTCAGCAGCCCTGTAAGAACATT 2142
Db AAGAGATGTCTGTGTGGTGGAAAGCCCTCAGTTTGTCTCAGCAGCCCTGTAAGAACATT 2100

QY 2143 TATTCTTTCATGTGGAAGCCAGTCCCTCACCATGAAGATGAGAGGCACATCACATCT 2202
Db TATTCTTTCATGTGGAAGCCAGTCCCTCACCATGAAGATGAGAGGCACATCACATCT 2160
QY 2203 GTAACACACCTGAAACCTTGTGATTCATGACCTACAGAAATCAACGGCTGCCGG 2257
Db GTAACACACCTGAAACCTTGTGATTCATGACCTACAGAAATCAACGGCTGCCGG 2215

RESULT 36
US-10-221-097-22
; Sequence 22, Application US/10221097
; GENERAL INFORMATION:
; APPLICANT: Agriwel; Pankaj
; APPLICANT: Mirdock; Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoqing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/10/221,097
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 22
; LENGTH: 2215
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-221-097-22

Query Match 57.1%; Score 2062; DB 42; Length 2215;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2212; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 43 ATGGGAAAGACTGTATATAAGCAAAATCACAGATGACCTATTGTGTATGAATTTCTGAAT 102
Db 1 ATGGGAAAGACTGTATATAAGCAAAATCACAGATGACCTATTGTGTATGAATTTCTGAAT 60
QY 103 CGGGAAGAGTAACACATCATTTGCTGCGAAGAGGTGAGCAGGATGCTGTAGAGGATC 162
Db 61 CGGGAAGAGTAACACATCATTTGCTGCGAAGAGGTGAGCAGGATGCTGTAGAGGATC 120
QY 163 ATTCACAAGATTTGAAAAAGGTTTCAGAGTCCCTGTAACTCTTCTTAAATCCCTTAAG 222
Db 121 ATTCACAAGATTTGAAAAAGGTTTCAGAGTCCCTGTAACTCTTCTTAAATCCCTTAAG 180
QY 223 GAGTGGAACTATCTCTTATTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCA 282
Db 181 GAGTGGAACTATCTCTTATTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCA 240
QY 283 GAAGGAGCTTGACAGATTTGGCTCAGGATTAAGGACTGTACCATCCCATCTTTT 342
Db 241 GAAGGAGCTTGACAGATTTGGCTCAGGATTAAGGACTGTACCATCCCACTTTT 300
QY 343 CTGAACCTTTATCCCTTGTGTGAAGATTTGACATTTATTTTAACTTGAAGACACCTTC 402
Db 301 CTGAACCTTTATCCCTTGTGTGAAGATTTGACATTTATTTTAACTTGAAGACACCTTC 360
QY 403 ACAGAACCTCTCTCTGTGGAGGAAGGACCAACACCATCACCCTGTGGAGCAGCTGACCTG 462
Db 361 ACAGAACCTCTCTCTGTGGAGGAAGGACCAACACCATCACCCTGTGGAGCAGCTGACCTG 420
QY 463 AATGGCTCTGACAGGCTCTTCAGAGCCCTGATCATTTGAAGGGGAATCTGGCAAGGC 522

Db	421		AATGGCCTCTG	CAGGCTCTT	CAGAGCCCTTCAT	CTTAAGGGGAATCTG	CGAAAGGC	480
Qy	523		AAGTCCACTCTG	TCAGCGCAT	TGCTCTGGGCTCCG	GAAAGTGAAGGCTCTG	582	
Db	481		AAGTCCACTCTG	TCAGCGAAT	TGCCATGCTCTGGGCTCG	GNAAGTGAAGGCTCTG	540	
Qy	583		ACCAAGTTCAAAT	TCGCTCTTCTCCGTC	TCAGCAGGGCCCAAGGTG	GAATTTTGA	642	
Db	541		ACCAAGTTCAAAT	TCGCTCTTCTCCGTC	TCAGCAGGGCCCAAGGTG	GAATTTTGA	600	
Qy	643		ACCTCTGTGAT	CAACTCTTG	GATATACCTG	GCACAAATCAGGAAGCAGACAT	TCAATGGCC	702
Db	601		ACCTCTGTGAT	CAACTCTTG	GATATACCTG	GCACAAATCAGGAAGCAGACAT	TCAATGGCC	660
Qy	703		ATGCTGTGAAG	TGCGG	CAGAGGGTCTCTTTCCTCT	TCTTGATGGCTACAATGAAT	TCAAG	762
Db	661		ATGCTGTGAAG	TGCGG	CAGAGGGTCTCTTTCCTCT	TCTTGATGGCTACAATGAAT	TCAAG	720
Qy	763		CCCCAGAATCT	GCCG	GAATTCGAGAGCCCTG	ATAAGGAAAAACCCGCTTCAAGAACATG	822	
Db	721		CCCCAGAATCT	GCCG	GAATTCGAGAGCCCTG	ATAAGGAAAAACCCGCTTCAAGAACATG	780	
Qy	823		GTATCTGTACC	ACTACC	ACTGAGTGCCTG	AGGCACATACGGCAGTTTGTC	CCCTGACT	882
Db	781		GTATCTGTACC	ACTACC	ACTGAGTGCCTG	AGGCACATACGGCAGTTTGTC	CCCTGACT	840
Qy	883		GCTGAGTGGGG	ATATG	CAGAAAGACAGCGCC	AGGCTCTCATCCGAGAAAGTCTG	CTGATC	942
Db	841		GCTGAGTGGGG	ATATG	CAGAAAGACAGCGCC	AGGCTCTCATCCGAGAAAGTCTG	CTGATC	900
Qy	943		AAGGAGCTGCT	G	GAAGGCTTGTGCTTCCAAAT	TCAGAAATCCAGTGCTTGAGGAATCTC	1002	
Db	901		AAGGAGCTGCT	G	GAAGGCTTGTGCTTCCAAAT	TCAGAAATCCAGTGCTTGAGGAATCTC	960	
Qy	1003		ATGAAGACCCCT	CTCTTT	TGGTGCATCACTTGTG	CAATCCAGATGGGTGAAGTGAAGTTC	1062	
Db	961		ATGAAGACCCCT	CTCTTT	TGGTGCATCACTTGTG	CAATCCAGATGGGTGAAGTGAAGTTC	1020	
Qy	1063		CACCTCACACACA	CAACCGCTGT	TCCATACCTTCTATGATCTG	TGATACAGAAAAAC	1122	
Db	1021		CACCTCACACACA	CAACCGCTGT	TCCATACCTTCTATGATCTG	TGATACAGAAAAAC	1080	
Qy	1123		AAACAAACAT	AAAGTG	TGGCTGCAAGTGA	CTTCAATTCGAGAGCCTGGACCACTGTGGA	1182	
Db	1081		AAACAAACAT	AAAGTG	TGGCTGCAAGTGA	CTTCAATTCGAGAGCCTGGACCACTGTGGA	1140	
Qy	1183		GACCTAGCTCG	GAGGGTG	TTCTCCCAAGTTTGATTT	CGAACTGCAGAGTGTGTC	1242	
Db	1141		GACCTAGCTCG	GAGGGTG	TTCTCCCAAGTTTGATTT	CGAACTGCAGAGTGTGTC	1200	
Qy	1243		AGCGTGAAT	CAGGATG	CTCTGTGCAACTGGGCT	CTCTGTAAATATACAGCTCAAAAG	1302	
Db	1201		AGCGTGAAT	CAGGATG	CTCTGTGCAACTGGGCT	CTCTGTAAATATACAGCTCAAAAG	1260	
Qy	1303		TTCAAGCCAAAG	TATAAATCT	TTCACAAAGTCAT	TCCAGGAGTACACAGCAGGCAAGA	1362	
Db	1261		TTCAAGCCAAAG	TATAAATCT	TTCACAAAGTCAT	TCCAGGAGTACACAGCAGGCAAGA	1320	
Qy	1363		CTCAGCAGTT	TTTATG	AGCTCTCATGAGCAGAGGTG	ACCAAGGGGAATGTGTTACTTG	1422	
Db	1321		CTCAGCAGTT	TTTATG	AGCTCTCATGAGCAGAGGTG	ACCAAGGGGAATGTGTTACTTG	1380	
Qy	1423		CAGAAATG	TTCATTT	TCGACATATACATCC	ACTTATAGCAGCTCTCCGGTACAC	1482	
Db	1381		CAGAAATG	TTCATTT	TCGACATATACATCC	ACTTATAGCAGCTCTCCGGTACAC	1440	
Qy	1483		TGTGGGTCA	CTCTGGA	AGCCACAGGGGCTGT	TATGAAGACACTCGCAGCAGTGTATCA	1542	
Db	1441		TGTGGGTCA	CTCTGGA	AGCCACAGGGGCTGT	TATGAAGACACTCGCAGCAGTGTATCA	1500	
Qy	1543		CACGGCTGC	CTTCG	GACTTTTCCATTCG	CCAAAGAGGCCCTCTCTGGAGACAGGAATCTTTG	1602	

Db	1501	CACGGCTCTCTCGGACGCTTCCATCGCCAGAGAGCGCTCTCTGGAGACAGGAATCTTTG	1560
Qy	1603	CAAAAGTGTGAAAACACCACTGACGCAAGAAATTTCTGAAAGCCATAAATCAATTCCTTT	1652
Db	1561	CAAAAGTGTGAAAACACCACTGACGCAAGAAATTTCTGAAAGCCATAAATCAATTCCTTT	1620
Qy	1663	GTAGAGTGTGGCATCATTTATATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAA	1722
Db	1621	GTAGAGTGTGGCATTCATTTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCCAAGAA	1680
Qy	1723	TTTCAAGCTTTCTTCAAGGTAAAGCTTATATATCAACTCAGGGAACATCCCGGATTAC	1782
Db	1681	TTTCAAGCTTTCTTCAAGGTAAAGCTTATATATCAACTCAGGGAACATCCCGGATTAC	1740
Qy	1783	TATTTGACTTCTTTGAAACATTTGCCAATTTGTGCAAGTGCTCTGGACTTCATTTAAACTG	1842
Db	1741	TATTTGACTTCTTTGAAACATTTGCCAATTTGTGCAAGTGCTCTGGACTTCATTTAAACTG	1800
Qy	1843	GACTTTTATGGGGAGCTATGGCTTTCATCGGAAAAGGCTGCAGAAGACACAGGTGGGAATC	1902
Db	1801	GACTTTTATGGGGAGCTATGGCTTTCATCGGAAAAGGCTGCAGAAGACACAGGTGGGAATC	1860
Qy	1903	CACATGGAAGAGGCCCCAGAAACCTACATTTCCCAGCGGCTGTATCTTTGTTCTTCAAC	1962
Db	1861	CACATGGAAGAGGCCCCAGAAACCTACATTTCCCAGCGGCTGTATCTTTGTTCTTCAAC	1920
Qy	1963	TGGAAGCAGAAATTCAGGACTCTGGAGGTCAACATCCCGGATTTTCAGCAAGTTGAATAAG	2022
Db	1921	TGGAAGCAGAAATTCAGGACTCTGGAGGTCAACATCCCGGATTTTCAGCAAGTTGAATAAG	1980
Qy	2023	CAAGATATCATATCTCGGGGAAAATATTACGCTCTGCCACAAGCTCAGGCTGCAAAATA	2082
Db	1981	CAAGATATCATATCTCGGGGAAAATATTACGCTCTGCCACAAGCTCAGGCTGCAAAATA	2040
Qy	2083	AAGAGATGTGCTGGTGTGGCTGGAAGCCCTCAGTTTGGTCCCTCAGCACCTGTGAAGAACATT	2142
Db	2041	AAGAGATGTGCTGGTGTGGCTGGAAGCCCTCAGTTTGGTCCCTCAGCACCTGTGAAGAACATT	2100
Qy	2143	TATTTCTCATGTGTGGAAGCCAGTCCCTCACCATAGAGAGTGCAGGCGCATCATCATCT	2202
Db	2101	TATTTCTCATGTGTGGAAGCCAGTCCCTCACCATAGAGAGTGCAGGCGCATCATCATCT	2160
Qy	2203	GTAACAAACCTGAAAACCTTTGAGTATTTCTATGACCTACAGAAATCAACGGCTCCGG	2257
Db	2161	GTAACAAACCTGAAAACCTTTGAGTATTTCTATGACCTACAGAAATCAACGGCTCCGG	2215

```

RESULT 37
US-09-578-789-73
; Sequence 73, Application US/09578789
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Frederick pio
; APPLICANT: Adam Godzik
; TITLE OF INVENTION: Novel Card Polypeptides
; FILE REFERENCE: P-LJ 4141
; CURRENT APPLICATION NUMBER: US/09/578,789
; CURRENT FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 6900
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6900)
; OTHER INFORMATION: n = A,T,C or G
US-09-578-789-73

```

Query Match 63.3%; Score 1946; DB 22; Length 6900;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1996: Conservative 0; Mismatches 1; Indels 0;

QY 263 GTCCTTTTCATCAGACATCAGAGGACCTTGGAGATTTGGCTCAGATTTTAAAGGACT 322
Db 2679 GTCCTTTTCATCAGACATCAGAGGACCTTGGAGATTTGGCTCAGATTTTAAAGGACT 2738
QY 323 TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATTGACATTAATTT 382
Db 2739 TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATTGACATTAATTT 2798
QY 383 TTAACCTTGAAGACACCTTTCACAGAACTGTCTGTGGAGGAAGGACCAACACCATCACC 442
Db 2799 TTAACCTTGAAGACACCTTTCACAGAACTGTCTGTGGAGGAAGGACCAACACCATCACC 2858
QY 443 GCGTGGAGCAGCTCACCCTGAATGCGCTCTGACAGGCTCTTCAGAGCCCTGCAATATTG 502
Db 2859 GCGTGGAGCAGCTCACCCTGAATGCGCTCTGACAGGCTCTTCAGAGCCCTGCAATATTG 2918
QY 503 AAGGGGAATCTGGCAAGGCAAGTCCACTCTGTGCGACGCAATGGCCATGCTCTGGGGCT 562
Db 2919 AAGGGGAATCTGGCAAGGCAAGTCCACTCTGTGCGACGCAATGGCCATGCTCTGGGGCT 2978
QY 563 CCGGAAGTGCAGGCTCTGACGAAGTTCRAATTCGTCTTCTCCTCGCTCAGCAGGG 622
Db 2979 CCGGAAGTGCAGGCTCTGACGAAGTTCRAATTCGTCTTCTCCTCGCTCAGCAGGG 3038
QY 623 CCCAGGCTGGACTTTTGAACCCCTGTGATCAACTCTCGGATATACCTGGGCACATCA 682
Db 3039 CCCAGGCTGGACTTTTGAACCCCTGTGATCAACTCTCGGATATACCTGGGCACATCA 3098
QY 683 GGAAGCAGACATCATGCGCATGCTGTGAAGCTGCGGCAAGAGGGTCTTTTCTCTCTTG 742
Db 3099 GGAAGCAGACATCATGCGCATGCTGTGAAGCTGCGGCAAGAGGGTCTTTTCTCTCTTG 3158
QY 743 ATGCTCAATGAATTCAGGCCCCAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAA 802
Db 3159 ATGCTCAATGAATTCAGGCCCCAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAA 3218
QY 803 ACCACCGCTTCAAGAACATGGTCTACCTGACCACTACCACTGAGTGGCTGAGGCACATAC 862
Db 3219 ACCACCGCTTCAAGAACATGGTCTACCTGACCACTACCACTGAGTGGCTGAGGCACATAC 3278
QY 863 GGCAGTTTGGTGCCTGACTGCTGAGTGGGGATATGACAGAAGACAGCGCCAGGCTC 922
Db 3279 GGCAGTTTGGTGCCTGACTGCTGAGTGGGGATATGACAGAAGACAGCGCCAGGCTC 3338
QY 923 TCATCCGAGAGTCTGATCAAGGAGCTTGTGAAGGCTTGTGCTCCAAATTCAGAAAT 982
Db 3339 TCATCCGAGAGTCTGATCAAGGAGCTTGTGAAGGCTTGTGCTCCAAATTCAGAAAT 3398
QY 983 CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTGTGGTCACTCATCTGTGCAATCC 1042
Db 3399 CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTGTGGTCACTCATCTGTGCAATCC 3458
QY 1043 AGATGGGTGAAGTGAAGTTCACCTCTCACACAAACAAAGCTGTTCCATACCTTCTATG 1102
Db 3459 AGATGGGTGAAGTGAAGTTCACCTCTCACACAAACAAAGCTGTTCCATACCTTCTATG 3518
QY 1103 ATCTGTTGATACAGAAAACAAACACAAATGAAGTGGCTGCAAGTGAAGTCAATTC 1162
Db 3519 ATCTGTTGATACAGAAAACAAACACAAATGAAGTGGCTGCAAGTGAAGTCAATTC 3578
QY 1163 GGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTGTTCTCCCAAGTTTGATT 1222
Db 3579 GGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTGTTCTCCCAAGTTTGATT 3638
QY 1223 TCGAACTGCAGGATGTCTCAGCGTGAATGAGGATGTCTGCTGACAACTGGGCTCTCT 1282
Db 3639 TCGAACTGCAGGATGTCTCAGCGTGAATGAGGATGTCTGCTGACAACTGGGCTCTCT 3698
QY 1283 GTAATATACAGCTCAAGGTTCAAGCACAAGTATAAATCTTTTCAACAAGTCAATTCAGG 1342
Db 3699 GTAATATACAGCTCAAGGTTCAAGCACAAGTATAAATCTTTTCAACAAGTCAATTCAGG 3758

QY 1343 AGTACACAGCAGGAGAGACTCAGAGTTTATTTAGCTCTCATCAGCCAGGAGGTGA 1402
Db 3759 AGTACACAGCAGGAGAGACTCAGAGTTTATTTAGCTCTCATCAGCCAGGAGGTGA 3818
QY 1403 CCAAGCGAATGGTTACTTGCAGAAAATGGTTCCATTTCCGACATTTACATCCACTTATA 1462
Db 3819 CCAAGCGAATGGTTACTTGCAGAAAATGGTTCCATTTCCGACATTTACATCCACTTATA 3878
QY 1463 GCAGCCGCTCCGGTACACCTGTGGGTCTATCTGTGGAAGCCAGGCTGTGTTGAAGC 1522
Db 3879 GCAGCCGCTCCGGTACACCTGTGGGTCTATCTGTGGAAGCCAGGCTGTGTTGAAGC 3938
QY 1523 ACCTCGTAGCAGTGTATCAACACGCTGCTCTCTCGGACTTTCCATCGCCAAAGGCGCTC 1582
Db 3939 ACCTCGTAGCAGTGTATCAACACGCTGCTCTCTCGGACTTTCCATCGCCAAAGGCGCTC 3998
QY 1583 TCTGGAJACAGGAATCTTTGCAAAAGTGTGAAAACACACACCTGACGAAAGTCTGAAAG 1642
Db 3999 TCTGGAJACAGGAATCTTTGCAAAAGTGTGAAAACACACACCTGACGAAAGTCTGAAAG 4058
QY 1643 GCATAAJCATCAATTCCTTTAGAGTGTGCAATCCATTTATATCAAGAGAGTACATCCA 1702
Db 4059 GCATAAJCATCAATTCCTTTAGAGTGTGCAATCCATTTATATCAAGAGAGTACATCCA 4118
QY 1703 AATCAGCCTGAGCCAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATCAACT 1762
Db 4119 AATCAGCCTGAGCCAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATCAACT 4178
QY 1763 CAGGGAJCATCCCGATTTACTTATTTGACTTCTTTGAACATTTGCCAAATTTGCAAGTG 1822
Db 4179 CAGGGAJCATCCCGATTTACTTATTTGACTTCTTTGAACATTTGCCAAATTTGCAAGTG 4238
QY 1823 CTCTGGAJTTCTTCAAACTGGAGCTTTTATGGGGAGCTATGGCTTCATGGGAAAAGCTG 1882
Db 4239 CTCTGGAJTTCTTCAAACTGGAGCTTTTATGGGGAGCTATGGCTTCATGGGAAAAGCTG 4298
QY 1883 CAGAAGAJACAGGTGGAATCCACATGGAAGAGGCCCCAGAAACCTACATTTCCAGCAGGG 1942
Db 4299 CAGAAGAJACAGGTGGAATCCACATGGAAGAGGCCCCAGAAACCTACATTTCCAGCAGGG 4358
QY 1943 CTGTATCTCTTCAACTGGAAGCAGGAATTTAGAGCTCTCTGGAGTCACTCCGCGG 2002
Db 4359 CTGTATCTCTTCAACTGGAAGCAGGAATTTAGAGCTCTCTGGAGTCACTCCGCGG 4418
QY 2003 ATTTTCAAGJAAAGTGAATATACATATCTGGGAAAATATTCAGCTCTGCCA 2062
Db 4419 ATTTTCAAGJAAAGTGAATATACATATCTGGGAAAATATTCAGCTCTGCCA 4478
QY 2063 CAGCCTCAGGCTCAATTAAGAGATGCTGCTGGTGGCTGGAGGCTCAGTTTGTTC 2122
Db 4479 CAGCCTCAGGCTCAATTAAGAGATGCTGCTGGTGGCTGGAGGCTCAGTTTGTTC 4538
QY 2123 TCAGCACCCTGAAGAACATTTTCTCTCATGTTGGTGAAGCCAGTCCCTCACCATAGAG 2182
Db 4539 TCAGCACCCTGAAGAACATTTTCTCTCATGTTGGTGAAGCCAGTCCCTCACCATAGAG 4598
QY 2183 ATGAGAGGJACATCAGATCTGTAAACAACCTGAAACCTTGAGTATTTCATGACCTACAGA 2242
Db 4599 ATGAGAGGJACATCAGATCTGTAAACAACCTGAAACCTTGAGTATTTCATGACCTACAGA 4658
QY 2243 ATCAACGGJTGCCGGGT 2259
Db 4659 ATCAACGGJTGCCGGGT 4675

RESULT 38

US-09-579-240-73
; Sequence 73, Application US/09579240
; GENERAL INFORMATION:
; APPLICANT: John S. Reed
; APPLICANT: Fredrick Plo
; APPLICANT: Adam Godzik
; TITLE OF INVENTION: Novel Card-Domain Containing

; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4211
; CURRENT APPLICATION NUMBER: US/09/579,240
; CURRENT FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 6900
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6900)
; OTHER INFORMATION: n = A,T,C or G
US-09-579-240-73

Query Match	63.3%	Score	1946;	DB	22;	Length	6900;
Best Local Similarity	99.9%	Pred. No.	0;				
Matches	1996;	Conservative	0;	Mismatches	1;	Indels	0;
				Gaps	0;		
QY	263	GTCTTTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT	322				
DB	2679	GTCTTTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT	2738				
QY	323	TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATTTGACATTTATTT	382				
DB	2739	TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATTTGACATTTATTT	2798				
QY	383	TTAATTGAAAGACCTTTCACAGAACCTGTCTGTGGAGGAAGGACCAACACATCACCC	442				
DB	2799	TTAATTGAAAGACCTTTCACAGAACCTGTCTGTGGAGGAAGGACCAACACATCACCC	2858				
QY	443	GCCTGGAGCAGCTCACCTCTGAATGGCTCTCTGCAGGCTTTCAGAGCCCTTGCATCATATG	502				
DB	2859	GCCTGGAGCAGCTCACCTCTGAATGGCTCTCTGCAGGCTTTCAGAGCCCTTGCATCATATG	2918				
QY	503	AAGGGGAATCTGGCAAGGCAAGTCCACTCTGTCTGCAGCGCATTTGCCATGCTCTGGGGCT	562				
DB	2919	AAGGGGAATCTGGCAAGGCAAGTCCACTCTGTCTGCAGCGCATTTGCCATGCTCTGGGGCT	2978				
QY	563	CCGAAAGTGCAGGCTCTGACCAAGTTCAAATTCGTCCTCCCTCCCTCCCTCCCTCCCTCCCT	622				
DB	2979	CCGAAAGTGCAGGCTCTGACCAAGTTCAAATTCGTCCTCCCTCCCTCCCTCCCTCCCTCCCT	3038				
QY	623	CCCAGGTGGACTTTTGAACCCCTCTGTGATCAACTCCCTGGATATACCTGGCACAATCA	682				
DB	3039	CCCAGGTGGACTTTTGAACCCCTCTGTGATCAACTCCCTGGATATACCTGGCACAATCA	3098				
QY	683	GGAAAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGGCAGAGGGTTCTTTTCTCTCTTG	742				
DB	3099	GGAAAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGGCAGAGGGTTCTTTTCTCTCTTG	3158				
QY	743	ATGCTACATGAATTCAGCCCCAGAACTGCCCAGAAATCGAAGCCCTGATAAAGGAA	802				
DB	3159	ATGCTACATGAATTCAGCCCCAGAACTGCCCAGAAATCGAAGCCCTGATAAAGGAA	3218				
QY	803	ACCACCGCTTCAAGAACATGCTACCTGCTACCACTACCCTGAGTGGCTGAGGCACATAC	862				
DB	3219	ACCACCGCTTCAAGAACATGCTACCTGCTACCACTACCCTGAGTGGCTGAGGCACATAC	3278				
QY	863	GGCAGTTTGGTGCCTGACTGCTGAGGTGGGGGATATGACAGAGACAGCGCCCGAGGCTC	922				
DB	3279	GGCAGTTTGGTGCCTGACTGCTGAGGTGGGGGATATGACAGAGACAGCGCCCGAGGCTC	3338				
QY	923	TCATCCGAGAAGTCTGATCAAGGAGCTTGTGTAAGGCTTGTTCCTCCAAATTCAGAAAT	982				
DB	3339	TCATCCGAGAAGTCTGATCAAGGAGCTTGTGTAAGGCTTGTTCCTCCAAATTCAGAAAT	3398				
QY	983	CCAGGTGCTTGAGAAATCTCATGAAGACCCCTCTCTTTGGGTGATCATCTGTGCAATCC	1042				
DB	3399	CCAGGTGCTTGAGAAATCTCATGAAGACCCCTCTCTTTGGGTGATCATCTGTGCAATCC	3458				
QY	1043	AGATGGGTGAAAGTGAGTCCACTCTCACACAAACACACGCTGTTCCATACCTTCATATG	1102				

DB	3459	AGATGGGTGAAAGTGAGTCCACTCTCACACAAACAAACGCTGTTCCATACCTTCATG	3518				
QY	1103	ATCTGTTGATACAGAAAACAAACACACAAACATAAAGTGTGGCTGCAAGTCACTTCAATC	1162				
DB	3519	ATCTGTTGATACAGAAAACAAACACAAACATAAAGTGTGGCTGCAAGTCACTTCAATC	3578				
QY	1163	GGAGCCTGGACCCACTGTGGAGACCTAGCTCTGGAGGGTGTCTTCTCCACAAAGTTTGATT	1222				
DB	3579	GGAGCCTGGACCCACTGTGGAGACCTAGCTCTGGAGGGTGTCTTCTCCACAAAGTTTGATT	3638				
QY	1223	TCGAACCTGCAGGATGTGTCCAGCCTGAATGAGGATGTCTCTGACAACTGGGCTCTCTCT	1282				
DB	3639	TCGAACCTGCAGGATGTGTCCAGCCTGAATGAGGATGTCTCTGACAACTGGGCTCTCTCT	3698				
QY	1283	GTAATAATACAGCTCAAGGTTCAAGCCAAAGTATAAATCTTTTCACAAGTCATTCCAGG	1342				
DB	3699	GTAATAATACAGCTCAAGGTTCAAGCCAAAGTATAAATCTTTTCACAAGTCATTCCAGG	3758				
QY	1343	AGTACACAGCAGGACGAGACTCAGCAGTTTATTTGACCTCTCATGAGCCAGAGAGGTGA	1402				
DB	3759	AGTACACAGCAGGACGAGACTCAGCAGTTTATTTGACCTCTCATGAGCCAGAGAGGTGA	3818				
QY	1403	CCAAGGGAATGTACTTTCAGAAAATGTGTTTCCATTTTCGGACATTTACATCCACTTATA	1462				
DB	3819	CCAAGGGAATGTACTTTCAGAAAATGTGTTTCCATTTTCGGACATTTACATCCACTTATA	3878				
QY	1463	GCAGCCTGCTCCGCTACACCTGTGGTGCATCTGTGGAGCCACACAGGCTCTTATGAAGC	1522				
DB	3879	GCAGCCTGCTCCGCTACACCTGTGGTGCATCTGTGGAGCCACACAGGCTCTTATGAAGC	3938				
QY	1523	ACCTCGCAGCAGTGTATCAACACGCTGCTCTCGGACTTTTCCATGCCAAGAGGCTC	1582				
DB	3939	ACCTCGCAGCAGTGTATCAACACGCTGCTCTCGGACTTTTCCATGCCAAGAGGCTC	3998				
QY	1583	TCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACACACTGAGCAAGAAATTTCTGAAG	1642				
DB	3999	TCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACACACTGAGCAAGAAATTTCTGAAG	4058				
QY	1643	CCATAACATCAATCTCTTGTAGAGTGGCATCCATTTATATCAAGAGAGTACATCCA	1702				
DB	4059	CCATAACATCAATCTCTTGTAGAGTGGCATCCATTTATATCAAGAGAGTACATCCA	4118				
QY	1703	AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAGGTAAAAGCTTATATATCAACT	1762				
DB	4119	AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAGGTAAAAGCTTATATATCAACT	4178				
QY	1763	CAGGAAACATCCCGATTACTTATTTGACTTCTTTTGAACATTTGCCAAATTTGTGCAAGTG	1822				
DB	4179	CAGGAAACATCCCGATTACTTATTTGACTTCTTTTGAACATTTGCCAAATTTGTGCAAGTG	4238				
QY	1823	CTCTGGACTTCATTTAAACTGGACCTTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTG	1882				
DB	4239	CTCTGGACTTCATTTAAACTGGACCTTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTG	4298				
QY	1883	CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCAGAAACCTACATTTCCACAGAGG	1942				
DB	4299	CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCAGAAACCTACATTTCCACAGAGG	4358				
QY	1943	CTGTATCTTTTCTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGCTCACACTCCGGG	2002				
DB	4359	CTGTATCTTTTCTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGCTCACACTCCGGG	4418				
QY	2003	ATTTTCAGCAAGTTGAATGAAGCAAGATATCATATCTCTGGGGAATAATATTCAGCTCTGCCA	2062				
DB	4419	ATTTTCAGCAAGTTGAATGAAGCAAGATATCATATCTCTGGGGAATAATATTCAGCTCTGCCA	4478				
QY	2063	CAAGCCTCAGCTGCAATTAAGAGATGTGCTGTGGTGGAGGCTCAGTTTGGTCC	2122				
DB	4479	CAAGCCTCAGCTGCAATTAAGAGATGTGCTGTGGTGGAGGCTCAGTTTGGTCC	4538				
QY	2123	TCAGCACCTGTGAAGAACATTTTATCTCTCATGGTGGAGGCCAGTCCCTCACCATPAGAAG	2182				

Db 4539 TCAGCACCTTAAGAGACATTTATTCTCTCATGGTGAAGCCAGTCCCTCACCATAGAAG 4598
QY 2183 ATGAGAGGCACATCACATCTGTAAACAACTGAAACCTTGAAGCTTATTCATGACCTACAGA 2242
Db 4599 ATGAGAGGCACATCACATCTGTAAACAACTGAAACCTTGAAGCTTATTCATGACCTACAGA 4658
QY 2243 ATCAACGGCTGCCGGT 2259
Db 4659 ATCAACGGCTGCCGGT 4675
RESULT 39
US-09-686-347-73
; Sequence 73, Application US/09586347
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Stehlik, Christian
; TITLE OF INVENTION: Novel Card-Domain Containing
; ; FILE REFERENCE: P-LJ 4271
; ; CURRENT APPLICATION NUMBER: US/09/686,347
; ; PRIOR FILING DATE: 2000-10-10
; ; PRIOR APPLICATION NUMBER: US 09/579,240
; ; NUMBER OF SEQ ID NOS: 109
; ; SOFTWARE: FastSeq for Windows Version 4.0
; ; SEQ ID NO 73
; ; LENGTH: 6900
; ; TYPE: DNA
; ; ORGANISM: Homo Sapien
; ; FEATURE:
; ; NAME/KEY: misc_feature
; ; LOCATION: (1)...(6900)
; ; OTHER INFORMATION: n = A,T,C or G
US-09-686-347-73
Query Match 63.3%; Score 1946; DB 27; Length 6900;
Best Local Similarity 99.9%; Pred No. 0;
Matches 1996; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 263 GTCCTTTTCATCAGACATCAGAGGAGACTTGGACGATTTGGCTCAGGATTTAAGGACT 322
Db 2679 GTCCTTTTCATCAGACATCAGAGGAGACTTGGACGATTTGGCTCAGGATTTAAGGACT 2738
QY 323 TGTACCATACCCCATCTTTCTGAACTTTATGCCCTTGGTGAAGATATGACATTTATTT 382
Db 2739 TGTACCATACCCCATCTTTCTGAACTTTATGCCCTTGGTGAAGATATGACATTTATTT 2798
QY 383 TTAACCTGAAAGACCTTTCACAGAACCTGTCTGTGGAGGAGGACCAACACCATCACC 442
Db 2799 TTAACCTGAAAGACCTTTCACAGAACCTGTCTGTGGAGGAGGACCAACACCATCACC 2858
QY 443 GCGTGGAGGAGCTGACCCCTGAATGGCTCTCTGCAGGCTCTTCAGAGCCCTGCATCATTTG 502
Db 2859 GCGTGGAGGAGCTGACCCCTGAATGGCTCTCTGCAGGCTCTTCAGAGCCCTGCATCATTTG 2918
QY 503 AAGGGGAATCTGGCAAAGGCAAGTCCACATCTGTCTGCAGGCGCATTTGCCATGCTCTGGGGCT 562
Db 2919 AAGGGGAATCTGGCAAAGGCAAGTCCACATCTGTCTGCAGGCGCATTTGCCATGCTCTGGGGCT 2978
QY 563 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGCTCTTCTCCCGCTCTCAGCAGGG 622
Db 2979 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGCTCTTCTCCCGCTCTCAGCAGGG 3038
QY 623 CCAGGGTGGACTTTTGAACCCCTGTGATCAACTCTGATACCTGGATATACCTGGCACAATCA 682
Db 3039 CCAGGGTGGACTTTTGAACCCCTGTGATCAACTCTGATACCTGGATATACCTGGCACAATCA 3098
QY 683 GGNAGCAGACATTCATGGCCATGCTCTGAAAGCTGCGGCAGAGGGTTCTTTTCTCTCTTG 742

Db 3099 GGAAG:AGACATTCATGGCCATGCTGCTGAAAGCTGCGGAGAGGGTTCTTTTCTCTCTTG 3158
QY 743 ATGGC:ACAAATGAATTCAGAGCCCAAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAA 802
Db 3159 ATGGC:ACAAATGAATTCAGAGCCCAAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAA 3218
QY 803 ACCAC:GCTTCAAGAACATGGTCATGTCACCACTACCACTAGTGGCTGAGGCACATAC 862
Db 3219 ACCAC:GCTTCAAGAACATGGTCATGTCACCACTACCACTAGTGGCTGAGGCACATAC 3278
QY 863 GGCAG:TTGGTGGCCCTGACTGCTGAGGTGGGGATATGACAGAAAGACAGCCCGCAGGCTC 922
Db 3279 GGCAG:TTGGTGGCCCTGACTGCTGAGGTGGGGATATGACAGAAAGACAGCCCGCAGGCTC 3338
QY 923 TCATCC:GAGAAGTGTGATCAAGGAGCTTGCCTGAAGGCTTGTTCCTCCAAATTCAGAAAT 982
Db 3339 TCATCC:GAGAAGTGTGATCAAGGAGCTTGCCTGAAGGCTTGTTCCTCCAAATTCAGAAAT 3398
QY 983 CCAGGT:GCTTGAAGGAATCTCATGAAGACCCCTCTCTTTTGTGGTTCATCCTTGTGCAATCC 1042
Db 3399 CCAGGT:GCTTGAAGGAATCTCATGAAGACCCCTCTCTTTTGTGGTTCATCCTTGTGCAATCC 3458
QY 1043 AGATGG:GTGAAAGTGAATTCCTCACTCTCACACAAAACAAACGCTGTTCCTCATACCTTCTATG 1102
Db 3459 AGATGG:GTGAAAGTGAATTCCTCACTCTCACACAAAACAAACGCTGTTCCTCATACCTTCTATG 3518
QY 1103 ATCTGT:IGATACAGAAAAACAAACACAAATATAAGGTGTGGCTGCAAGTGAAGTTCATTC 1162
Db 3519 ATCTGT:IGATACAGAAAAACAAACACAAATATAAGGTGTGGCTGCAAGTGAAGTTCATTC 3578
QY 1163 GGAGCC:GGACCACTGTGGAGACCTAGCTCTGGAGGCTGTGTTCTCCCAAGTTTGAAT 1222
Db 3579 GGAGCC:GGACCACTGTGGAGACCTAGCTCTGGAGGCTGTGTTCTCCCAAGTTTGAAT 3638
QY 1223 TCGAAC:TCAGGATGTGTCAGGCTGAAGGAGTCTCTGCTGCAAACTGGCTCCTCT 1282
Db 3639 TCGAAC:TCAGGATGTGTCAGGCTGAAGGAGTCTCTGCTGCAAACTGGCTCCTCT 3698
QY 1343 AGTAC:AGCAGGACGAAGACTCAGAGTTTATGAGTCTCATGAGCAGAGGAGGTGA 1402
Db 3759 AGTAC:AGCAGGACGAAGACTCAGAGTTTATGAGTCTCATGAGCAGAGGAGGTGA 3818
QY 1403 CCAAGG:GAATGGTTACTTGCAGAAAATGGTTTCCATTTCCGACATTCATCCACTATA 1462
Db 3819 CCAAGG:GAATGGTTACTTGCAGAAAATGGTTTCCATTTCCGACATTCATCCACTATA 3878
QY 1463 GCAGCC:GCTCCGGTACACCTGTGGGTCTATCTGTGGAAGCCACAGGGGCTGTATGAAGC 1522
Db 3879 GCAGCC:GCTCCGGTACACCTGTGGGTCTATCTGTGGAAGCCACAGGGGCTGTATGAAGC 3938
QY 1523 AGCTCG:AGCAGTGTATCAACACAGGCTGCTTCTCGGACTTTTCATCGCAAGAGGCTC 1582
Db 3939 AGCTCG:AGCAGTGTATCAACACAGGCTGCTTCTCGGACTTTTCATCGCAAGAGGCTC 3998
QY 1583 TCTGGA:ACAGAAATCTTTTGCAAAAGTGTGAAAACACCACTGAGCAAGAAATTCCTCAAG 1642
Db 3999 TCTGGA:ACAGAAATCTTTTGCAAAAGTGTGAAAACACCACTGAGCAAGAAATTCCTCAAG 4058
QY 1643 CCATAA:CATCAATCTTTGTAGAGTGGGATCCATTTATATCAAGAGATACATCCA 1702
Db 4059 CCATAA:CATCAATCTTTGTAGAGTGGGATCCATTTATATCAAGAGATACATCCA 4118
QY 1703 AATCAG:CTGAGCCCAAGAAATTTGAGCTTCTTCAAGGTAAAGCTTATATCAACT 1762
Db 4119 AATCAG:CTGAGCCCAAGAAATTTGAGCTTCTTCAAGGTAAAGCTTATATCAACT 4178
QY 1763 CAGGAA:ATCCCGGATTTACTTATTTGACTTCTTTGAACATTTGCCAATTTGTGCAAGTG 1822

Db 4179 CAGGGAACATCCCCGATFACCTATTGAGCTCTTTTGAACATTTGCCCAATTTGTGCAAGTG 4238
Qy 1823 CTCGTGACTTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTG 1882
Db 4239 CTCGTGACTTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAGGCTG 4298
Qy 1883 CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAACCTACATTTCCACGAGGG 1942
Db 4299 CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAACCTACATTTCCACGAGGG 4358
Qy 1943 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGAGCTCTGAGGTTCACATTCGCGG 2002
Db 4359 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGAGCTCTGAGGTTCACATTCGCGG 4418
Qy 2003 ATTTTCAGCAAGTTGAATGAAGCAAGATATCACATATCTGGGAAATATTCAGCTCTGCCA 2062
Db 4419 ATTTTCAGCAAGTTGAATGAAGCAAGATATCACATATCTGGGAAATATTCAGCTCTGCCA 4478
Qy 2063 CAAGCCTCAGGCTGCAAAATAAAGAGATGCTGTGGTGGGAAAGCCCTCAGTTTGGTCC 2122
Db 4479 CAAGCCTCAGGCTGCAAAATAAAGAGATGCTGTGGTGGGAAAGCCCTCAGTTTGGTCC 4538
Qy 2123 TCAGCACCTGTAAGAACATTTATCTCTCATGTTGGTGGAGCCAGTCCCTCCACCATAGAG 2182
Db 4539 TCAGCACCTGTAAGAACATTTATCTCTCATGTTGGTGGAGCCAGTCCCTCCACCATAGAG 4598
Qy 2183 ATGAGAGGCATCATCATCTGTAAACAACTGAAACCTTGAGTATTCATGACCTACACAGA 2242
Db 4599 ATGAGAGGCATCATCATCTGTAAACAACTGAAACCTTGAGTATTCATGACCTACACAGA 4658
Qy 2243 ATCAACGGCTGCGGGT 2259
Db 4659 ATCAACGGCTGCGGGT 4675

RESULT 40

US-09-557-676-906

; Sequence 906, Application US/09557676

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith

; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-136

; CURRENT APPLICATION NUMBER: US/09/557,676

; CURRENT FILING DATE: 2000-04-25

; NUMBER OF SEQ ID NOS: 986

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 906

; LENGTH: 4098

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-557-676-906

Query Match 63.3%; Score 1945; DB 22; Length 4098;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1995; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 263 GTCTTTTTCATCAGACATCAGAGGAGACTTGGCAGTATGGCTCAGGATTTAAAGGACT 322
Db 275 GTCTTTTTCATCAGACATCAGAGGAGACTTGGCAGTATGGCTCAGGATTTAAAGGACT 334
Qy 323 TGTACCATACCCACTTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATATT 382
Db 335 TGTACCATACCCACTTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATATT 394
Qy 383 TTAACCTGAAAGACACCTTCACAGAACCTGTCCTGTGGAGGAAGCAACACCATCACC 442
Db 395 TTAACCTGAAAGACACCTTCACAGAACCTGTCCTGTGGAGGAAGCAACACCATCACC 454
Qy 443 CGGTGGACAGTGAACCTGATGGCTCTCCAGGCTCTTCAGAGCCCTTCATCAT 502
Db 455 CGGTGGACAGTGAACCTGATGGCTCTCCAGGCTCTTCAGAGCCCTTCATCAT 514
Qy 503 AAGGGGAATCTGGGAAAGGCAAGTCCACTCTGCTGCAGCGCATTTGCCATGCTGGGCT 562

Db 515 AAGGGGAATCTGGGAAAGGCAAGTCCACTCTGCTGCAGCGCATTTGCCATGCTCTGGGCT 574
Qy 563 CGGGAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTTCTTCTCCGTCGTCACAGGG 622
Db 575 CGGGAAGTGAAGGCTCTGACCAAGTTCAAAATTCGTTCTTCTCCGTCGTCACAGGG 634
Qy 623 CCCAGGGTGGACTTTTGTAAACCCCTCTGTGATCAAACTCTCTGGATATACCTGGCACAATCA 682
Db 635 CCCAGGGTGGACTTTTGTAAACCCCTCTGTGATCAAACTCTCTGGATATACCTGGCACAATCA 694
Qy 683 GGAAGCAGACATTCATGCGCATGCTGTAAGCTGCGGAGAGGGTCTTTTCTCTCTG 742
Db 695 GGAAGCAGACATTCATGCGCATGCTGTAAGCTGCGGAGAGGGTCTTTTCTCTCTG 754
Qy 743 ATGGCTACAAATTCAGCCCGAGAGCTGCCAGAAATCGAAGCCCTGATAAAGGAA 802
Db 755 ATGGCTACAAATTCAGCCCGAGAGCTGCCAGAAATCGAAGCCCTGATAAAGGAA 814
Qy 803 ACCACCGCTTCAAGAACATGCTCATCGTCACCACTACCACTGAGTGCCTGAGGCAACATAC 862
Db 815 ACCACCGCTTCAAGAACATGCTCATCGTCACCACTACCACTGAGTGCCTGAGGCAACATAC 874
Qy 863 GGCAGTTTGGTCCCTGACTGCTGAGGTGGGGATATGACAGAAGACAGCGCCAGGCTC 922
Db 875 GGCAGTTTGGTCCCTGACTGCTGAGGTGGGGATATGACAGAAGACAGCGCCAGGCTC 934
Qy 923 TCATCCGAGAGTGTGATCAAGAGGCTTGTGTAAGGCTTGTGCTCCAAATTCAGAAAT 982
Db 935 TCATCCGAGAGTGTGATCAAGAGGCTTGTGTAAGGCTTGTGCTCCAAATTCAGAAAT 994
Qy 983 CCAGTGTCTGAGGAATCTCATGAAGAGCCCTCTCTTGTGGTGCATCACTTGTGCAATCC 1042
Db 995 CCAGTGTCTGAGGAATCTCATGAAGAGCCCTCTCTTGTGGTGCATCACTTGTGCAATCC 1054
Qy 1043 AGATGGTGAAGTGAAGTTCACACTCTCACACAAACAAACAGCTGTTCATACCTTCTATG 1102
Db 1055 AGATGGTGAAGTGAAGTTCACACTCTCACACAAACAAACAGCTGTTCATACCTTCTATG 1114
Qy 1103 ATCTCTTATACAGAAACAAACAAACAAACAAAGTGTGGCTGCAAGTGAAGTTCATTC 1162
Db 1115 ATCTCTTATACAGAAACAAACAAACAAACAAAGTGTGGCTGCAAGTGAAGTTCATTC 1174
Qy 1163 GGAGCTTGACACCTGTGGAGACCTAGTCTCGAGGGTGTGTTCTCCCAAGTGTGATT 1222
Db 1175 GGAGCTTGACACCTGTGGAGACCTAGTCTCGAGGGTGTGTTCTCCCAAGTGTGATT 1234
Qy 1223 TCGAACTGCAGGATGTCTCCAGCGTGAATGAGGATGTCTGCTGACAACTGGGCTCCTCT 1282
Db 1235 TCGAACTGCAGGATGTCTCCAGCGTGAATGAGGATGTCTGCTGACAACTGGGCTCCTCT 1294
Qy 1283 GTAAATATACAGCTCAAGGTTCAAGCCAAAGATATAAATTCCTTCACAGTCAATTCAGG 1342
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Qy 1343 AGTACACAGCAGGAGCAAGACTCAGCAGTTTATTCACGCTCTCATGAGCCAGAGGAGTGA 1402
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Qy 1403 CCAAGGGGAATGGTTTACTTTCAGAAATGGTTTCCATTTTCGACATTTACATCCACTTATA 1462
Db 1415 CCAAGGGGAATGGTTTACTTTCAGAAATGGTTTCCATTTTCGACATTTACATCCACTTATA 1474
Qy 1463 GCAGCCTGCTCGGTGACACCTGTGGGTGATCTGTGGAAGCCACAGGGCTGTATTAAGC 1522
Db 1475 GCAGCCTGCTCGGTGACACCTGTGGGTGATCTGTGGAAGCCACAGGGCTGTATTAAGC 1534
Qy 1523 ACCTGCAGCAGTGTATCAACACGGCTGCCTTCTCGGACTTTTCCATTCGCAAGAGGCTC 1582
Db 1535 ACCTGCAGCAGTGTATCAACACGGCTGCCTTCTCGGACTTTTCCATTCGCAAGAGGCTC 1594
Qy 1583 TCTGAGACAGGAATCTTTTGAAGTGTGAAGAAACACCACTGAGCAAGAAATTCGAAAG 1642

Db 1595 TCCTGGAGACAGGAATCTTTGCAAGGTGTGAAAAACACCACCTAGCAAGAAATTTCTGAAAG 1654
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Db 1655 CCATAAACATCAATCTCTTTGTAGAGTGTGGCATCTTATATCAAGAGGTACATCCA 1714
QY 1703 AATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT 1762
Db 1715 AATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATATCAACT 1774
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Db 1775 CAGGGAACATCCCGGATTTACTTTTGAACCTTTCTTTGAACATTTTCCCAATTTGCAAGTG 1834
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QY 1883 CAGAAGACACAGGTGAATCCACATGGAAGAGGCCCGGAGAACTACATCCCGAGAGG 1942
Db 1895 CAGAAGACACAGGTGAATCCACATGGAAGAGGCCCGGAGAACTACATCCCGAGAGG 1954
QY 1943 CTGTATCTTTGTTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTCACACTCCGGG 2002
Db 1955 CTGTATCTTTGTTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTCACACTCCGGG 2014
QY 2003 ATTTAGCAAGTTGAATAAGCAAGATATACATATCTGGGGAATAATTCAGCTCTGCCA 2062
Db 2015 ATTTAGCAAGTTGAATAAGCAAGATATACATATCTGGGGAATAATTCAGCTCTGCCA 2074
QY 2063 CAAGCCTCAGGCTGCAAAATAAGAGATGTCTGTGGCTGGAAGCCTCAGTTTGGTCC 2122
Db 2075 CAAGCCTCAGGCTGCAAAATAAGAGATGTCTGTGGCTGGAAGCCTCAGTTTGGTCC 2134
QY 2123 TCAGCAGCTGTAAGAACATTTATCTCTCATGTGGAAGCAGTCCCTCACCATAGAAG 2182
Db 2135 TCAGCAGCTGTAAGAACATTTATCTCTCATGTGGAAGCAGTCCCTCACCATAGAAG 2194
QY 2183 ATGAGAGGCACATCAGATCTGTAACAACTGAAACCTTGAGTATTTATGAGCTTACAGA 2242
Db 2195 ATGAGAGGCACATCAGATCTGTAACAACTGAAACCTTGAGTATTTATGAGCTTACAGA 2254
QY 2243 ATCAAGGCTGCCGGG 2258
Db 2255 ATCAAGGCTGCCGGG 2270

RESULT 41

US-09-557-676-912
; Sequence 912, Application US/09557676

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith

; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-136

; CURRENT APPLICATION NUMBER: US/09/557,676

; CURRENT FILING DATE: 2000-04-25

; NUMBER OF SEQ ID NOS: 986

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 912

; LENGTH: 4098

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-557-676-912

Query Match

Best Local Similarity 53.3%; Score 1945; DB 22; Length 4098;

Matches 1995; Conservative 0; Pred. No. 0;

Mismatches 1; Indels 0; Gaps 0;

QY 263 GTCTTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 332

Db 275 GTCTTTTCATCAGACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 334

QY 323 TGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGTGGAAGATATTGACATTATTT 382

Db 335 TGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGTGGAAGATATTGACATTATTT 394
QY 383 TTAACCTGAAAAGCAGCTTTTACAGAAACCTGTCTGTGGAGAAAGGACCAACACCATCACC 442
Db 395 TTAACCTGAAAAGCAGCTTTTACAGAAACCTGTCTGTGGAGAAAGGACCAACACCATCACC 454
QY 443 GCCTGAGCAGCTGAGCCCTGAAATGGCTCTCTGAGGCTCTTTCAGAGCCCTGCATCATTTG 502
Db 455 GCCTGAGCAGCTGAGCCCTGAAATGGCTCTCTGAGGCTCTTTCAGAGCCCTGCATCATTTG 514
QY 503 AAGGGGAATCTGCAAGAGCAAGTCCACCTCTGCTGAGAGCAATTTGCGATCTCTGGGCT 562
Db 515 AAGGGGAATCTGCAAGAGCAAGTCCACCTCTGCTGAGAGCAATTTGCGATCTCTGGGCT 574
QY 563 CCGGAAAGTGCAGAGCTCTGACCAAGTTCAAATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 622
Db 575 CCGGAAAGTGCAGAGCTCTGACCAAGTTCAAATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 634
QY 623 CCGAGGATGAGCTTTTGAACCTCTGTGATCAACTCTCTGGATATATCTGGGACATCA 682
Db 635 CCGAGGATGAGCTTTTGAACCTCTGTGATCAACTCTCTGGATATATCTGGGACATCA 694
QY 683 GGAAGCAGCATTTATGGCCATCTGCTGAAGCTGGGCGAGAGGTTCTTTCTCTCTCTCT 742
Db 695 GGAAGCAGCATTTATGGCCATCTGCTGAAGCTGGGCGAGAGGTTCTTTCTCTCTCTCT 754
QY 743 ATGGCTCAATGAATTCAGCCCGAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAA 802
Db 755 ATGGCTCAATGAATTCAGCCCGAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAAA 814
QY 803 ACCACCTCTTCAAGAACATCTGCTCATCTACCACCTACCACTGAGTGCCTGAGGACATAC 862
Db 815 ACCACCTCTTCAAGAACATCTGCTCATCTACCACCTACCACTGAGTGCCTGAGGACATAC 874
QY 863 GGCAGTCTGCTGCTCTGAGTGGGGATATGACAGAAAGACAGCGCCAGGCTC 922
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QY 923 TCATCCAGAGAGTCTGATCAAGGCTTGTCTGAAGCTTGTTCCTCAATTTCAAGAAAT 982
Db 935 TCATCCAGAGAGTCTGATCAAGGCTTGTCTGAAGCTTGTTCCTCAATTTCAAGAAAT 994
QY 983 CAGGCTCTTGAAGAACATCTGATGAAGCCCTCTCTTTGTGGTCATCAGTGTGCAATCC 1042
Db 995 CAGGCTCTTGAAGAACATCTGATGAAGCCCTCTCTTTGTGGTCATCAGTGTGCAATCC 1054
QY 1043 AGATGGCTGAAGTGTGCTCTCACACAAACAGCTGTGCTCCATACCTTCTATG 1102
Db 1055 AGATGGCTGAAGTGTGCTCTCACACAAACAGCTGTGCTCCATACCTTCTATG 1114
QY 1103 ATCTGTTATACAGAAAAACAAACACAAACATAAAGGTGTGGCTGCAAGTGACTTCAATC 1162
Db 1115 ATCTGTTATACAGAAAAACAAACACAAACATAAAGGTGTGGCTGCAAGTGACTTCAATC 1174
QY 1163 GGAGCCTGAGCCACTGTGGAGACCTAGCTCTGGAGGCTGTGTCTCCCAAGTTTGATT 1222
Db 1175 GGAGCCTGAGCCACTGTGGAGACCTAGCTCTGGAGGCTGTGTCTCCCAAGTTTGATT 1234
QY 1223 TCGAACTTCAGGATGTCCAGGCTGAATGAGGATGTCTGCTGCAACTGGGCTCTCT 1282
Db 1235 TCGAACTTCAGGATGTCCAGGCTGAATGAGGATGTCTGCTGCAACTGGGCTCTCT 1294
QY 1283 GTAATAATACAGCTCAAGGTTCAAGCCAAAGTATAAATTTCTTTCACAAAGTTCATCCAG 1342
Db 1295 GTAATAATACAGCTCAAGGTTCAAGCCAAAGTATAAATTTCTTTCACAAAGTTCATCCAG 1354
QY 1343 AGTACACAGCAGGACGAAGACTCAGCAGTTTATTGACGCTCTCATGAGCCAGAGAGGTGA 1402
Db 1355 AGTACACAGCAGGACGAAGACTCAGCAGTTTATTGACGCTCTCATGAGCCAGAGAGGTGA 1414
QY 1403 CCAAGGGTAATGTTTACTTGCAGAAAATGGTTTCCATTTTCGGACATTATACATCCACTATA 1462

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Db 1415 CCAAGGGGAATGGTTACTTTCGAGAAAATGGTTTCCATTTCGGACATTACATCCACTTATA 1474
QY 1463 GCAGCTGCTCGGTACACTGCGGCTCATCTCTGGAAGCCACCAGGGGCTGTATGAAGC 1522
Db 1475 GCAGCTGCTCGGTACACTGCGGCTCATCTCTGGAAGCCACCAGGGGCTGTATGAAGC 1534
QY 1523 ACCTCGCAGCAGTGTATCAACAGCGGTGCTTCTCGGACTTTCCATCGCCAGAGGCCCTC 1582
Db 1535 ACCTCGCAGCAGTGTATCAACAGCGGTGCTTCTCGGACTTTCCATCGCCAGAGGCCCTC 1594
QY 1583 TCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCCTAGTGAAGAAATCTCTCAAAG 1642
Db 1595 TCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCCTAGTGAAGAAATCTCTCAAAG 1654
QY 1643 CCATTAACATCAATTCCTTTGTAGAGTGTGGCATCTTATATCAAGAGAGTACATCCA 1702
Db 1655 CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCTTATATCAAGAGAGTACATCCA 1714
QY 1703 AATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAGGTAAAACTTTATATCAACT 1762
Db 1715 AATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTTCAAGGTAAAACTTTATATCAACT 1774
QY 1763 CAGGGAACATCCCGGATTAATTTGACTTCTTTGAAACATTTGCCAAATTTGTGCAAGTG 1822
Db 1775 CAGGGAACATCCCGGATTAATTTGACTTCTTTGAAACATTTGCCAAATTTGTGCAAGTG 1834
QY 1823 CTCTGACATTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1882
Db 1835 CTCTGACATTCATTAACCTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1894
QY 1883 CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAAACCTACATTCCAGCAGGG 1942
Db 1895 CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAAACCTACATTCCAGCAGGG 1954
QY 1943 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGAGGTCACACTCCGGG 2002
Db 1955 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGAGGTCACACTCCGGG 2014
QY 2003 ATTTACAGCAAGTTGAATAAGCAAGATATCACATATCTGSGGAAAATATTCAGCTCTGCCA 2062
Db 2015 ATTTACAGCAAGTTGAATAAGCAAGATATCACATATCTGSGGAAAATATTCAGCTCTGCCA 2074
QY 2063 CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGGCTGGAAGCCCTCAGTTTGGTCC 2122
Db 2075 CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGGCTGGAAGCCCTCAGTTTGGTCC 2134
QY 2123 TCAGCACCCTGTAGAACATTTATTTCTCATGTGTGGAAGCCAGTCCCTCACCATAGAAG 2182
Db 2135 TCAGCACCCTGTAGAACATTTATTTCTCATGTGTGGAAGCCAGTCCCTCACCATAGAAG 2194
QY 2183 ATGAGAGGCACATCACATCTGTAACAAACCTGAAAACCTTGAGTATTTCATGACCTACAGA 2242
Db 2195 ATGAGAGGCACATCACATCTGTAACAAACCTGAAAACCTTGAGTATTTCATGACCTACAGA 2254
QY 2243 ATCAACGGCTGCCGGG 2258
Db 2255 ATCAACGGCTGCCGGG 2270
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RESULT 42

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US-10-042-938-906
; Sequence 906, Application US/10042938
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith
; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-136
; CURRENT APPLICATION NUMBER: US/10/042,938
; PRIOR FILING DATE: 2002-01-09
; PRIOR FILING DATE: 09/557,676
; PRIOR FILING DATE: 2000-APR-25
; NUMBER OF SEQ ID NOS: 986
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 906
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; LENGTH: 4098
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-042-938-906

Query Match 63.3%; Score 1945; DB 38; Length 4098;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1995; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 263 GTCCTTTTTCATCAGACATCAGAGGAGACTTGGACCAATTTGGCTCAGGATTTTAAAGGACT 322
Db 275 GTCCTTTTTCATCAGACATCAGAGGAGACTTGGACCAATTTGGCTCAGGATTTTAAAGGACT 334
QY 323 TGTACCATACCCCATCTTTTCTGAACTTTATCCCTTGGTGAAGATATTGACATTATTT 382
Db 335 TGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGGTGAAGATATTGACATTATTT 394
QY 383 TTTAACTTGAAGACACCTTTACAGAAACCTGTCTCTGGAGGAAGGACCACACCATCAC 442
Db 395 TTTAACTTGAAGACACCTTTACAGAAACCTGTCTCTGGAGGAAGGACCACACCATCAC 454
QY 443 GCGTGAGCAGCTGACCCCTGAATGGCTCTCTGCAGGCTCTTCAGAGCCCTTGCATCATTTG 502
Db 455 GCGTGAGCAGCTGACCCCTGAATGGCTCTCTGCAGGCTCTTCAGAGCCCTTGCATCATTTG 514
QY 503 AAGGGGAATCTGSCAAAGGCAAGTCCACCTCTGCTGCAGGCAATTTGCCATGCTCTGGGGCT 562
Db 515 AAGGGGAATCTGSCAAAGGCAAGTCCACCTCTGCTGCAGGCAATTTGCCATGCTCTGGGGCT 574
QY 563 CCGAAAGTGCAGGCTCTGACCAAGTTCAAAATTCCTTCTTCCCTCCGTTCTCAGCAGGG 622
Db 575 CCGAAAGTGCAGGCTCTGACCAAGTTCAAAATTCCTTCTTCCCTCCGTTCTCAGCAGGG 634
QY 623 CCAGGGTGAGCTTTTGTAAACCCCTGTGTGATCAACTCTCTGGATATACCTGGCACAATCA 682
Db 635 CCAGGGTGAGCTTTTGTAAACCCCTGTGTGATCAACTCTCTGGATATACCTGGCACAATCA 694
QY 683 GGAAGCAGACATTCATGTGGCATCTGCTGAAGCTGCGGAGAGGGTCTTTTCTCTCTTG 742
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Db 755 ATGGCTACAATGAATTCAGAGCCCAAGAACTGCCCAGAAATCGAAGCCCTGTATAAGGAAA 814
QY 803 ACCACCGCTTCAGAACATGGTTCATGTCACCACTACCACTGAGTGCCTGAGGCACATAC 862
Db 815 ACCACCGCTTCAGAACATGGTTCATGTCACCACTACCACTGAGTGCCTGAGGCACATAC 874
QY 863 GGCAGTTTGGTGGCCCTGACTGCTGAGTGGGGATATGACAGAAAGACAGCGCCAGGCTC 922
Db 875 GGCAGTTTGGTGGCCCTGACTGCTGAGTGGGGATATGACAGAAAGACAGCGCCAGGCTC 934
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Db 995 CCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTTGTGGTCACTACTTGTGCAATCC 1054
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Db 1055 AGATGGGTGAAAGTGAATTCCTCACTCTCACACAAACACGCTGTTCATACCTTCTATG 1114
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Db 1535 ACCTCCAGAGTGTATCAACAGGCTGCTCTCGAGCTTTCATCGCCACAGAGGCTC 1594
QY 1583 TCTGGAGACAGGAATCTTTGCAAGTGTGAAACACCACTGAGCAAGAAATTTCTCAAG 1642
Db 1595 TCTGGAGACAGGAATCTTTGCAAGTGTGAAACACCACTGAGCAAGAAATTTCTCAAG 1654
QY 1643 CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGATACATCCA 1702
Db 1655 CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGATACATCCA 1714
QY 1703 AATCAGCCCTGAGCAGAAATTTGAAGCTTCTTTCAAGGTAAAGCTTATATCAACT 1762
Db 1715 AATCAGCCCTGAGCAGAAATTTGAAGCTTCTTTCAAGGTAAAGCTTATATCAACT 1774
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Db 1775 CAGGGAACATCCCGATTACTTATTTGACTTCTTTGAACATTTGCCAATTTGTGCAAGTG 1834
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QY 1883 CAGAAGACACAGGTGGAATTCACATGGAAGAGGCCCCAGAAACCTTACATTTCCAGCAGG 1942
Db 1895 CAGAAGACACAGGTGGAATTCACATGGAAGAGGCCCCAGAAACCTTACATTTCCAGCAGG 1954
QY 1943 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTCACTCCGG 2002
Db 1955 CTGTATCTTTGTTCTTCAACTGGAAGCAGGAATTCAGGACTCTGGAGGTCACTCCGG 2014
QY 2003 ATTTACAGCAAGTTGAATAAGCAAGATATCACATATCTGGGAAAATATTTCAGCTCTGCCA 2062
Db 2015 ATTTACAGCAAGTTGAATAAGCAAGATATCACATATCTGGGAAAATATTTCAGCTCTGCCA 2074
QY 2063 CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGTGCTGGAAGCCTCAGTTGGTCC 2122
Db 2075 CAAGCCTCAGGCTGCAAAATAAGAGATGTGCTGGTGTGCTGGAAGCCTCAGTTGGTCC 2134

QY 2123 TCAGCACCTGTAGAACATTTATTTCTCTCATGGTGAAGCCAGTCCCTCACCATAGAAG 2182
Db 2135 TCAGCACCTGTAGAACATTTATTTCTCTCATGGTGAAGCCAGTCCCTCACCATAGAAG 2194
QY 2183 ATGAGAGGCACATCACATCTGTAAACAACTGAAACCTTGAATTTATGATGACCTACAGA 2242
Db 2195 ATGAGAGGCACATCACATCTGTAAACAACTGAAACCTTGAATTTATGATGACCTACAGA 2254
QY 2243 ATCAACGGCTGCGGG 2258
Db 2255 ATCAACGGCTGCGGG 2270
RESULT 44
US-10-029-386-25135/c
; Sequence 25135, Application US/10029386
; GENERAL INFORMATION:
; APPLICANT: Penn, David R.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
; FILE REFERENCE: AEOmica-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 25135
; LENGTH: 2002
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121653.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.36
; OTHER INFORMATION: EST_HUMAN HIT: AV656315.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q9JIB6, EVALUE 2.00e-40
; OTHER INFORMATION: NT HIT: g115296399, EVALUE 0.00e+00
US-10-029-386-25135

Query Match 60.0%; Score 1844; DB 38; Length 2002;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1994; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 263 GTCTTTTTCATCAGACATCAGAGGAGACTTGGACCATTTGGCTCAGGATTTAAAGSACT 322
Db 2000 GTCTTTTTCATCAGACATCAGAGGAGACTTGGACCATTTGGCTCAGGATTTAAAGSACT 1941
QY 323 TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATTGACATTATTT 382
Db 1940 TGTACCATACCCCATCTTTTCTGAACCTTTATCCCTTGGTGAAGATATTGACATTATTT 1881
QY 383 TTAACCTGAAAGCACCTTCACAGAACCCTGCTGTGGAGGAAGGACCAACCATCACC 442
Db 1880 TTAACCTGAAAGCACCTTCACAGAACCCTGCTGTGGAGGAAGGACCAACCATCACC 1821
QY 443 GGTGAGCAGCTGACCCCTGAATGGCTCCTGCAGGCTCTTCAGAGCCCTGCATCATTTG 502
Db 1820 GGTGAGCAGCTGACCCCTGAATGGCTCCTGCAGGCTCTTCAGAGCCCTGCATCATTTG 1761
QY 503 AAGGGAAATCTGGCAAGGCAAGTCCACCTCTGCTGAGGCGCATTTGCATGCTCTGGGGCT 562
Db 1760 AAGGGAAATCTGGCAAGGCAAGTCCACCTCTGCTGAGGCGCATTTGCATGCTCTGGGGCT 1701
QY 563 CCGGAAAGTGCAGGCTCTGACCAAGTTCAAATTCGCTCTTCTCTCCCTCCGCTCAGCAGG 632
Db 1700 CCGGAAAGTGCAGGCTCTGACCAAGTTCAAATTCGCTCTTCTCTCCCTCCGCTCAGCAGG 1641
QY 623 CCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACAATCA 682
Db 1640 CCCAGGCTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGGATATACCTGGCACAATCA 1581
QY 683 GGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGCGGAGAGGGTTCTTTTCTCTCTTG 742

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Db 1580 GGAAGCAGACATTCATGCCCATGCTGTAAGCTGGCGCAGAGGGTCTTTTCTCTCTTG 1521
QY 743 ATGGCTACAATGAATTAAGCCCGCAGAACTGCCAGAAATCGAAGCCCTGTATAAAGGAA 802
Db 1520 ATGGCTACAATGAATTAAGCCCGCAGAACTGCCAGAAATCGAAGCCCTGTATAAAGGAA 1461
QY 803 ACCACCGCTTCAAGAACATGTCTATCGTCAACCTACCATCGAGTGGCTGAGGCACATAC 862
Db 1460 ACCACCGCTTCAAGAACATGTCTATCGTCAACCTACCATCGAGTGGCTGAGGCACATAC 1401
QY 863 GGCAGTTTGGTGGCCCTGACTGCTGAGTGGGGGATATGACAGAGAGACAGCGCCACAGGCTC 922
Db 1400 GGCAGTTTGGTGGCCCTGACTGCTGAGTGGGGGATATGACAGAGAGACAGCGCCACAGGCTC 1341
QY 923 TCATCCGAGAAAGTGCTGATCAAGAGCTTGCTGAAGGCTTGCTGCCAAATTCAGAAAT 982
Db 1340 TCATCCGAGAAAGTGCTGATCAAGAGCTTGCTGAAGGCTTGCTGCCAAATTCAGAAAT 1281
QY 983 CCAGTGGCTTCAGGAATCTCATGAAGACCCCTCTCTTTGTGTCATCACTTGTGCAATCC 1042
Db 1280 CCAGTGGCTTCAGGAATCTCATGAAGACCCCTCTCTTTGTGTCATCACTTGTGCAATCC 1221
QY 1043 AGATGGGTGAAGTGAAGTTCACCTCTCACACACAAACAAAGCTGTTCATACCTTCATG 1102
Db 1220 AGATGGGTGAAGTGAAGTTCACCTCTCACACACAAACAAAGCTGTTCATACCTTCATG 1161
QY 1103 ATCTGTTGATACAGAAACAAACACAAACATAAAGTGTGGCTGCAAGTGAAGTTCATTC 1162
Db 1160 ATCTGTTGATACAGAAACAAACACAAACATAAAGTGTGGCTGCAAGTGAAGTTCATTC 1101
QY 1163 GGAGCTGGACCTGTGGAGACCTAGCTCTGAGGGTGTGTTCTCCCAACAAGTTTGATT 1222
Db 1100 GGAGCTGGACCTGTGGAGACCTAGCTCTGAGGGTGTGTTCTCCCAACAAGTTTGATT 1041
QY 1223 TCGAACTGCAGGATGTGCTCAGCGTGATGAGGATGTCTCTGACAACTGGGCTCCCTCT 1282
Db 1040 TCGAACTGCAGGATGTGCTCAGCGTGATGAGGATGTCTCTGACAACTGGGCTCCCTCT 981
QY 1283 GTAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAATCTTTCACAAAGTCATTCCAGG 1342
Db 980 GTAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAATCTTTCACAAAGTCATTCCAGG 921
QY 1343 AGTACACAGCAGGACGAAAGCTCAGCAGTTTATTGACGTCTCATGAGCAGAGGAGTGA 1402
Db 920 AGTACACAGCAGGACGAAAGCTCAGCAGTTTATTGACGTCTCATGAGCAGAGGAGTGA 861
QY 1403 CCAAGGGGAATGGTTACTTTCAGAAATGGTTTCCATTTCGACATACATCCACTTATA 1462
Db 860 CCAAGGGGAATGGTTACTTTCAGAAATGGTTTCCATTTCGACATACATCCACTTATA 801
QY 1463 GCAGCTGCTCCGTACACCTGTGGGTCACTGTGGAGCCACAGGGCTGTATGAAGC 1522
Db 800 GCAGCTGCTCCGTACACCTGTGGGTCACTGTGGAGCCACAGGGCTGTATGAAGC 741
QY 1523 ACCTCGACGAGTGTATCAACACGGCTGCTTCTCGGACTTTCATCGCCAAAGAGGCTC 1582
Db 740 ACCTCGACGAGTGTATCAACACGGCTGCTTCTCGGACTTTCATCGCCAAAGAGGCTC 681
QY 1583 TCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCACTGAGCAAGAAATCTGAAAG 1642
Db 680 TCTGGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACCACTGAGCAAGAAATCTGAAAG 621
QY 1643 CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCCTTTATATCAAGAGAGTACATCCA 1702
Db 620 CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCCTTTATATCAAGAGAGTACATCCA 561
QY 1703 AATCAGCCCTGAGCAGAAATTTGAAGCTTCTTTTCAAGGTAAAAAGCTTATATCAACT 1762
Db 560 AATCAGCCCTGAGCAGAAATTTGAAGCTTCTTTTCAAGGTAAAAAGCTTATATCAACT 501
QY 1763 CAGGAACATCCCGGATTACTTATTGACTCTTTTGAACATTTGCCCAATTTGTCAGAGT 1822
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Db 500 CAGGGAACATCCCGCATTAATTGACTTCTTTGAACATTTGCCCAATTTGTGCAAGTG 441
QY 1823 CTCTGGACTTCATTAACTGGACTTTTATATGGGGAGCTATGCTTCATGGGAAAAGGCTG 1882
Db 440 CCCTGGACTTCATTAACTGGACTTTTATGGGGAGCTATGCTTCATGGGAAAAGGCTG 381
QY 1883 CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAAACCTACATTTCCACAGAGG 1942
Db 380 CAGAAGACACAGGTGGAATCCACATGGAAGAGGCCCCAGAAAACCTACATTTCCACAGAGG 321
QY 1943 CTGTATTTTCTTCAACTGGAAGCAGGAATTCAGAGCTCTGTGAGTTCACACTCCCGGG 2002
Db 320 CTGTATTTTCTTCAACTGGAAGCAGGAATTCAGAGCTCTGTGAGTTCACACTCCCGGG 261
QY 2003 ATTTCAACAAGTTCAATAAGCAAGATATACATATCTGGGAAAATATTTCAGCTCTGCCA 2062
Db 260 ATTTCAACAAGTTCAATAAGCAAGATATACATATCTGGGAAAATATTTCAGCTCTGCCA 201
QY 2063 CAAGCCY CAGGCTCAATAAAGAGATGTCTGTGCTGTGGCTGGAGCCTCAGTTTGGTCC 2122
Db 200 CAAGCCY CAGGCTCAATAAAGAGATGTCTGTGCTGTGGCTGGAGCCTCAGTTTGGTCC 141
QY 2123 TCAGCACCTGTGAAGCAATTTATTTCTCTCATGTTGGAGCCAGTCCCTCACCATAGAAG 2182
Db 140 TCAGCACCTGTGAAGCAATTTATTTCTCTCATGTTGGAGCCAGTCCCTCACCATAGAAG 81
QY 2183 ATGAGAGCAGCATCACATCTGTAAACAACTGTAAACCTTGAGTATTTCATGACCTACAGA 2242
Db 80 ATGAGAGCAGCATCACATCTGTAAACAACTGTAAACCTTGAGTATTTCATGACCTACAGA 21
QY 2243 ATCAACGCTGCGCGGGT 2259
Db 20 ATCAACGCTGCGCGGGT 4
RESULT 45
US-10-029-386-228 30/c
; Sequence 22860, Application us/10029386
; GENERAL INFORMATION:
; APPLICANT: Penil, Sharon G.
; APPLICANT: Raik, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: AROMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ. D.NOS: 34288
; SOFTWARE: Amonax Sequence Listing Engine vers. 1.1
; SEQ. ID NO 22860
; LENGTH: 1976
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121653.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: SWISSPROT HIT: Q9JIB6, EVALUATE 2.00e-40
; OTHER INFORMATION: NT HIT: g115296399, EVALUATE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AV656315.1, EVALUATE 0.00e+00
US-10-029-386-22860
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Query Match 59.3% Score 1823; DB 38; Length 1976;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1973; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 263 GTCCTTTTATCACACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 322
Db 1976 GTCCTTTTATCACACATCAGAAGGAGACTTGGACGATTTGGCTCAGGATTTAAAGGACT 1917
QY 323 TGTACCATCCCCATCTTTCTGAACCTTTATCCCTTGGTGAAGATATTGCACATTATTT 382
Db 1916 TGTACCATCCCCATCTTTCTGAACCTTTATCCCTTGGTGAAGATATTGCACATTATTT 1857
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QY 383 TTAACCTTGAAGACACCTTACAGAACCTGTCTCTGGAGGAAGACCAACACCATCAC 442
DB 1856 TTAACCTTGAAGACACCTTACAGAACCTGTCTCTGGAGGAAGACCAACACCATCAC 1797
QY 443 GCGTGGAGAGCTGACCGTGAATGCGCTCTCTGAGGCTCTTTCAGAGCCCTGCATCATG 502
DB 1796 GCGTGGAGAGCTGACCGTGAATGCGCTCTCTGAGGCTCTTTCAGAGCCCTGCATCATG 1737
QY 503 AAGGGAATCTGGCAAGGCAAGTCCACTCTCTGCGAGGCAATGCCATGCTCTGGGCT 562
DB 1736 AAGGGAATCTGGCAAGGCAAGTCCACTCTCTGCGAGGCAATGCCATGCTCTGGGCT 1677
QY 563 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGCTCTCTCTGCGTCTFCAGCAGG 622
DB 1676 CCGGAAAGTGAAGGCTCTGACCAAGTTCAAATTCGCTCTCTCTGCGTCTFCAGCAGG 1617
QY 623 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGATATACCTGGCAACAATCA 682
DB 1616 CCCAGGGTGGACTTTTGAACCCCTCTGTGATCAACTCTCTGATATACCTGGCAACAATCA 1557
QY 683 GGAACAGACATTCATGCGCATGCTGAAGCTGCGCAGAGGCTCTTTTCCCTCTTG 742
DB 1556 GGAACAGACATTCATGCGCATGCTGAAGCTGCGCAGAGGCTCTTTTCCCTCTTG 1497
QY 743 ATGGCTACAATGAATTCAGGCCCTCAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAA 802
DB 1496 ATGGCTACAATGAATTCAGGCCCTCAGAACTGCCAGAAATCGAAGCCCTGATAAAGGAA 1437
QY 803 ACCACGGTTCAGAACATGTCATGTCACCACTACCACTGAGTGCCTGAGGCACATAC 862
DB 1436 ACCACGGTTCAGAACATGTCATGTCACCACTACCACTGAGTGCCTGAGGCACATAC 1377
QY 863 GCGAGTTGGTCCCTGACTGCTGAGTGGGGATGACACAAGACGCGCCAGGCTC 922
DB 1376 GCGAGTTGGTCCCTGACTGCTGAGTGGGGATGACACAAGACGCGCCAGGCTC 1317
QY 923 TCATCCGAGAAGTGTGATCAAGAGCTGCTGAAAGGCTGTGTCTCCAAATTCAGAAAT 982
DB 1316 TCATCCGAGAAGTGTGATCAAGAGCTGCTGAAAGGCTGTGTCTCCAAATTCAGAAAT 1257
QY 983 CCAGTGTCTGAGGAATCTCATGAAGCCCTCTCTTTGTGTATCATCTGTGCAATCC 1042
DB 1256 CCAGTGTCTGAGGAATCTCATGAAGCCCTCTCTTTGTGTATCATCTGTGCAATCC 1197
QY 1043 AGATGGTGAAGTGAAGTCCACTCTCACACAACACGCTGTCCATACCTTCTATG 1102
DB 1196 AGATGGTGAAGTGAAGTCCACTCTCACACAACACGCTGTCCATACCTTCTATG 1137
QY 1103 ATCTGTGTATACAGAAAAACAAACAAATATAAAGTGTGGCTGCAAGTGAATTCATTC 1162
DB 1136 ATCTGTGTATACAGAAAAACAAACAAATATAAAGTGTGGCTGCAAGTGAATTCATTC 1077
QY 1163 GGAGCTGGACACTGTGGAGACCTAGCTCTGGAGGCTGTGTCTCCCAAGTTGAT 1222
DB 1076 GGAGCTGGACACTGTGGAGACCTAGCTCTGGAGGCTGTGTCTCCCAAGTTGAT 1017
QY 1223 TCGAACTGAGATGTGCCAGCGTGAATGAGGATGCTCTGTGACAACTGGGCTCTCT 1282
DB 1016 TCGAACTGAGATGTGCCAGCGTGAATGAGGATGCTCTGTGACAACTGGGCTCTCT 957
QY 1283 GTAATATACACTCAAAAGTTCAAGCCAAAGTATAAATTCCTCACAGTCAATCCAGG 1342
DB 956 GTAATATACACTCAAAAGTTCAAGCCAAAGTATAAATTCCTCACAGTCAATCCAGG 897
QY 1343 AGTACACAGCAGGACGAAGACTCAGCAGTTTATTGACGCTCTCATGAGCAGAGGAGTGA 1402
DB 896 AGTACACAGCAGGACGAAGACTCAGCAGTTTATTGACGCTCTCATGAGCAGAGGAGTGA 837
QY 1403 CCAAGGGGAATGGTTACTTGCAGAAAAATGGTTTCCATTTCCGACATTAATCCACTTATA 1462
DB 836 CCAAGGGGAATGGTTACTTGCAGAAAAATGGTTTCCATTTCCGACATTAATCCACTTATA 777

QY 1463 GCAGCGTCTCGGTACACCTCTGGGTATCTGTGGAAGCCACCCAGGCTGTTATGAAGC 1522
DB 776 GCAGCGTCTCGGTACACCTCTGGGTATCTGTGGAAGCCACCCAGGCTGTTATGAAGC 717
QY 1523 ACCTCGCAGCAGTGTATCAACACGCGTGCCTCTCTGGACTTTCCATCGCAAGAGCCCTC 1582
DB 716 ACCTCGCAGCAGTGTATCAACACGCGTGCCTCTCTGGACTTTCCATCGCAAGAGCCCTC 657
QY 1583 TCTGGAGACAGAAATCTTTGCAAAAGTGTGAAAAACACCACTGAGCAAGAAATTCGAAAG 1642
DB 656 TCTGGAGACAGAAATCTTTGCAAAAGTGTGAAAAACACCACTGAGCAAGAAATTCGAAAG 597
QY 1643 CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGATACATCCA 1702
DB 596 CCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGATACATCCA 537
QY 1703 AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATCAACT 1762
DB 536 AATCAGCCCTGAGCCAAAGAAATTTGAAGCTTTCTTTCAAGGTAAAGCTTATATCAACT 477
QY 1763 CAGGGAACATCCCGATTAATTTGACTTCTTTGAACATTTGCCCAATTTGCAAGTG 1822
DB 476 CAGGGAACATCCCGATTAATTTGACTTCTTTGAACATTTGCCCAATTTGCAAGTG 417
QY 1823 CTCTGAGCTTCAATAAAGTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 1882
DB 416 CCCTGGACTTCAATAAAGTGGACTTTTATGGGGAGCTATGGCTTCATGGGAAAAGGCTG 357
QY 1883 CAGAAGACACAGCTGGAATCCACATGGAAGAGGCCCCAGAAACCTTACATTCAGCAGG 1942
DB 356 CAGAAGACACAGCTGGAATCCACATGGAAGAGGCCCCAGAAACCTTACATTCAGCAGG 297
QY 1943 CTGTATCTTTGCTTCAACTGGAAGAGCAATTCAGGACTCTGGAGGTCAACATCCGCG 2002
DB 296 CTGTATCTTTGCTTCAACTGGAAGAGCAATTCAGGACTCTGGAGGTCAACATCCGCG 237
QY 2003 ATTTCCAGCAAGTGAATTAAGCAAGATATCACATATCTGCGGAAAATATTTCAGCTCTGCCA 2062
DB 236 ATTTCCAGCAAGTGAATTAAGCAAGATATCACATATCTGCGGAAAATATTTCAGCTCTGCCA 177
QY 2063 CAAGCTCAGGCTGCAATTAAGAGATGTGCTGGTGGCTGGAAGCCCTCAGTTTGGTCC 2122
DB 176 CAAGCTCAGGCTGCAATTAAGAGATGTGCTGGTGGCTGGAAGCCCTCAGTTTGGTCC 117
QY 2123 TCAGCAGCTGTAAGAACATTTATCTCTCATGCTGGAAGCCAGTCCCTCAGCAGTAGAG 2182
DB 116 TCAGCAGCTGTAAGAACATTTATCTCTCATGCTGGAAGCCAGTCCCTCAGCAGTAGAG 57
QY 2183 ATGAGGAGCACATCATCTGTAAACAACTGAAACCTTTGAGTATTTCATGACCTA 2238
DB 56 ATGAGGAGCACATCATCTGTAAACAACTGAAACCTTTGAGTATTTCATGACCTA 1

RESULT 46

PCT-US00-35017A-416
; Sequence 416, Application PC/TUS0035017A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: PCT/US00/35017A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 416
; LENGTH: 2950
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-35017A-416

Query Match 58.0%; Score 1781; DB 1; Length 2950; Best Local Similarity 99.9%; Pred. No. 0; Matches 1881; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	1190	CTCTGGAGGGTGTCTTCCACAAAGTTTGATTTTCGAACCTGCAGAGTGTGTCCACGGCTGA	1249						
Db	45	CTCTGGAGGGTGTCTTCCACAAAGTTTGATTTTCGAACCTGCAGAGTGTGTCCACGGCTGA	104						
Qy	1250	ATGAGGATGCTCTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGC	1309						
Db	105	ATGAGGATGCTCTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGC	164						
Qy	1310	CAAAAGTAAATTCCTTCAGAACTCAATTCAGAGTACACAGCAGGAGAGACTCAGCA	1369						
Db	165	CAAAAGTAAATTCCTTCAGAACTCAATTCAGAGTACACAGCAGGAGAGACTCAGCA	224						
Qy	1370	GTTTATTGACGTCATGAGCCAGAGAGGTGACCAAGGGGAATGGTTACTTGCAGAAA	1429						
Db	225	GTTTATTGACGTCATGAGCCAGAGAGGTGACCAAGGGGAATGGTTACTTGCAGAAA	284						
Qy	1430	TGGTTTCGATTCGAGCAATACATCCACTATATAGACGCTGCTCCGGTACACCTGTGGT	1489						
Db	285	TGGTTTCGATTCGAGCAATACATCCACTATATAGACGCTGCTCCGGTACACCTGTGGT	344						
Qy	1490	CATCTGGGAAGCCACGAGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGCGT	1549						
Db	345	CATCTGGGAAGCCACGAGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGCGT	404						
Qy	1550	GCCTTCTCGGACTTTCATGCCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGT	1609						
Db	405	GCCTTCTCGGACTTTCATGCCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAAAGT	464						
Qy	1610	TGAAAAACACCACCTGAGCAAGAAATCTGAAAGCCATTAACATCAATTCCTTTAGAGT	1669						
Db	465	TGAAAAACACCACCTGAGCAAGAAATCTGAAAGCCATTAACATCAATTCCTTTAGAGT	524						
Qy	1670	GTGCATCTCAATTTATCAAGAGAGTACATCCAAATCAGCCCTCAGCAAGAAATTTCAAG	1729						
Db	525	GTGCATCTCAATTTATCAAGAGAGTACATCCAAATCAGCCCTCAGCAAGAAATTTCAAG	584						
Qy	1730	CTTTCTTTCAAGGTAAGGCTTATATCAACTCAGGGAACATCCCGATTAATTTT	1789						
Db	585	CTTTCTTTCAAGGTAAGGCTTATATCAACTCAGGGAACATCCCGATTAATTTT	644						
Qy	1790	ACTTCTTTGACATTTGCCCAATTTGCAAGTGTCTGGCTTCATTAAGCTGACATTT	1849						
Db	645	ACTTCTTTGACATTTGCCCAATTTGCAAGTGTCTGGCTTCATTAAGCTGACATTT	704						
Qy	1850	ATGGGGAGCTATGGCTTCATGGAAAGGCTGCAGAAAGACAGGTGGAAATCCACATGG	1909						
Db	705	ATGGGGAGCTATGGCTTCATGGAAAGGCTGCAGAAAGACAGGTGGAAATCCACATGG	764						
Qy	1910	AAGAGCCCCAGAAACCTACATTCGCCAGCGGCTGTATCTTTCTTCAACTGGAAGC	1969						
Db	765	AAGAGCCCCAGAAACCTACATTCGCCAGCGGCTGTATCTTTCTTCAACTGGAAGC	824						
Qy	1970	AGGAATTGAGGACTCTGGAGGTACACTCCGGGATTTTCAAGGTTGAATAAGCAAGATA	2029						
Db	825	AGGAATTGAGGACTCTGGAGGTACACTCCGGGATTTTCAAGGTTGAATAAGCAAGATA	884						
Qy	2030	TCACATATCTGGGAAATATTCAGCTCTGCCAAGGCTCAGGCTGCAATAAAGAGAT	2089						
Db	885	TCACATATCTGGGAAATATTCAGCTCTGCCAAGGCTCAGGCTGCAATAAAGAGAT	944						
Qy	2090	GTGCTGTGGTGGGAGCTCAGTTTGGTCTCAGCAGCTGTAAGCAATTTATCTC	2149						
Db	945	GTGCTGTGGTGGGAGCTCAGTTTGGTCTCAGCAGCTGTAAGCAATTTATCTC	1004						
Qy	2150	TCATGTTGGAGCCAGTCCCTCACCATAGAGATGAGGACATCAGATCTGTACAA	2209						
Db	1005	TCATGTTGGAGCCAGTCCCTCACCATAGAGATGAGGACATCAGATCTGTACAA	1064						
Qy	2210	ACCTGAAAACCTTGAGTATTTCATGACCTACAGAAATCAACGGCTCCCGGTCTGACTG	2269						

RESULT 47
US-09-471-275-709;
; Sequence 7095, Application US/09471275
; GENERAL INFORMATION:
; APPLICANT: Hys-q, Inc.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE OF INVENTION: From Various Libraries
; FILE REFERENCE 782
; CURRENT APPLICATION NUMBER: US/09/471.275
; EARLIER FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: US 09/235,076
; EARLIER FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: US 09/234,611

[illegible]

QY	2210	ACCTGAAAACCTTTGAGTATTTCATGACCTACAGAATCAACGGCTGCCGGGTGGTCTGACTG	2280
Db	1065	ACCTGAAAACCTTTGAGTATTTCATGACCTACAGAATCAACGGCTGCCGGGTGGTCTGACTG	1124
QY	2270	ACAGCTTGGGTAACTTCAAGAACCTTTACAAAGCTCATATGATCAACATAAAGATGATG	2329
Db	1125	ACAGCTTGGGTAACTTCAAGAACCTTTACAAAGCTCATATGATCAACATAAAGATGATG	1184
QY	2330	AAGAAGATGCTATAAAACCTAGCTGAAGGCGCTGAAAAACCTGAAGAAGATGTGTTATTTC	2389
Db	1195	AAGAAGATGCTATAAAACCTAGCTGAAGGCGCTGAAAAACCTGAAGAAGATGTGTTATTTC	1244
QY	2390	ATTTGACCCACTTGTCTGACATTTGAGAGGGGAATGGATTACATGCTCAAGTCTCTGTCAA	2449
Db	1245	ATTTGACCCACTTGTCTGACATTTGAGAGGGGAATGGATTACATGCTCAAGTCTCTGTCAA	1304
QY	2450	GTGAACCCCTGTGACCTTGAAGAAATTCATTTAGTCTCCTGCTGCTGTCGCAAAATGCAG	2509
Db	1305	GTGAACCCCTGTGACCTTGAAGAAATTCATTTAGTCTCCTGCTGCTGTCGCAAAATGCAG	1364
QY	2510	TGAAAATCCTAGCTCAGAAATCTTCAAAATTTGGTCAAACTGAGCAATCTTGATTATTTCAG	2569
Db	1365	TGAAAATCCTAGCTCAGAAATCTTCAAAATTTGGTCAAACTGAGCAATCTTGATTATTTCAG	1424
QY	2570	AAAAATTACCTGGAAAAAGATGGAAATGAAGCTCTTCATGAACCTGATCGACAGGATGAACG	2629
Db	1425	AAAAATTACCTGGAAAAAGATGGAAATGAAGCTCTTCATGAACCTGATCGACAGGATGAACG	1484
QY	2630	TGCTAGAACAGCTTCACGGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGCAGCCTGA	2689
Db	1485	TGCTAGAACAGCTTCACGGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGCAGCCTGA	1544
QY	2690	GCAGCCTGTTGAAACATTTTGGAGGAGGTCCTCCACAACTCGTCAAGCTTGGGTTGAAAAACT	2749
Db	1545	GCAGCCTGTTGAAACATTTTGGAGGAGGTCCTCCACAACTCGTCAAGCTTGGGTTGAAAAACT	1604
QY	2750	GGAGACTCACAGATACAGAGATTTTAGTGTCATTTTTTGGGAAGAACCTCTCTGA	2809

Db 1605 GGAGACTCACAGATACAGAGATTAGAATTTTAGTGCAATTTTGGAAAGAACCCCTCTGA 1664
Qy 2810 AAAACTTCCAGCAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGTATGGATGGCTTGCT 2869
Db 1665 AAAACTTCCAGCAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGTATGGATGGCTTGCT 1724
Qy 2870 TCATGGGTGATTTAGAGAACTTAAAGCAATAGTGTATTTTGGACTTTAGTACTAAAGAA 2929
Db 1725 TCATGGGTGATTTAGAGAACTTAAAGCAATAGTGTATTTTGGACTTTAGTACTAAAGAA 1784
Qy 2930 TTCTACCTGATCCAGCAGTGTATCTAGCAAACTTAGCCAGTGTATCCAGTTAACTTTTC 2989
Db 1795 TTCTACCTGATCCAGCAGTGTATCTAGCAAACTTAGCCAGTGTATCCAGTTAACTTTTC 1844
Qy 2990 TGCARAAGCTAGGCTTGTGGTGGCAATTTGATGATGATGATCTCAGTGTATTACAG 3049
Db 1845 TGCARAAGCTAGGCTTGTGGTGGCAATTTGATGATGATGATGATCTCAGTGTATTACAG 1904
Qy 3050 GTGCTTTTAACTAGTACTGCT 3072
Db 1905 GTGCTTTTAACTAGTAACTGCT 1927

RESULT 48
PCT-US02-09921-429/c
; Sequence 429, Application PC/TUS0209921.

; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAFFO, Abel
; APPLICANT: JONES, Anissa L.
; APPLICANT: TRAN, Alanna-Phung B.
; APPLICANT: DAHL, Christopher R.
; APPLICANT: GIETZEN, Darryl
; APPLICANT: CHINN, Joyce
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: TUASON, Olivia
; APPLICANT: YAP, Pierre E.
; APPLICANT: AMSEH, Stefan R.
; APPLICANT: DAUGHERTY, Sean C.
; APPLICANT: DAM, Tam C.
; APPLICANT: LIU, Tommy F.
; APPLICANT: NGUYEN, Duy-Viet An
; APPLICANT: KLEEFELD, Yael
; APPLICANT: GERSTIN JR., Edward H.
; APPLICANT: PERALTA, Careyna H.
; APPLICANT: DAVID, Marie H.
; APPLICANT: LEWIS, Samantha A.
; APPLICANT: CHEN, Alice J.
; APPLICANT: PANZER, Scott R.
; APPLICANT: HARRIS, Bernard
; APPLICANT: FLORES, Vincent
; APPLICANT: MARWAHA, Rakesh
; APPLICANT: LO, Audrey
; APPLICANT: LAN, Ruth Y.
; APPLICANT: URASHKA, Michael
; TITLE OF INVENTION: SECRETORY MOLECULES
; FILE REFERENCE: PT-1232 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09921
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/280,067; 60/280,068; 60/291,280; 60/291,849;
; 60/291,829; 60/299,428; 60/300,001; 60/299,776
; PRIOR FILING DATE: 2001-03-29; 2001-03-29; 2001-05-16; 2001-05-17;
; 2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
; NUMBER OF SEQ ID NOS: 1146
; SOFTWARE: PERL Program
; SEQ ID NO 429
; LENGTH: 4626
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No: LG:332701.3:2001JUN22
; NAME/KEY: us:usure
; LOCATION: 114, 199, 224, 231, 237-238, 255, 258-259
; OTHER INFORMATION: a, t, c, g, or other
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Query Match 41.2%; Score 1267; DB 1; Length 4626;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1755 TATCA/CTCAGGGAACATCCCGGATTTACTTTTGTGACTTCTTTGACATTTTGGACATTTTGGCCAAATGG 1814
Db 4626 TATCA/CTCAGGGAACATCCCGGATTTACTTTTGTGACTTCTTTGACATTTTGGACATTTTGGCCAAATGG 4567
Qy 1815 TGCAG/TCCTCTGGACTTCATTTAACTGGAGCTTTTATGGGGAGCTATGGCTTCATGGGA 1874
Db 4566 TGCAG/TCCTCTGGACTTCATTTAACTGGAGCTTTTATGGGGAGCTATGGCTTCATGGGA 4507
Qy 1875 AAAGGC TGCAGAAGACAGAGTGGAAATCCACATGGAAGAGCCCAAGAACTACATTC 1934
Db 4506 AAAGGC TGCAGAAGACAGAGTGGAAATCCACATGGAAGAGCCCAAGAACTACATTC 4447
Qy 1935 CAGCAG/3GCTGTATCTTTTGTCTTCACTGGAAGCAGGAATTCAGGACTCTGGAGGTCCAC 1994
Db 4446 CAGCAG/3GCTGTATCTTTTGTCTTCACTGGAAGCAGGAATTCAGGACTCTGGAGGTCCAC 4387
Qy 1995 ACTCCG/3GATTTTCAGCAAGTTGAATTAAGCAAGATATACATATCTGGGGAATAATTTTCAG 2054
Db 4386 ACTCCG/3GATTTTCAGCAAGTTGAATTAAGCAAGATATACATATCTGGGGAATAATTTTCAG 4327
Qy 2055 CTCGTC/ACAAAGCCTCAGGCTGCAAAATAAGAGATGTCTGTGTGGTGGAGGCTCCAG 2114
Db 4326 CTCGTC/ACAAAGCCTCAGGCTGCAAAATAAGAGATGTCTGTGTGGTGGAGGCTCCAG 4267
Qy 2115 TTTGGT/CTCAGCAGCTGTAAAGACATTTATCTCTCAGTGGAGGACAGCTCCCTCCAC 2174
Db 4266 TTTGGT/CTCAGCAGCTGTAAAGACATTTATCTCTCAGTGGAGGACAGCTCCCTCCAC 4207
Qy 2175 CATAGA/IGATGAGAGGCACATCATCTGTAAACAACCTGAAACCTTGAGTATTTCATGA 2234
Db 4206 CATAGA/IGATGAGAGGCACATCATCTGTAAACAACCTGAAACCTTGAGTATTTCATGA 4147
Qy 2235 CCTACA/AAATCAACGGCTGCGGGTGGTCTGACTGACAGCTTGGTAACTTGAAGAACT 2294
Db 4146 CCTACA/AAATCAACGGCTGCGGGTGGTCTGACTGACAGCTTGGTAACTTGAAGAACT 4087
Qy 2295 TACAAA/CTCATAATGGATAACATAAAGATGAATGAAGAAGATGCTATATAAACTAGCTGA 2354
Db 4086 TACAAA/CTCATAATGGATAACATAAAGATGAATGAAGAAGATGCTATATAAACTAGCTGA 4027
Qy 2355 AGGCCT/AAAAACCTGGAAGAAGATGTGTATTATTTTCATTTGACCCCACTTGTCTGCATTTGG 2414
Db 4026 AGGCCT/AAAAACCTGGAAGAAGATGTGTATTATTTTCATTTGACCCCACTTGTCTGCATTTGG 3967
Qy 2415 AGAGGG/ATGGATTACATAGTCAAGTCTCTCAAGTGAACCCCTGTGACCTTGAAGAAAT 2474
Db 3966 AGAGGG/ATGGATTACATAGTCAAGTCTCTCAAGTGAACCCCTGTGACCTTGAAGAAAT 3907
Qy 2475 TCAATT/3GCTCTCCTGCTGTCTGTGCAAAATGCAGTGAATAATCCTAGCTCAGAACTTTCA 2534
Db 3906 TCAATT/3GCTCTCCTGCTGTCTGTGCAAAATGCAGTGAATAATCCTAGCTCAGAACTTTCA 3847
Qy 2535 CAATTT/3TCAAACTGAGCATCTTGTATTTATCATGAAAAATTTACCTGGAAAAAGATGGAAA 2594
Db 3846 CAATTT/3TCAAACTGAGCATCTTGTATTTATCAGAAAAATTTACCTGGAAAAAGATGGAAA 3787
Qy 2595 TGAAGCT/TTTCATGAACCTGATCGACAGGATGAAGCTGTAGAACAGCTCACCGCACTGAT 2654
Db 3786 TGAAGCT/TTTCATGAACCTGATCGACAGGATGAAGCTGTAGAACAGCTCACCGCACTGAT 3727
Qy 2655 GCTGCCC TGGGGCTGTGACGTGCAAGGAGCAGCTGAGAGCCTGTGTGAACATTTTGGAGGA 2714
Db 3726 GCTGCCC TGGGGCTGTGACGTGCAAGGAGCAGCTGAGAGCCTGTGTGAACATTTTGGAGGA 3667

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QY 2715 GTCCACAACTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACAGATACAGAGATTAG 2774
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QY 2775 AATTTAGTGCAATTTTGGGAAGAACCCCTCTGAAAACTTCCAGCAGTTGAATTTGGC 2834
Db 3606 AATTTAGTGCAATTTTGGGAAGAACCCCTCTGAAAACTTCCAGCAGTTGAATTTGGC 3547
QY 2835 GGGAAATCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTTGAGAACTTAA 2894
Db 3546 GGGAAATCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTGATTTGAGAACTTAA 3487
QY 2895 GCAATTAGTGTCTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGTATCCAGCATTAGTTCAG 2954
Db 3486 GCAATTAGTGTCTTTTGGACTTTAGTACTAAAGAAATTTCTACCTGTATCCAGCATTAGTTCAG 3427
QY 2955 AAACTTAGCAGAGTGTATTCAGATTAATTTCTGCAAGAGCTAGGCTTGTGGGTG 3014
Db 3426 AAACTTAGCAGAGTGTATTCAGATTAATTTCTGCAAGAGCTAGGCTTGTGGGTG 3367
QY 3015 GCAATTGATGATGATCTAGTCTATACAGTGTCTTTAAACTAGTAACTGCT 3072
Db 3366 GCAATTGATGATGATCTAGTCTATACAGTGTCTTTAAACTAGTAACTGCT 3309

RESULT 49
US-09-864-921-179
; Sequence 179, Application US/09864921
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Pawlowski, Hideki
; APPLICANT: Hayashi, Hideki
; TITLE OF INVENTION: Novel Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(891)
US-09-864-921-179

Query Match 27.3%; Score 840; DB 33; Length 891;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 890; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 481 CTTACAGCCCTCGATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 540
Db 1 CTTACAGCCCTCGATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 60
QY 541 CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGGCTCTGACCAAGTTCAAATTCGTC 600
Db 61 CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGGCTCTGACCAAGTTCAAATTCGTC 120
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QY 601 TTCTTCTCGTCTCAGAGGGCCCGAGGGTGGACTTTTGAACCCCTCTCTGTGATCAACTC 660
Db 121 TTCTTCTCGTCTCAGAGGGCCCGAGGGTGGACTTTTGAACCCCTCTCTGTGATCAACTC 180
QY 661 CTGGATATACCTGGCAATTCAGGAAGCAGACATTTATGCGCCATGCTGCTGAAGCTGCGG 720
Db 181 CTGGATATACCTGGCAATTCAGGAAGCAGACATTTATGCGCCATGCTGCTGAAGCTGCGG 240
QY 721 CAGAGGGTCTCTTCTTCTTGTGATGCTACAATTAAGTCAAGCCCGAGAACTGCCAGAA 780
Db 241 CAGAGGGTCTCTTCTTCTTGTGATGCTACAATTAAGTCAAGCCCGAGAACTGCCAGAA 300
QY 781 ATCGAAGCCCTGTATAAGGAAACACCCGCTTCAAGAACAATGGTCACTCGTCAACCTACC 840
Db 301 ATCGAAGCCCTGTATAAGGAAACACCCGCTTCAAGAACAATGGTCACTCGTCAACCTACC 360
QY 841 ACTGAGTGCTGAGGACATACGCGAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATG 900
Db 361 ACTGAGTGCTGAGGACATACGCGAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATG 420
QY 901 ACAGAAGACAGCCCGCAGGCTCTATCCGAGAAAGTGTGATCAAGGAGCTTGTGGAAGC 960
Db 421 ACAGAAGACAGCCCGCAGGCTCTATCCGAGAAAGTGTGATCAAGGAGCTTGTGGAAGC 480
QY 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 1020
Db 481 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT 540
QY 1021 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAAGTTCACACTCTCACACAAACA 1080
Db 541 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAAGTTCACACTCTCACACAAACA 600
QY 1081 ACGCTGCTGCATACCTTCTATGATCTGTGATACAGAAAAACACACAAACATAAAGT 1140
Db 601 ACGCTGCTGCATACCTTCTATGATCTGTGATACAGAAAAACACACAAACATAAAGT 660
QY 1141 GTGGCTGCAAGTGACTTTCATTCGGAGCCCTGAGACCTGTGGAGACCTAGTCTGGAGGT 1200
Db 661 GTGGCTGCAAGTGACTTTCATTCGGAGCCCTGAGACCTGTGGAGACCTAGTCTGGAGGT 720
QY 1201 GTGTTCTCCCAAGTTTGAATTCGAACTGCGAGGATGTGCCAGCGTGAATGAGGATGTC 1260
Db 721 GTGTTCTCCCAAGTTTGAATTCGAACTGCGAGGATGTGCCAGCGTGAATGAGGATGTC 780
QY 1261 CTGCTGACAACTGGGCTCTCTCTAAATATACAGCTCAAAGTTCAAGCCAAAAGTATAA 1320
Db 781 CTGCTGACAACTGGGCTCTCTCTAAATATACAGCTCAAAGTTCAAGCCAAAAGTATAA 840
QY 1321 TTCTTTTCAAAAGTCAATTCAGGAGTACACAGCAGGAGAGACTCAGCAGT 1371
Db 841 TTCTTTTCAAAAGTCAATTCAGGAGTACACAGCAGGAGAGACTCAGCAGT 891

RESULT 50
US-09-686-347-98
; Sequence 98, Application US/09686347
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Stehlik, Christian
; TITLE OF INVENTION: Novel Card-Domain Containing
; FILE REFERENCE: P-LJ 4271
; CURRENT APPLICATION NUMBER: US/09/686,347
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
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; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(1353)
US-09-686-347-98

Query Match      26.5%; Score 815; DB 27; Length 1395;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 815; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2318 TAAAGATGAATGAAGAACTGCTATATAAAGCTAGCTGAAGGCTGAAAAACCTGAAGAAGA 2377
Db 599 TAAAGATGAATGAAGAACTGCTATATAAAGCTAGCTGAAGGCTGAAAAACCTGAAGAAGA 658
QY 2378 TGTGTTTATTTCAATTGACCCACCTTGTCTGACATTTGGAGAGGAATGATACATAGTCA 2437
Db 659 TGTGTTTATTTCAATTGACCCACCTTGTCTGACATTTGGAGAGGAATGATACATAGTCA 718
QY 2438 AGTCTCTGCAAGTGAAGCCCTGTGACCTTGAAGAAATTCAAATAGTCTCCTGCTGTGT 2497
Db 719 AGTCTCTGCAAGTGAAGCCCTGTGACCTTGAAGAAATTCAAATAGTCTCCTGCTGTGT 778
QY 2498 CTGCAAAATGCAAGTGAAGAAATTCCTAGCTCAGAAATCTTCAAAATTTGGTCAAACTGAGCATTC 2557
Db 779 CTGCAAAATGCAAGTGAAGAAATTCCTAGCTCAGAAATCTTCAAAATTTGGTCAAACTGAGCATTC 838
QY 2558 TTGATTTATCAGAAATTTACCTGGAAAGATGGAATGAAGCTCTTCATGAAGTATCG 2617
Db 839 TTGATTTATCAGAAATTTACCTGGAAAGATGGAATGAAGCTCTTCATGAAGTATCG 898
QY 2618 ACAGATGAAGCTGCTAGAACAGCTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGC 2677
Db 899 ACAGATGAAGCTGCTAGAACAGCTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGC 958
QY 2678 AAGGCAAGCTGAGCAGCCTGTTGAAACATTTGGAGAGGTCCTCCACAACTCGTCAAGCTTG 2737
Db 959 AAGGCAAGCTGAGCAGCCTGTTGAAACATTTGGAGAGGTCCTCCACAACTCGTCAAGCTTG 1018
QY 2738 GGTGAAAACTGGAGACTCACAGATACAGAGATTAGAAATTTTAGGTGCATTTTTTGGAA 2797
Db 1019 GGTGAAAACTGGAGACTCACAGATACAGAGATTAGAAATTTTAGGTGCATTTTTTGGAA 1078
QY 2798 AGAACCCCTCTGAAAACTTCCAGCAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGTG 2857
Db 1079 AGAACCCCTCTGAAAACTTCCAGCAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGTG 1138
QY 2858 GATGGCTTGCCTTCATGGTGTATTTGAGAAATCTTAAGCAATTTAGTGTTTTTTGACTTTA 2917
Db 1139 GATGGCTTGCCTTCATGGTGTATTTGAGAAATCTTAAGCAATTTAGTGTTTTTTGACTTTA 1198
QY 2918 GTACTTAAGAATTTCTACCTCATCCAGCATTTAGTCAAGAACTTAGCAAGTGTATCCA 2977
Db 1199 GTACTTAAGAATTTCTACCTCATCCAGCATTTAGTCAAGAACTTAGCAAGTGTATCCA 1258
QY 2978 AGTTAACTTTCTGCAAGAACTAGGCTTGTGGTGGCAATTTGATGATGATCATCTCA 3037
Db 1259 AGTTAACTTTCTGCAAGAACTAGGCTTGTGGTGGCAATTTGATGATGATCATCTCA 1318
QY 3038 GTGTATTACAGGTGCTTTTAACTAGTAAGTCT 3072
Db 1319 GTGTATTACAGGTGCTTTTAACTAGTAAGTCT 1353
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Job time : 6602 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2003, 23:02:25 ; search time 469 seconds
(without alignments)
7985.160 Million cell updates/sec

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Perfect score: 3072
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2500250 seqs, 609544256 residues

Word size : 12

Total number of hits satisfying chosen parameters: 207489

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Pending_Patents_NA_New.*

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- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	2919	95.0	3075	1 PCT-US02-21946A-1
2	2919	95.0	3219	1 PCT-US02-21946A-14
3	2919	95.0	3545	6 US-10-276-781-111
4	242	7.9	421	6 US-10-203-138A-4307
5	220	7.2	220	6 US-10-203-138A-9429
6	20	0.7	601	5 US-09-949-004-6715
7	20	0.7	209798	5 US-09-949-004-693
8	19	0.6	230	5 US-09-531-113-38966
9	19	0.6	369	6 US-10-240-425-462
10	19	0.6	5513	5 US-09-724-676-16013
11	19	0.6	5513	5 US-09-724-676A-16013
12	19	0.6	8632	1 PCT-US02-32727-122
13	19	0.6	8632	6 US-10-057-488-122
14	19	0.6	30310	6 US-10-293-783-96
15	19	0.6	302603	1 PCT-US02-32700-8
16	19	0.6	302603	6 US-10-271-416-8
17	19	0.6	428573	5 US-09-948-134-119
18	18	0.6	19	6 US-10-303-778-15466
19	18	0.6	19	6 US-10-310-188-29161
20	18	0.6	25	7 US-60-427-836-33474
21	18	0.6	116	5 US-09-513-999C-19061
22	18	0.6	124	6 US-10-286-136-502
23	18	0.6	143	6 US-10-266-131-1575
24	18	0.6	199	5 US-09-531-113-19390
25	18	0.6	246	5 US-09-531-113-22263
26	18	0.6	256	5 US-09-531-113-25999

27	18	0.6	270	5	US-09-531-113-37454	Sequence 37454, A
28	18	0.6	446	5	US-09-513-999C-13408	Sequence 13408, A
29	18	0.6	454	6	US-10-203-138A-4790	Sequence 4790, Ap
30	18	0.6	466	5	US-09-513-999C-1807	Sequence 1807, Ap
31	18	0.6	472	6	US-10-203-138A-1760	Sequence 1760, Ap
32	18	0.6	481	5	US-09-747-358A-688	Sequence 688, App
33	18	0.6	601	5	US-09-949-002-8756	Sequence 8756, Ap
34	18	0.6	601	5	US-09-949-002-8757	Sequence 8757, Ap
35	18	0.6	885	5	US-09-134-000C-1076	Sequence 1076, Ap
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37	18	0.6	986	5	US-09-724-676-3688	Sequence 3688, Ap
38	18	0.6	986	5	US-09-724-676-3693	Sequence 3693, Ap
39	18	0.6	986	5	US-09-724-676A-3688	Sequence 3688, Ap
40	18	0.6	986	5	US-09-724-676A-3693	Sequence 3693, Ap
41	18	0.6	998	5	US-09-724-676A-3693	Sequence 3693, Ap
42	18	0.6	998	5	US-09-724-676-3694	Sequence 3694, Ap
43	18	0.6	998	5	US-09-724-676A-3689	Sequence 3689, Ap
44	18	0.6	998	5	US-09-724-676A-3694	Sequence 3694, Ap
45	18	0.6	1243	6	US-10-264-237-181	Sequence 181, App
46	18	0.6	1297	1	PCT-US02-38446-98	Sequence 98, Appl
47	18	0.6	1610	5	US-09-724-676-3691	Sequence 3691, Ap
48	18	0.6	1610	5	US-09-724-676A-3691	Sequence 3691, Ap
49	18	0.6	1619	5	US-09-743-247A-23	Sequence 23, Appl
50	18	0.6	1622	5	US-09-724-676-3692	Sequence 3692, Ap
51	18	0.6	1622	5	US-09-724-676A-3692	Sequence 3692, Ap
52	18	0.6	2068	5	US-09-724-676-2475	Sequence 2475, Ap
53	18	0.6	2068	5	US-09-724-676A-2475	Sequence 2475, Ap
54	18	0.6	3001	5	US-09-539-333D-188	Sequence 188, App
55	18	0.6	3001	5	US-09-539-333D-199	Sequence 199, App
56	18	0.6	3001	5	US-09-539-333D-188	Sequence 188, App
57	18	0.6	3001	5	US-09-539-333D-199	Sequence 199, App
58	18	0.6	4089	1	PCT-US02-40225-240	Sequence 240, App
59	18	0.6	4089	1	US-10-320-797-240	Sequence 240, App
60	18	0.6	4215	5	US-09-620-312D-295	Sequence 295, App
61	18	0.6	8868	1	PCT-US02-32257-1	Sequence 1, Appl
62	18	0.6	8868	6	US-10-267-488-1	Sequence 1, Appl
63	18	0.6	9084	6	US-10-311-455-1577	Sequence 1577, Ap
64	18	0.6	13732	6	US-10-152-724-22	Sequence 22, Appl
65	18	0.6	50000	6	US-10-152-724-22	Sequence 22, Appl
66	18	0.6	50000	6	US-10-152-724A-22	Sequence 22, Appl
67	18	0.6	121434	6	US-10-303-165-11	Sequence 11, Appl
68	18	0.6	142299	5	US-09-911-077A-14	Sequence 14, Appl
69	18	0.6	202001	6	US-10-274-990-3	Sequence 3, Appl
70	18	0.6	209631	5	US-09-949-002-574	Sequence 574, App
71	18	0.6	209632	5	US-09-949-002-802	Sequence 802, App
72	18	0.6	438464	5	US-09-948-124-7	Sequence 7, Appl
73	17	0.6	25	7	US-60-427-808-180867	Sequence 180867, App
74	17	0.6	25	7	US-60-427-808-562753	Sequence 562753, App
75	17	0.6	25	7	US-60-427-808-725906	Sequence 725906, App
76	17	0.6	25	7	US-60-427-808-785497	Sequence 785497, App
77	17	0.6	25	7	US-60-427-836-393338	Sequence 393338, App
78	17	0.6	47	6	US-10-349-143-2385	Sequence 2285, Ap
79	17	0.6	50	6	US-10-325-899-992	Sequence 992, App
80	17	0.6	121	5	US-09-513-999C-14286	Sequence 14286, A
81	17	0.6	173	5	US-09-531-113-37369	Sequence 37369, A
82	17	0.6	195	5	US-09-531-113-33755	Sequence 33755, A
83	17	0.6	203	5	US-09-531-113-25917	Sequence 25917, A
84	17	0.6	212	5	US-09-513-999C-17822	Sequence 17822, A
85	17	0.6	223	5	US-09-531-113-32604	Sequence 32604, A
86	17	0.6	223	5	US-09-531-113-36189	Sequence 36189, A
87	17	0.6	224	5	US-09-531-113-32945	Sequence 32945, A
88	17	0.6	225	5	US-09-531-113-28221	Sequence 28221, A
89	17	0.6	225	5	US-09-531-113-38627	Sequence 38627, A
90	17	0.6	229	6	US-10-305-720-814	Sequence 814, App
91	17	0.6	232	5	US-09-531-113-35287	Sequence 35287, A
92	17	0.6	233	5	US-09-531-113-33033	Sequence 33033, A
93	17	0.6	233	5	US-09-531-113-35306	Sequence 35306, A
94	17	0.6	233	5	US-09-531-113-35724	Sequence 35724, A
95	17	0.6	234	5	US-09-531-113-27764	Sequence 27764, A
96	17	0.6	239	5	US-09-531-113-33445	Sequence 33445, A
97	17	0.6	240	5	US-09-531-113-39757	Sequence 39757, A
98	17	0.6	241	5	US-09-531-113-34933	Sequence 34933, A
99	17	0.6	242	5	US-09-531-113-36455	Sequence 36455, A

c 100	17	0.6	243	5	US-09-531-113-34944	Sequence 34944, A	c 173	17	0.6	2291	1	PCT-US02-40194-17	Sequence 17, Appl
c 101	17	0.6	244	5	US-09-531-113-27930	Sequence 27930, A	c 174	17	0.6	2291	6	US-10-320-351-16	Sequence 16, Appl
c 102	17	0.6	244	5	US-09-531-113-33819	Sequence 33819, A	c 175	17	0.6	2291	6	US-10-320-351-17	Sequence 17, Appl
c 103	17	0.6	244	5	US-09-531-113-36575	Sequence 36575, A	c 176	17	0.6	2291	6	US-10-320-351-19	Sequence 9, Appl
c 104	17	0.6	245	5	US-09-531-113-35612	Sequence 35612, A	c 177	17	0.6	2471	6	US-10-297-880-8	Sequence 8, Appl
c 105	17	0.6	246	5	US-09-531-113-15493	Sequence 15493, A	c 178	17	0.6	2491	1	PCT-US02-32851-87	Sequence 87, Appl
c 106	17	0.6	246	5	US-09-531-113-21269	Sequence 21269, A	c 179	17	0.6	2493	7	US-60-417-155-1	Sequence 1, Appl
c 107	17	0.6	246	5	US-09-531-113-35320	Sequence 35320, A	c 180	17	0.6	2553	7	US-60-417-155-4	Sequence 4, Appl
c 108	17	0.6	248	5	US-09-531-113-34131	Sequence 34131, A	c 181	17	0.6	2604	5	US-09-950-084-582	Sequence 582, App
c 109	17	0.6	249	5	US-09-531-113-38328	Sequence 38328, A	c 182	17	0.6	2605	5	US-09-724-676-46843	Sequence 46843, A
c 110	17	0.6	251	5	US-09-531-113-28359	Sequence 28359, A	c 183	17	0.6	2605	6	US-09-724-676A-46843	Sequence 46843, A
c 111	17	0.6	251	5	US-09-531-113-33175	Sequence 33175, A	c 184	17	0.6	3458	6	US-10-240-965-273	Sequence 273, App
c 112	17	0.6	251	5	US-09-531-113-34843	Sequence 34843, A	c 185	17	0.6	3456	1	PCT-US02-31338-154	Sequence 154, App
c 113	17	0.6	251	5	US-09-531-113-38478	Sequence 38478, A	c 186	17	0.6	3456	6	US-10-188-832-154	Sequence 154, App
c 114	17	0.6	252	5	US-09-531-113-31855	Sequence 31855, A	c 187	17	0.6	3580	5	US-09-724-676-35627	Sequence 35627, A
c 115	17	0.6	252	5	US-09-531-113-37099	Sequence 37099, A	c 188	17	0.6	3580	5	US-09-724-676A-35627	Sequence 35627, A
c 116	17	0.6	255	5	US-09-531-113-38481	Sequence 38481, A	c 189	17	0.6	3593	5	US-09-949-002-278	Sequence 278, App
c 117	17	0.6	256	5	US-09-531-113-1857	Sequence 1857, Ap	c 190	17	0.6	3853	1	PCT-US02-39126-43	Sequence 43, Appl
c 118	17	0.6	259	5	US-09-531-113-28418	Sequence 28418, A	c 191	17	0.6	4000	1	PCT-US02-39126-44	Sequence 44, Appl
c 119	17	0.6	259	5	US-09-531-113-34016	Sequence 34016, A	c 192	17	0.6	4003	5	US-09-724-676-24597	Sequence 24597, A
c 120	17	0.6	260	5	US-09-531-113-33628	Sequence 33628, A	c 193	17	0.6	4003	5	US-09-724-676A-24597	Sequence 24597, A
c 121	17	0.6	260	5	US-09-531-113-39015	Sequence 39015, A	c 194	17	0.6	4307	5	US-09-949-002-94	Sequence 94, Appl
c 122	17	0.6	261	5	US-09-531-113-39275	Sequence 39275, A	c 195	17	0.6	4307	5	US-09-724-676-35628	Sequence 35628, A
c 123	17	0.6	263	5	US-09-531-113-26650	Sequence 26650, A	c 196	17	0.6	4335	5	US-09-724-676A-35628	Sequence 35628, A
c 124	17	0.6	263	5	US-09-531-113-37536	Sequence 37536, A	c 197	17	0.6	4335	6	US-10-218-140-2273	Sequence 2273, Ap
c 125	17	0.6	266	5	US-09-531-113-37038	Sequence 37038, A	c 198	17	0.6	4407	6	US-10-125-923A-351	Sequence 351, App
c 126	17	0.6	267	5	US-09-531-113-37406	Sequence 37406, A	c 199	17	0.6	4407	6	US-10-205-892-351	Sequence 351, App
c 127	17	0.6	275	5	US-09-531-113-47210	Sequence 47210, A	c 200	17	0.6	4407	6	US-10-174-575-351	Sequence 351, App
c 128	17	0.6	276	5	US-09-531-113-32949	Sequence 32949, A	c 201	17	0.6	4407	6	US-10-174-575A-351	Sequence 351, App
c 129	17	0.6	283	5	US-09-531-113-14915	Sequence 14915, A	c 202	17	0.6	4407	6	US-10-015-610A-316	Sequence 316, App
c 130	17	0.6	284	5	US-10-335-066-386	Sequence 386, App	c 203	17	0.6	4407	6	US-10-226-254A-316	Sequence 316, App
c 131	17	0.6	333	5	US-09-513-9996-26762	Sequence 26762, A	c 204	17	0.6	4407	6	US-10-187-755-351	Sequence 351, App
c 132	17	0.6	351	5	US-09-724-676-16100	Sequence 16100, A	c 205	17	0.6	4407	6	US-10-187-749-351	Sequence 351, App
c 133	17	0.6	351	5	US-09-724-676A-16100	Sequence 16100, A	c 206	17	0.6	4407	6	US-10-017-253A-316	Sequence 316, App
c 134	17	0.6	387	5	US-09-513-9996-33562	Sequence 33562, A	c 207	17	0.6	4407	6	US-10-199-672-351	Sequence 351, App
c 135	17	0.6	435	6	US-10-203-138A-4763	Sequence 4763, Ap	c 208	17	0.6	5388	6	US-10-311-455-218	Sequence 218, App
c 136	17	0.6	467	6	US-10-266-131-2487	Sequence 2487, Ap	c 209	17	0.6	5729	6	US-10-152-319A-1943	Sequence 1943, Ap
c 137	17	0.6	472	5	US-09-531-113-7632	Sequence 7632, Ap	c 210	17	0.6	5729	6	US-10-301-856-1101	Sequence 1101, Ap
c 138	17	0.6	482	5	US-09-531-113-3643	Sequence 3643, Ap	c 211	17	0.6	5803	6	US-10-144-779-709	Sequence 709, App
c 139	17	0.6	541	6	US-10-203-138A-9876	Sequence 9876, Ap	c 212	17	0.6	5804	6	US-10-329-624-249	Sequence 249, App
c 140	17	0.6	542	6	US-10-150-811-17	Sequence 17, Appl	c 213	17	0.6	6065	6	US-10-311-455-477	Sequence 477, App
c 141	17	0.6	542	6	US-10-131-409-17	Sequence 17, Appl	c 214	17	0.6	6079	6	US-10-311-455-231	Sequence 231, App
c 142	17	0.6	542	6	US-10-139-854-17	Sequence 17, Appl	c 215	17	0.6	6079	6	US-10-257-166-73	Sequence 73, App
c 143	17	0.6	542	6	US-10-150-813-17	Sequence 17, Appl	c 216	17	0.6	6283	6	US-10-311-455-73	Sequence 73, App
c 144	17	0.6	542	6	US-10-150-164-17	Sequence 17, Appl	c 217	17	0.6	6283	6	US-10-194-163-479	Sequence 479, App
c 145	17	0.6	548	5	US-09-531-113-7411	Sequence 7411, Ap	c 218	17	0.6	7320	5	US-09-724-676-24595	Sequence 24595, A
c 146	17	0.6	549	5	US-09-531-113-7431	Sequence 7431, Ap	c 219	17	0.6	7320	5	US-09-724-676A-24595	Sequence 24595, A
c 147	17	0.6	551	6	US-10-240-425-152	Sequence 152, App	c 220	17	0.6	7434	5	US-09-724-676-24596	Sequence 24596, A
c 148	17	0.6	551	6	US-10-152-319A-866	Sequence 866, App	c 221	17	0.6	7434	5	US-09-724-676A-24596	Sequence 24596, A
c 149	17	0.6	554	5	US-09-531-113-10735	Sequence 10735, A	c 222	17	0.6	7669	6	US-10-311-455-1819	Sequence 1819, Ap
c 150	17	0.6	601	5	US-09-949-004-6531	Sequence 6531, Ap	c 223	17	0.6	8395	6	US-10-311-455-148	Sequence 148, App
c 151	17	0.6	865	5	US-09-724-676-46629	Sequence 46629, A	c 224	17	0.6	8705	6	US-10-240-851-10	Sequence 10, Appl
c 152	17	0.6	865	5	US-10-092-411A-621	Sequence 621, App	c 225	17	0.6	10026	6	US-10-311-455-1849	Sequence 1849, App
c 153	17	0.6	939	6	US-10-194-163-138	Sequence 138, App	c 226	17	0.6	10710	6	US-10-311-455-866	Sequence 866, App
c 154	17	0.6	963	6	US-10-157-104-28	Sequence 28, Appl	c 227	17	0.6	10766	6	US-10-293-017-27	Sequence 27, Appl
c 155	17	0.6	1013	6	US-10-276-774-646	Sequence 646, App	c 228	17	0.6	10766	6	US-10-293-071-27	Sequence 27, Appl
c 156	17	0.6	1245	6	US-10-092-411A-828	Sequence 828, App	c 229	17	0.6	11976	6	US-10-311-455-568	Sequence 568, App
c 157	17	0.6	1302	6	US-09-724-676-40541	Sequence 40541, A	c 230	17	0.6	12570	5	US-09-949-002-850	Sequence 850, App
c 158	17	0.6	1310	5	US-09-724-676A-40541	Sequence 40541, A	c 231	17	0.6	12857	6	US-10-017-161-2391	Sequence 2391, Ap
c 159	17	0.6	1425	6	US-10-240-425-410	Sequence 410, App	c 232	17	0.6	14307	6	US-10-311-455-701	Sequence 701, App
c 160	17	0.6	1425	6	US-09-724-676-40542	Sequence 40542, A	c 233	17	0.6	14551	6	US-10-240-485-138	Sequence 138, App
c 161	17	0.6	1526	5	US-09-724-676A-40542	Sequence 40542, A	c 234	17	0.6	15475	6	US-10-144-779-232	Sequence 232, App
c 162	17	0.6	1536	5	US-09-724-676A-40542	Sequence 40542, A	c 235	17	0.6	17534	6	US-10-257-166-108	Sequence 108, App
c 163	17	0.6	1835	1	PCT-US02-18666-7	Sequence 7, Appl	c 236	17	0.6	19803	6	US-10-017-161-1023	Sequence 1023, App
c 164	17	0.6	1894	1	PCT-US02-18666-1	Sequence 1, Appl	c 237	17	0.6	20407	5	US-09-949-002-666	Sequence 666, App
c 165	17	0.6	1938	1	PCT-US02-39126-69	Sequence 69, Appl	c 238	17	0.6	23574	6	US-10-277-216-6	Sequence 6, Appl
c 166	17	0.6	1942	5	US-09-598-075-245	Sequence 245, App	c 239	17	0.6	29836	7	US-60-417-155-3	Sequence 3, Appl
c 167	17	0.6	1950	6	US-10-311-764-18	Sequence 18, Appl	c 240	17	0.6	31129	6	US-10-298-192-3	Sequence 3, Appl
c 168	17	0.6	2115	7	US-60-417-155-5	Sequence 5, Appl	c 241	17	0.6	35956	6	US-10-017-161-761	Sequence 761, Appl
c 169	17	0.6	2177	5	US-09-724-676-12884	Sequence 12884, A	c 242	17	0.6	38611	5	US-09-949-002-649	Sequence 649, App
c 170	17	0.6	2177	5	US-09-724-676A-12884	Sequence 12884, A	c 243	17	0.6	38611	5	US-09-949-002-809	Sequence 809, App
c 171	17	0.6	2152	6	US-10-240-965-134	Sequence 134, App	c 244	17	0.6	45802	6	US-10-144-779-133	Sequence 133, App
c 172	17	0.6	2231	1	PCT-US02-40194-16	Sequence 16, Appl	c 245	17	0.6	46199	6	US-10-144-779-212	Sequence 212, App

c 246	17	0.6	46718	6	US-10-274-873-3	Sequence 3, Appli	c 319	16	0.5	25	7	US-60-427-836-431423	Sequence 431423,
c 247	17	0.6	48478	6	US-10-144-779-135	Sequence 135, App	320	16	0.5	25	7	US-60-427-836-45088	Sequence 465088,
c 248	17	0.6	48478	6	US-10-144-779-149	Sequence 149, App	c 321	16	0.5	25	7	US-60-427-836-491993	Sequence 491993,
c 249	17	0.6	51723	5	US-09-949-004-569	Sequence 569, App	c 322	16	0.5	25	7	US-60-427-836-522567	Sequence 522567,
c 250	17	0.6	51810	5	US-09-949-002-752	Sequence 752, App	c 323	16	0.5	25	7	US-60-427-836-559202	Sequence 559202,
c 251	17	0.6	51810	5	US-09-949-002-753	Sequence 753, App	c 324	16	0.5	25	7	US-60-427-836-581964	Sequence 581964,
c 252	17	0.6	57501	6	US-10-304-126-11	Sequence 11, Appl	c 325	16	0.5	25	7	US-60-427-836-699023	Sequence 699023,
c 253	17	0.6	78197	5	US-09-949-004-572	Sequence 572, App	c 326	16	0.5	25	7	US-09-864-636A-457	Sequence 457, App
c 254	17	0.6	78333	1	PCT-US02-36935-3	Sequence 3, Appli	c 327	16	0.5	27	6	US-09-864-636A-458	Sequence 458, App
c 255	17	0.6	78333	6	US-10-298-123-3	Sequence 3, Appli	c 328	16	0.5	27	6	US-10-084-839-457	Sequence 457, App
c 256	17	0.6	106323	6	US-10-300-827-3	Sequence 3, Appli	c 329	16	0.5	27	6	US-10-084-839-458	Sequence 458, App
c 257	17	0.6	126461	6	US-10-144-779-277	Sequence 277, App	c 330	16	0.5	40	6	US-10-247-019-19	Sequence 19, Appl
c 258	17	0.6	131009	6	US-10-144-779-287	Sequence 287, App	c 331	16	0.5	42	5	US-09-864-636A-389	Sequence 389, App
c 259	17	0.6	136990	5	US-09-949-004-690	Sequence 690, App	c 332	16	0.5	42	5	US-09-864-636A-390	Sequence 390, App
c 260	17	0.6	136997	5	US-09-949-004-488	Sequence 488, App	c 333	16	0.5	42	6	US-10-084-839-389	Sequence 389, App
c 261	17	0.6	207433	6	US-10-277-216-5	Sequence 5, Appli	c 334	16	0.5	42	6	US-10-084-839-390	Sequence 390, Appl
c 262	17	0.6	221636	5	US-09-948-124-104	Sequence 104, App	c 335	16	0.5	61	6	US-10-205-562-9	Sequence 9, Appli
c 263	17	0.6	268685	6	US-10-025-966A-22	Sequence 22, Appl	c 336	16	0.5	73	6	US-10-303-778-11850	Sequence 11850, A
c 264	17	0.6	321900	5	US-09-948-124-10	Sequence 10, Appl	c 337	16	0.5	73	6	US-10-310-188-21741	Sequence 21741, A
c 265	17	0.6	475970	5	US-09-950-084-7438	Sequence 7438, Ap	c 338	16	0.5	129	6	US-10-327-713-820	Sequence 820, App
c 266	17	0.6	611259	5	US-09-948-124-8	Sequence 8, Appli	c 339	16	0.5	138	6	US-10-205-562-7	Sequence 7, Appli
c 267	17	0.6	646370	5	US-09-948-124-108	Sequence 108, App	c 340	16	0.5	138	6	US-10-205-563-10	Sequence 10, Appl
c 268	17	0.6	646370	5	US-09-948-124-108	Sequence 108, App	c 341	16	0.5	141	6	US-10-203-138A-8655	Sequence 8655, Ap
c 269	16	0.5	19	6	US-10-310-188-55122	Sequence 55122, A	c 342	16	0.5	147	6	US-10-266-131-738	Sequence 738, App
c 270	16	0.5	25	7	US-60-417-190-18146	Sequence 18146, A	c 343	16	0.5	183	6	US-09-534-850-14142	Sequence 14142, A
c 271	16	0.5	25	7	US-60-417-190-18147	Sequence 18147, A	c 344	16	0.5	202	5	US-09-513-999C-12540	Sequence 12540, A
c 272	16	0.5	25	7	US-60-417-190-18148	Sequence 18148, A	c 345	16	0.5	208	5	US-09-534-850-14163	Sequence 14163, A
c 273	16	0.5	25	7	US-60-417-190-18149	Sequence 18149, A	c 346	16	0.5	216	5	US-09-534-850-14161	Sequence 14161, A
c 274	16	0.5	25	7	US-60-417-190-18150	Sequence 18150, A	c 347	16	0.5	217	5	US-09-534-850-20474	Sequence 20474, A
c 275	16	0.5	25	7	US-60-417-190-76888	Sequence 76888, A	c 348	16	0.5	217	5	US-09-534-850-20511	Sequence 20511, A
c 276	16	0.5	25	7	US-60-417-190-76889	Sequence 76889, A	c 349	16	0.5	219	5	US-09-534-850-14108	Sequence 14108, A
c 277	16	0.5	25	7	US-60-417-190-76890	Sequence 76890, A	c 350	16	0.5	220	6	US-10-203-138A-8358	Sequence 8358, Ap
c 278	16	0.5	25	7	US-60-417-190-76891	Sequence 76891, A	c 351	16	0.5	232	5	US-09-534-850-14113	Sequence 14113, A
c 279	16	0.5	25	7	US-60-417-190-109583	Sequence 109583, A	c 352	16	0.5	236	5	US-09-534-850-14167	Sequence 14167, A
c 280	16	0.5	25	7	US-60-417-190-109584	Sequence 109584, A	c 353	16	0.5	236	5	US-09-531-113-13805	Sequence 13805, A
c 281	16	0.5	25	7	US-60-417-190-109585	Sequence 109585, A	c 354	16	0.5	236	5	US-09-531-113-34374	Sequence 34374, A
c 282	16	0.5	25	7	US-60-417-190-109586	Sequence 109586, A	c 355	16	0.5	239	5	US-09-534-850-14148	Sequence 14148, A
c 283	16	0.5	25	7	US-60-417-190-109587	Sequence 109587, A	c 356	16	0.5	239	5	US-09-531-113-38807	Sequence 38807, A
c 284	16	0.5	25	7	US-60-417-190-109588	Sequence 109588, A	c 357	16	0.5	242	5	US-09-531-113-35841	Sequence 35841, A
c 285	16	0.5	25	7	US-60-427-808-6042	Sequence 6042, Ap	c 358	16	0.5	243	5	US-09-531-113-33143	Sequence 33143, A
c 286	16	0.5	25	7	US-60-427-808-27819	Sequence 27819, A	c 359	16	0.5	244	5	US-09-534-850-14118	Sequence 14118, A
c 287	16	0.5	25	7	US-60-427-808-30853	Sequence 30853, A	c 360	16	0.5	244	5	US-09-534-850-14127	Sequence 14127, A
c 288	16	0.5	25	7	US-60-427-808-96867	Sequence 96867, A	c 361	16	0.5	245	5	US-09-534-850-20473	Sequence 20473, A
c 289	16	0.5	25	7	US-60-427-808-128295	Sequence 128295, A	c 362	16	0.5	247	5	US-09-513-999C-34995	Sequence 34995, A
c 290	16	0.5	25	7	US-60-427-808-157246	Sequence 157246, A	c 363	16	0.5	247	5	US-09-531-113-37893	Sequence 37893, A
c 291	16	0.5	25	7	US-60-427-808-156677	Sequence 156677, A	c 364	16	0.5	250	5	US-09-534-850-14166	Sequence 14166, A
c 292	16	0.5	25	7	US-60-427-808-226607	Sequence 226607, A	c 365	16	0.5	250	5	US-09-531-113-15336	Sequence 15336, A
c 293	16	0.5	25	7	US-60-427-808-261911	Sequence 261911, A	c 366	16	0.5	251	5	US-09-531-113-21411	Sequence 21411, A
c 294	16	0.5	25	7	US-60-427-808-323347	Sequence 323347, A	c 367	16	0.5	251	5	US-09-531-113-36520	Sequence 36520, A
c 295	16	0.5	25	7	US-60-427-808-406973	Sequence 406973, A	c 368	16	0.5	251	5	US-09-531-113-40669	Sequence 40669, A
c 296	16	0.5	25	7	US-60-427-808-609848	Sequence 609848, A	c 369	16	0.5	252	5	US-09-534-850-13505	Sequence 13505, A
c 297	16	0.5	25	7	US-60-427-808-638248	Sequence 638248, A	c 370	16	0.5	252	5	US-09-531-113-36954	Sequence 36954, A
c 298	16	0.5	25	7	US-60-427-808-638519	Sequence 638519, A	c 371	16	0.5	252	6	US-10-203-138A-7707	Sequence 7707, Ap
c 299	16	0.5	25	7	US-60-427-808-687341	Sequence 687341, A	c 372	16	0.5	254	5	US-09-531-113-1061	Sequence 1061, Ap
c 300	16	0.5	25	7	US-60-427-808-898894	Sequence 898894, A	c 373	16	0.5	254	5	US-09-531-113-19121	Sequence 19121, A
c 301	16	0.5	25	7	US-60-427-808-939179	Sequence 939179, A	c 374	16	0.5	255	5	US-09-531-113-24210	Sequence 24210, A
c 302	16	0.5	25	7	US-60-427-808-943215	Sequence 943215, A	c 375	16	0.5	255	5	US-09-747-358A-263	Sequence 263, App
c 303	16	0.5	25	7	US-60-427-808-982255	Sequence 982255, A	c 376	16	0.5	255	5	US-09-531-113-22670	Sequence 22670, A
c 304	16	0.5	25	7	US-60-427-808-7102	Sequence 7102, Ap	c 377	16	0.5	256	5	US-09-531-113-26109	Sequence 26109, A
c 305	16	0.5	25	7	US-60-427-836-66322	Sequence 66322, A	c 378	16	0.5	258	5	US-09-513-999C-3556	Sequence 3556, Ap
c 306	16	0.5	25	7	US-60-427-836-100573	Sequence 100573, A	c 379	16	0.5	260	5	US-09-513-999C-3556	Sequence 3556, Ap
c 307	16	0.5	25	7	US-60-427-836-115604	Sequence 115604, A	c 380	16	0.5	260	5	US-09-534-850-14153	Sequence 14153, A
c 308	16	0.5	25	7	US-60-427-836-135906	Sequence 125906, A	c 381	16	0.5	261	5	US-09-531-113-303	Sequence 303, App
c 309	16	0.5	25	7	US-60-427-836-143583	Sequence 143583, A	c 382	16	0.5	261	5	US-09-531-113-44808	Sequence 44808, A
c 310	16	0.5	25	7	US-60-427-836-189920	Sequence 189920, A	c 383	16	0.5	262	5	US-09-531-113-24588	Sequence 24588, A
c 311	16	0.5	25	7	US-60-427-836-194689	Sequence 194689, A	c 384	16	0.5	263	5	US-09-531-113-20441	Sequence 20441, A
c 312	16	0.5	25	7	US-60-427-836-229530	Sequence 229530, A	c 385	16	0.5	265	5	US-09-534-850-14124	Sequence 14124, A
c 313	16	0.5	25	7	US-60-427-836-255656	Sequence 255656, A	c 386	16	0.5	267	5	US-09-531-113-668	Sequence 668, App
c 314	16	0.5	25	7	US-60-427-836-268477	Sequence 268477, A	c 387	16	0.5	267	5	US-09-531-113-43592	Sequence 43592, A
c 315	16	0.5	25	7	US-60-427-836-346739	Sequence 346739, A	c 388	16	0.5	269	5	US-09-534-850-14119	Sequence 14119, A
c 316	16	0.5	25	7	US-60-427-836-347632	Sequence 347632, A	c 389	16	0.5	269	5	US-09-531-113-15951	Sequence 15951, A
c 317	16	0.5	25	7	US-60-427-836-377335	Sequence 377335, A	c 390	16	0.5	270	5	US-09-531-113-46774	Sequence 46774, A
c 318	16	0.5	25	7	US-60-427-836-403963	Sequence 403963, A	c 391	16	0.5	271	5	US-09-534-850-14112	Sequence 14112, A

392	16	0.5	271	6	US-10-203-138A-6861	Sequence 6861, App	465	16	0.5	543	5	US-09-134-000C-394	Sequence 394, App
393	16	0.5	274	5	US-09-531-113-23604	Sequence 23604, A	466	16	0.5	543	5	US-09-134-000C-394	Sequence 394, App
C 394	16	0.5	278	6	US-10-335-066-1954	Sequence 1954, App	467	16	0.5	552	5	US-09-531-113-6221	Sequence 6221, App
C 395	16	0.5	282	6	US-10-266-131-2350	Sequence 2350, App	468	16	0.5	562	6	US-10-240-425-708	Sequence 708, App
C 396	16	0.5	287	5	US-09-531-113-45594	Sequence 45594, A	469	16	0.5	563	5	US-09-531-113-4122	Sequence 4122, App
C 397	16	0.5	290	5	US-09-534-850-25516	Sequence 25516, A	c 470	16	0.5	573	4	US-08-906-1568-67	Sequence 67, Appl
C 398	16	0.5	302	6	US-10-071-510-11	Sequence 11, Appl	c 471	16	0.5	573	4	US-08-906-1568-67	Sequence 67, Appl
C 399	16	0.5	306	5	US-09-513-999C-27209	Sequence 27209, A	c 472	16	0.5	574	6	US-10-266-131-2355	Sequence 2355, App
C 400	16	0.5	321	5	US-09-134-000C-3172	Sequence 3172, App	c 473	16	0.5	578	1	PCT-US02-31467-58	Sequence 58, Appl
C 401	16	0.5	321	5	US-09-134-000C-3276	Sequence 3276, App	c 474	16	0.5	585	5	US-09-531-113-29196	Sequence 19, Appl
C 402	16	0.5	321	5	US-09-134-000C-3172	Sequence 3172, App	c 475	16	0.5	590	4	US-08-906-1568-19	Sequence 19, Appl
C 403	16	0.5	321	5	US-09-134-000C-3276	Sequence 3276, App	c 476	16	0.5	590	4	US-08-906-1568-19	Sequence 19, Appl
C 404	16	0.5	322	6	US-10-209-582-54	Sequence 54, Appl	c 477	16	0.5	597	6	US-10-203-138A-10251	Sequence 10251, A
C 405	16	0.5	331	6	US-10-071-510-6	Sequence 6, Appl	c 478	16	0.5	600	6	US-10-310-673-1401	Sequence 1401, A
C 406	16	0.5	335	6	US-10-329-624-4258	Sequence 4258, App	c 479	16	0.5	601	5	US-09-949-002-3848	Sequence 3848, App
C 407	16	0.5	336	6	US-10-329-624-2989	Sequence 2989, App	c 480	16	0.5	601	5	US-09-949-002-8561	Sequence 8561, App
C 408	16	0.5	363	5	US-09-534-850-14158	Sequence 14158, A	c 481	16	0.5	601	5	US-09-949-004-848	Sequence 848, App
C 409	16	0.5	367	6	US-10-329-624-4109	Sequence 4109, App	c 482	16	0.5	601	5	US-09-949-004-1605	Sequence 1605, App
C 410	16	0.5	383	6	US-10-276-774-1210	Sequence 1210, App	c 483	16	0.5	601	5	US-09-949-004-1605	Sequence 1605, App
C 411	16	0.5	394	5	US-09-513-999C-34127	Sequence 34127, A	c 484	16	0.5	601	5	US-09-949-004-1729	Sequence 1729, App
C 412	16	0.5	397	5	US-09-724-676-30388	Sequence 30388, A	c 485	16	0.5	601	5	US-09-949-004-1851	Sequence 1851, App
C 413	16	0.5	397	5	US-09-724-676-30388	Sequence 30388, A	c 486	16	0.5	601	5	US-09-949-004-1896	Sequence 1896, App
C 414	16	0.5	403	6	US-10-276-781-857	Sequence 857, App	c 487	16	0.5	601	5	US-09-949-004-3181	Sequence 3181, App
C 415	16	0.5	411	5	US-09-513-999C-31900	Sequence 31900, A	c 488	16	0.5	601	5	US-09-949-004-3182	Sequence 3182, App
C 416	16	0.5	415	5	US-09-134-000C-3142	Sequence 3142, App	c 489	16	0.5	601	5	US-09-949-004-5506	Sequence 5506, App
C 417	16	0.5	415	5	US-09-134-000C-3142	Sequence 3142, App	c 490	16	0.5	604	6	US-10-203-138A-5437	Sequence 5437, App
C 418	16	0.5	415	6	US-10-203-138A-3207	Sequence 3207, App	c 491	16	0.5	607	5	US-09-531-113-12530	Sequence 12530, A
C 419	16	0.5	416	7	US-06-422-176-2757	Sequence 2757, App	c 492	16	0.5	626	5	US-09-724-676-17161	Sequence 17161, A
C 420	16	0.5	417	5	US-09-513-999C-1951	Sequence 1951, App	c 493	16	0.5	626	5	US-09-724-676-17161	Sequence 17161, A
C 421	16	0.5	422	5	US-09-724-676-30391	Sequence 30391, A	c 494	16	0.5	631	5	US-09-531-113-7814	Sequence 7814, App
C 422	16	0.5	425	5	US-09-724-676A-30391	Sequence 30391, A	c 495	16	0.5	634	5	US-09-724-676-30385	Sequence 30385, A
C 423	16	0.5	425	6	US-09-513-999C-12134	Sequence 12134, A	c 496	16	0.5	634	5	US-09-724-676A-30385	Sequence 30385, A
C 424	16	0.5	425	6	US-10-218-140-619	Sequence 619, App	c 497	16	0.5	634	6	US-10-203-138A-7222	Sequence 7222, App
C 425	16	0.5	437	6	US-10-152-319A-486	Sequence 486, App	c 498	16	0.5	635	6	US-10-218-140-2453	Sequence 2453, App
C 426	16	0.5	437	6	US-10-301-856-307	Sequence 307, App	c 499	16	0.5	635	6	US-10-230-437-115	Sequence 115, App
C 427	16	0.5	439	6	US-09-949-002-6987	Sequence 6987, App	c 500	16	0.5	638	6	US-10-223-089-195	Sequence 195, App
C 428	16	0.5	439	6	US-10-264-237-49	Sequence 49, Appl	c 501	16	0.5	728	6	US-10-219-076-115	Sequence 115, App
C 429	16	0.5	441	5	US-09-724-676-30386	Sequence 30386, A	c 502	16	0.5	728	6	US-10-219-076-115	Sequence 115, App
C 430	16	0.5	441	5	US-09-724-676A-30386	Sequence 30386, A	c 503	16	0.5	728	6	US-10-219-076-115	Sequence 115, App
C 431	16	0.5	443	6	US-10-240-425-868	Sequence 868, App	c 504	16	0.5	770	6	US-10-219-076-115	Sequence 115, App
C 432	16	0.5	446	6	US-10-203-138A-2206	Sequence 2206, App	c 505	16	0.5	770	6	PCT-US02-28859-13	Sequence 13, Appl
C 433	16	0.5	446	6	US-10-071-510-7	Sequence 7, Appl	c 506	16	0.5	799	1	PCT-US02-18668-5	Sequence 5, Appl
C 434	16	0.5	447	6	US-10-092-411A-1190	Sequence 1190, App	c 507	16	0.5	803	6	US-10-194-163-684	Sequence 684, App
C 435	16	0.5	449	5	US-09-534-850-22738	Sequence 22738, App	c 508	16	0.5	825	5	US-09-950-084-2672	Sequence 2672, App
C 436	16	0.5	456	5	US-09-531-113-9224	Sequence 9224, App	c 509	16	0.5	837	5	US-09-134-000C-319	Sequence 319, App
C 437	16	0.5	458	6	US-09-531-113-43241	Sequence 43241, App	c 510	16	0.5	837	5	US-09-134-000C-319	Sequence 319, App
C 438	16	0.5	458	6	US-10-071-510-10	Sequence 10, Appl	c 511	16	0.5	844	5	US-10-264-237-551	Sequence 551, App
C 439	16	0.5	465	5	US-09-531-113-29074	Sequence 29074, A	c 512	16	0.5	855	5	US-09-724-676A-25411	Sequence 25411, A
C 440	16	0.5	465	6	US-10-203-138A-664	Sequence 664, App	c 513	16	0.5	855	5	US-09-724-676A-25411	Sequence 25411, A
C 441	16	0.5	465	6	US-10-203-138A-3339	Sequence 3339, App	c 514	16	0.5	881	6	US-10-264-237-428	Sequence 428, App
C 442	16	0.5	466	5	US-09-724-676-30389	Sequence 30389, A	c 515	16	0.5	881	6	US-10-240-425-658	Sequence 658, App
C 443	16	0.5	466	5	US-09-724-676A-3514	Sequence 3514, App	c 516	16	0.5	901	5	US-09-620-120-814	Sequence 814, App
C 444	16	0.5	467	6	US-10-203-138A-3514	Sequence 3514, App	c 517	16	0.5	915	6	US-10-329-624-739	Sequence 739, App
C 445	16	0.5	469	6	US-10-203-138A-2929	Sequence 2929, App	c 518	16	0.5	915	6	US-10-329-624-739	Sequence 739, App
C 446	16	0.5	471	6	US-10-203-138A-2441	Sequence 2441, App	c 519	16	0.5	943	6	US-10-017-161-1851	Sequence 1851, App
C 447	16	0.5	474	6	US-10-203-138A-1734	Sequence 1734, App	c 520	16	0.5	962	5	US-09-724-676-15881	Sequence 15881, A
C 448	16	0.5	475	6	US-10-203-138A-2608	Sequence 2608, App	c 521	16	0.5	962	5	US-09-724-676A-15881	Sequence 15881, A
C 449	16	0.5	477	6	US-10-203-138A-147	Sequence 147, App	c 522	16	0.5	972	6	US-10-203-138A-2107	Sequence 2107, App
C 450	16	0.5	482	6	US-09-949-002-6986	Sequence 6986, App	c 523	16	0.5	993	5	US-09-950-084-2296	Sequence 2296, App
C 451	16	0.5	482	6	US-10-203-138A-9245	Sequence 9245, App	c 524	16	0.5	998	6	US-10-278-173-147	Sequence 147, Appl
C 452	16	0.5	491	6	US-10-266-131-2388	Sequence 2388, App	c 525	16	0.5	998	6	US-10-278-173-147	Sequence 147, Appl
C 453	16	0.5	492	5	US-09-534-850-23347	Sequence 23347, A	c 526	16	0.5	1044	5	US-10-278-536A-91	Sequence 91, Appl
C 454	16	0.5	495	6	US-10-152-319A-57	Sequence 57, Appl	c 527	16	0.5	1050	5	US-09-950-084-3303	Sequence 3303, App
C 455	16	0.5	502	5	US-09-534-850-23348	Sequence 23348, A	c 528	16	0.5	1057	1	PCT-US02-35606-39	Sequence 39, Appl
C 456	16	0.5	504	6	US-10-321-854-3709	Sequence 3709, App	c 529	16	0.5	1073	1	PCT-US02-18666-9	Sequence 9, Appl
C 457	16	0.5	504	6	US-10-321-854-3709	Sequence 3709, App	c 530	16	0.5	1084	6	US-10-152-319A-1992	Sequence 1992, App
C 458	16	0.5	506	7	US-60-422-176-1544	Sequence 1544, App	c 531	16	0.5	1089	5	US-09-724-676-40650	Sequence 40650, A
C 459	16	0.5	510	6	US-09-531-113-4372	Sequence 4372, App	c 532	16	0.5	1089	6	US-10-305-720-1381	Sequence 1381, App
C 460	16	0.5	511	6	US-10-327-713-82	Sequence 82, Appl	c 533	16	0.5	1089	6	US-10-305-720-1381	Sequence 1381, App
C 461	16	0.5	514	6	US-09-534-850-23355	Sequence 23355, A	c 534	16	0.5	1133	6	US-10-092-411A-586	Sequence 586, App
C 462	16	0.5	524	5	US-08-531-113-12563	Sequence 12563, A	c 535	16	0.5	1133	6	US-10-017-161-2355	Sequence 2355, App
C 463	16	0.5	529	5	US-09-534-850-22737	Sequence 22737, A	c 536	16	0.5	1134	6	US-10-302-267-119	Sequence 119, App
C 464	16	0.5	536	5	US-09-531-113-30061	Sequence 30061, A	c 537	16	0.5	1134	6	US-10-287-274-258	Sequence 258, App

538	16	0.5	1138	5	US-09-724-676-35837	Sequence 35837, A	c 611	16	0.5	1762	5	US-09-724-676A-23874	Sequence 23874, A
539	16	0.5	1138	5	US-09-724-676A-35837	Sequence 35837, A	612	16	0.5	1781	6	US-10-276-774-1080	Sequence 1080, Ap
540	16	0.5	1146	5	US-09-134-000C-1824	Sequence 1824, Ap	613	16	0.5	1811	6	US-10-131-985-52	Sequence 52, Appl
541	16	0.5	1146	5	US-09-134-000C-1824	Sequence 1824, Ap	614	16	0.5	1840	6	US-10-305-720-1367	Sequence 1367, Ap
542	16	0.5	1149	5	US-09-134-000C-1632	Sequence 1632, Ap	615	16	0.5	1858	5	US-09-724-676-25412	Sequence 25412, A
543	16	0.5	1149	5	US-09-134-000C-1632	Sequence 1632, Ap	616	16	0.5	1858	5	US-09-724-676A-23412	Sequence 23412, A
c 544	16	0.5	1171	1	PCT-US02-18666-11	Sequence 11, Appl	c 617	16	0.5	1870	5	US-09-724-676-23904	Sequence 23904, A
545	16	0.5	1232	6	US-09-620-312D-672	Sequence 672, App	c 618	16	0.5	1870	5	US-09-724-676A-23904	Sequence 23904, A
546	16	0.5	1233	6	US-10-072-012-195	Sequence 195, App	619	16	0.5	1874	5	US-09-724-676-20569	Sequence 20569, A
547	16	0.5	1233	6	US-10-203-138A-8047	Sequence 8047, App	620	16	0.5	1874	5	US-09-724-676A-20569	Sequence 20569, A
c 548	16	0.5	1279	5	US-09-724-676-11678	Sequence 11678, A	c 621	16	0.5	1875	5	US-09-724-676-14582	Sequence 14582, A
c 549	16	0.5	1279	5	US-09-724-676A-11678	Sequence 11678, A	c 622	16	0.5	1875	5	US-09-724-676A-14582	Sequence 14582, A
550	16	0.5	1305	5	US-09-724-676-30638	Sequence 30638, A	c 623	16	0.5	1876	5	US-09-724-676-47490	Sequence 47490, A
551	16	0.5	1305	5	US-09-724-676A-30638	Sequence 30638, A	c 624	16	0.5	1876	5	US-09-724-676A-47490	Sequence 47490, A
c 552	16	0.5	1311	6	US-10-092-411A-386	Sequence 386, App	c 625	16	0.5	1888	6	US-10-315-664-38	Sequence 38, Appl
553	16	0.5	1311	6	US-10-304-105-4	Sequence 4, Appli	626	16	0.5	1893	5	US-09-724-676-15888	Sequence 15888, A
554	16	0.5	1321	5	US-09-724-676-17163	Sequence 17163, A	627	16	0.5	1893	5	US-09-724-676A-15888	Sequence 15888, A
555	16	0.5	1321	5	US-09-724-676A-17163	Sequence 17163, A	c 628	16	0.5	1901	5	US-09-724-676-14581	Sequence 14581, A
556	16	0.5	1322	7	US-60-427-982-120	Sequence 120, App	c 629	16	0.5	1901	5	US-09-724-676A-14581	Sequence 14581, A
557	16	0.5	1333	6	US-10-017-161-545	Sequence 545, App	630	16	0.5	1906	5	US-09-724-676-30384	Sequence 30384, A
c 558	16	0.5	1339	5	US-09-724-676-11676	Sequence 11676, A	c 631	16	0.5	1906	5	US-09-724-676A-30384	Sequence 30384, A
c 559	16	0.5	1339	5	US-09-724-676A-11676	Sequence 11676, A	c 632	16	0.5	1914	6	US-10-287-818-1298	Sequence 1298, Ap
560	16	0.5	1339	6	US-10-264-237-1242	Sequence 1242, Ap	633	16	0.5	1915	6	US-10-325-899-9261	Sequence 9261, Ap
c 561	16	0.5	1350	5	US-09-950-084-1603	Sequence 1603, Ap	c 634	16	0.5	1924	5	US-09-724-676-23909	Sequence 23909, A
562	16	0.5	1352	6	US-10-218-140-2879	Sequence 2879, Ap	c 635	16	0.5	1924	5	US-09-724-676A-23909	Sequence 23909, A
c 563	16	0.5	1363	5	US-09-724-676-15890	Sequence 15890, A	636	16	0.5	1928	6	US-10-218-140-4309	Sequence 4309, Ap
564	16	0.5	1363	5	US-09-724-676A-15890	Sequence 15890, A	c 637	16	0.5	1951	6	US-10-278-536A-45	Sequence 45, Appl
c 565	16	0.5	1380	6	US-10-288-252-22	Sequence 22, Appl	c 638	16	0.5	1951	6	US-10-278-536A-45	Sequence 45, Appl
c 566	16	0.5	1380	5	US-09-724-676-11683	Sequence 11683, A	c 639	16	0.5	1963	6	US-10-203-138A-2893	Sequence 2893, Ap
c 567	16	0.5	1390	5	US-09-724-676A-11683	Sequence 11683, A	c 640	16	0.5	1964	5	US-09-911-514-1	Sequence 1, Appli
568	16	0.5	1394	5	US-09-620-312D-364	Sequence 364, App	c 641	16	0.5	1966	7	US-60-427-982-109	Sequence 109, App
569	16	0.5	1404	5	US-09-948-124-146	Sequence 146, App	c 642	16	0.5	1969	6	US-10-203-138A-3479	Sequence 3479, Ap
c 570	16	0.5	1422	7	US-60-427-045-147	Sequence 147, App	c 643	16	0.5	1972	6	US-10-203-138A-5151	Sequence 5151, Ap
c 571	16	0.5	1450	5	US-09-724-676-11681	Sequence 11681, A	c 644	16	0.5	1988	5	US-09-724-676-23894	Sequence 23894, A
c 572	16	0.5	1450	6	US-09-724-676A-11681	Sequence 11681, A	c 645	16	0.5	1988	5	US-09-724-676A-23894	Sequence 23894, A
573	16	0.5	1455	6	US-10-305-720-1287	Sequence 1287, Ap	646	16	0.5	1989	6	US-10-218-140-5283	Sequence 5283, Ap
c 574	16	0.5	1458	5	US-09-724-676-12266	Sequence 12266, A	c 647	16	0.5	2042	5	US-09-724-676-23899	Sequence 23899, A
c 575	16	0.5	1458	5	US-09-724-676-23875	Sequence 23875, A	c 648	16	0.5	2042	5	US-09-724-676A-23899	Sequence 23899, A
c 576	16	0.5	1500	6	US-10-209-582-40	Sequence 40, Appl	c 649	16	0.5	2047	6	US-10-203-138A-8620	Sequence 8620, Ap
c 577	16	0.5	1500	6	US-10-209-582-40	Sequence 40, Appl	c 650	16	0.5	2050	6	US-10-264-237-1009	Sequence 1009, Ap
578	16	0.5	1513	6	US-10-218-140-5481	Sequence 5481, Ap	c 651	16	0.5	2070	1	PCT-US02-29560-44	Sequence 44, Appl
579	16	0.5	1523	5	US-09-724-676-12266	Sequence 12266, A	c 652	16	0.5	2070	6	US-10-245-882-44	Sequence 44, Appl
c 580	16	0.5	1523	5	US-09-724-676A-12266	Sequence 12266, A	c 653	16	0.5	2076	5	US-09-724-676-23905	Sequence 23905, A
c 581	16	0.5	1551	6	US-10-029-397B-29	Sequence 29, Appl	c 654	16	0.5	2076	5	US-09-724-676A-23905	Sequence 23905, A
582	16	0.5	1574	5	US-09-724-676-12272	Sequence 12272, A	655	16	0.5	2078	5	US-09-724-676-12269	Sequence 12269, A
583	16	0.5	1574	5	US-09-724-676A-12272	Sequence 12272, A	656	16	0.5	2078	5	US-09-724-676A-12269	Sequence 12269, A
584	16	0.5	1594	5	US-09-724-676-33114	Sequence 33114, A	c 657	16	0.5	2088	6	US-10-287-818-1312	Sequence 1312, Ap
585	16	0.5	1594	5	US-09-724-676A-33114	Sequence 33114, A	c 658	16	0.5	2104	5	US-09-724-676-30364	Sequence 30364, A
586	16	0.5	1597	5	US-09-921-406C-39	Sequence 39, Appl	c 659	16	0.5	2104	5	US-09-724-676A-30364	Sequence 30364, A
587	16	0.5	1599	5	US-09-724-676-12268	Sequence 12268, A	c 660	16	0.5	2115	6	US-10-287-818-1313	Sequence 1313, Ap
c 588	16	0.5	1599	5	US-09-724-676-12268	Sequence 12268, A	c 661	16	0.5	2115	5	US-09-724-676-23902	Sequence 23902, A
c 589	16	0.5	1618	5	US-09-814-915A-48	Sequence 48, Appl	c 662	16	0.5	2115	5	US-09-724-676A-23902	Sequence 23902, A
c 590	16	0.5	1636	5	US-09-911-514-7	Sequence 7, Appli	c 663	16	0.5	2125	5	US-09-724-676-34195	Sequence 34195, A
c 591	16	0.5	1642	5	US-09-911-514-5	Sequence 5, Appli	c 664	16	0.5	2125	5	US-09-724-676A-34195	Sequence 34195, A
c 592	16	0.5	1642	5	US-09-911-514-9	Sequence 9, Appli	665	16	0.5	2128	5	US-09-724-676-12267	Sequence 12267, A
c 593	16	0.5	1643	5	US-09-911-514-3	Sequence 3, Appli	666	16	0.5	2128	5	US-09-724-676A-12267	Sequence 12267, A
594	16	0.5	1650	5	US-09-724-676-12275	Sequence 12275, A	c 667	16	0.5	2129	5	US-09-724-676-12261	Sequence 12261, A
595	16	0.5	1650	5	US-09-724-676A-12275	Sequence 12275, A	668	16	0.5	2129	5	US-09-724-676A-12261	Sequence 12261, A
c 596	16	0.5	1655	5	US-09-724-676-27588	Sequence 27588, A	c 669	16	0.5	2130	5	US-09-724-676-23910	Sequence 23910, A
c 597	16	0.5	1655	5	US-09-724-676A-27588	Sequence 27588, A	c 670	16	0.5	2130	5	US-09-724-676A-23910	Sequence 23910, A
c 598	16	0.5	1664	5	US-09-724-676-23876	Sequence 23876, A	c 671	16	0.5	2151	5	US-09-724-676-12264	Sequence 12264, A
c 599	16	0.5	1664	5	US-09-724-676A-23876	Sequence 23876, A	672	16	0.5	2151	5	US-09-724-676A-12264	Sequence 12264, A
600	16	0.5	1672	5	US-09-724-676-12263	Sequence 12263, A	c 673	16	0.5	2163	1	PCT-US02-40225-2287	Sequence 2287, Ap
c 601	16	0.5	1672	6	US-09-724-676A-12263	Sequence 12263, A	c 674	16	0.5	2163	6	US-10-320-797-2287	Sequence 2287, Ap
c 602	16	0.5	1678	5	US-10-218-140-1593	Sequence 1593, Ap	c 675	16	0.5	2169	5	US-09-724-676-23907	Sequence 23907, A
c 603	16	0.5	1703	5	US-09-724-676-23873	Sequence 23873, A	c 676	16	0.5	2169	5	US-09-724-676A-23907	Sequence 23907, A
c 604	16	0.5	1703	5	US-09-724-676A-23873	Sequence 23873, A	c 677	16	0.5	2174	5	US-09-724-676-23903	Sequence 23903, A
605	16	0.5	1723	5	US-09-724-676-12273	Sequence 12273, A	c 678	16	0.5	2174	5	US-09-724-676A-23903	Sequence 23903, A
606	16	0.5	1728	5	US-09-724-676A-12273	Sequence 12273, A	679	16	0.5	2179	5	US-09-724-676-12270	Sequence 12270, A
c 607	16	0.5	1728	5	US-10-210-120-23	Sequence 23, Appl	680	16	0.5	2179	5	US-09-724-676A-12270	Sequence 12270, A
c 608	16	0.5	1735	1	PCT-US02-18666-3	Sequence 3, Appli	681	16	0.5	2184	5	US-09-134-000C-3320	Sequence 3320, Ap
c 609	16	0.5	1740	5	US-09-950-084-2114	Sequence 2114, Ap	682	16	0.5	2184	5	US-09-134-000C-3320	Sequence 3320, Ap
c 610	16	0.5	1762	5	US-09-724-676-23874	Sequence 23874, A	c 683	16	0.5	2194	5	US-09-724-676-23895	Sequence 23895, A

c 684	16	0.5	2194	5	US-09-724-676A-23895	Sequence 23895, A	757	16	0.5	2677	5	US-09-724-676A-20568	Sequence 20568, A
c 685	16	0.5	2200	5	US-09-949-004-2022	Sequence 202, App	758	16	0.5	2678	6	US-10-017-161-1647	Sequence 1647, App
c 686	16	0.5	2201	5	US-09-724-676-12262	Sequence 12262, A	759	16	0.5	2681	6	US-10-152-319A-1631	Sequence 1631, App
c 687	16	0.5	2201	5	US-09-724-676A-12262	Sequence 12262, A	760	16	0.5	2686	5	US-09-724-676-30503	Sequence 30503, A
c 688	16	0.5	2202	5	US-09-724-676-12274	Sequence 12274, A	761	16	0.5	2686	5	US-09-724-676A-30503	Sequence 30503, A
c 689	16	0.5	2202	5	US-09-724-676A-12274	Sequence 12274, A	c 762	16	0.5	2705	1	PCT-US02-40225-1287	Sequence 1287, App
c 690	16	0.5	2205	5	US-09-724-676-29646	Sequence 29646, A	c 763	16	0.5	2705	6	US-10-320-797-1287	Sequence 1287, App
c 691	16	0.5	2205	5	US-09-724-676A-29646	Sequence 29646, A	c 764	16	0.5	2723	5	US-09-724-676-30536	Sequence 30536, A
c 692	16	0.5	2222	6	US-10-324-130-1	Sequence 1, Appl	765	16	0.5	2723	5	US-09-724-676A-30536	Sequence 30536, A
c 693	16	0.5	2228	5	US-09-724-676-23908	Sequence 23908, A	766	16	0.5	2738	5	US-09-724-676-30509	Sequence 30509, A
c 694	16	0.5	2233	5	US-09-724-676A-23908	Sequence 23908, A	767	16	0.5	2738	5	US-09-724-676A-30509	Sequence 30509, A
c 695	16	0.5	2233	5	US-09-724-676-23892	Sequence 23892, A	768	16	0.5	2742	1	PCT-US02-21420-20	Sequence 20, Appl
c 696	16	0.5	2233	5	US-09-724-676A-23892	Sequence 23892, A	769	16	0.5	2742	6	US-10-190-305A-15	Sequence 15, Appl
c 697	16	0.5	2239	5	US-09-724-676-40652	Sequence 40652, A	770	16	0.5	2742	6	US-10-190-435-20	Sequence 20, Appl
c 698	16	0.5	2239	5	US-09-724-676A-40652	Sequence 40652, A	c 771	16	0.5	2748	5	US-09-724-676-47489	Sequence 47489, A
c 699	16	0.5	2248	5	US-09-724-676-23900	Sequence 23900, A	c 772	16	0.5	2748	5	US-09-724-676A-47489	Sequence 47489, A
c 700	16	0.5	2248	5	US-09-724-676A-23900	Sequence 23900, A	c 773	16	0.5	2762	5	US-09-724-676-30511	Sequence 30511, A
c 701	16	0.5	2253	6	US-10-171-404A-1	Sequence 1, Appl	c 774	16	0.5	2762	5	US-09-724-676A-30511	Sequence 30511, A
c 702	16	0.5	2277	6	US-10-276-774-97	Sequence 97, Appl	c 775	16	0.5	2775	5	US-09-724-676-23880	Sequence 23880, A
c 703	16	0.5	2279	1	PCT-US02-28859-6	Sequence 6, Appl	c 776	16	0.5	2775	5	US-09-724-676A-23880	Sequence 23880, A
c 704	16	0.5	2279	6	US-10-241-220-6	Sequence 6, Appl	c 777	16	0.5	2814	5	US-09-724-676-30522	Sequence 30522, A
c 705	16	0.5	2287	5	US-09-724-676-23897	Sequence 23897, A	c 778	16	0.5	2814	5	US-09-724-676-30522	Sequence 30522, A
c 706	16	0.5	2287	5	US-09-724-676-8957	Sequence 8957, App	c 779	16	0.5	2818	5	US-09-724-676-30520	Sequence 30520, A
c 707	16	0.5	2291	5	US-09-724-676A-8957	Sequence 8957, App	c 780	16	0.5	2818	5	US-09-724-676-30520	Sequence 30520, A
c 708	16	0.5	2291	5	US-09-724-676A-23893	Sequence 23893, A	c 781	16	0.5	2818	5	US-09-724-676A-30513	Sequence 30513, A
c 709	16	0.5	2292	5	US-09-724-676-23893	Sequence 23893, A	c 782	16	0.5	2829	5	US-09-724-676A-30520	Sequence 30520, A
c 710	16	0.5	2307	5	US-09-724-676-34193	Sequence 34193, A	c 783	16	0.5	2829	5	US-09-724-676A-23885	Sequence 23885, A
c 711	16	0.5	2307	5	US-09-724-676-34193	Sequence 34193, A	c 784	16	0.5	2835	6	US-10-240-965-126	Sequence 126, App
c 712	16	0.5	2307	5	US-09-724-676A-34193	Sequence 34193, A	c 785	16	0.5	2835	6	US-10-240-965-126	Sequence 126, App
c 713	16	0.5	2346	5	US-09-724-676A-23898	Sequence 23898, A	c 786	16	0.5	2840	6	US-10-152-319A-1540	Sequence 1540, App
c 714	16	0.5	2346	5	US-09-724-676A-23898	Sequence 23898, A	c 787	16	0.5	2840	6	US-09-724-676-30530	Sequence 30530, A
c 715	16	0.5	2356	5	US-09-136-159-68	Sequence 68, Appl	c 788	16	0.5	2870	5	US-09-724-676-30538	Sequence 30538, A
c 716	16	0.5	2356	5	US-09-136-159A-68	Sequence 68, Appl	c 789	16	0.5	2870	5	US-09-724-676A-30530	Sequence 30530, A
c 717	16	0.5	2356	6	US-10-136-159A-68	Sequence 68, Appl	c 790	16	0.5	2870	5	US-09-724-676A-30538	Sequence 30538, A
c 718	16	0.5	2367	5	US-09-724-676-30518	Sequence 30518, A	c 791	16	0.5	2874	5	US-09-724-676-30523	Sequence 30523, A
c 719	16	0.5	2367	5	US-09-724-676A-30518	Sequence 30518, A	c 792	16	0.5	2874	5	US-09-724-676A-30523	Sequence 30523, A
c 720	16	0.5	2375	5	US-09-724-676-14580	Sequence 14580, A	c 793	16	0.5	2878	5	US-09-724-676-30501	Sequence 30501, A
c 721	16	0.5	2375	5	US-09-724-676A-14580	Sequence 14580, A	c 794	16	0.5	2878	5	US-09-724-676-30501	Sequence 30501, A
c 722	16	0.5	2401	5	US-09-724-676A-14579	Sequence 14579, A	c 795	16	0.5	2900	6	US-10-276-774-892	Sequence 892, App
c 723	16	0.5	2401	5	US-09-724-676A-14579	Sequence 14579, A	c 796	16	0.5	2926	5	US-09-724-676-30532	Sequence 30532, A
c 724	16	0.5	2419	5	US-09-724-676-30498	Sequence 30498, A	c 797	16	0.5	2926	5	US-09-724-676A-30532	Sequence 30532, A
c 725	16	0.5	2419	5	US-09-724-676-30498	Sequence 30498, A	c 798	16	0.5	2930	5	US-09-724-676-30507	Sequence 30507, A
c 726	16	0.5	2423	5	US-09-724-676-30528	Sequence 30528, A	c 799	16	0.5	2930	5	US-09-724-676A-30507	Sequence 30507, A
c 727	16	0.5	2423	7	US-60-427-313-157	Sequence 157, App	c 800	16	0.5	2934	5	US-09-724-676-30502	Sequence 30502, A
c 728	16	0.5	2423	7	US-60-427-313-157	Sequence 157, App	c 801	16	0.5	2934	5	US-09-724-676A-30502	Sequence 30502, A
c 729	16	0.5	2475	5	US-09-724-676A-30537	Sequence 30537, A	c 802	16	0.5	2977	5	US-09-724-676-34198	Sequence 34198, A
c 730	16	0.5	2475	5	US-09-724-676A-30537	Sequence 30537, A	c 803	16	0.5	2977	5	US-09-724-676-34198	Sequence 34198, A
c 731	16	0.5	2494	5	US-09-724-676-30372	Sequence 30372, A	c 804	16	0.5	2981	5	US-09-724-676A-23881	Sequence 23881, A
c 732	16	0.5	2494	5	US-09-724-676-30372	Sequence 30372, A	c 805	16	0.5	2981	5	US-09-724-676A-23881	Sequence 23881, A
c 733	16	0.5	2526	5	US-09-864-636A-391	Sequence 391, App	c 806	16	0.5	2986	5	US-09-724-676-30508	Sequence 30508, A
c 734	16	0.5	2526	5	US-09-864-636A-459	Sequence 459, App	c 807	16	0.5	2986	5	US-09-724-676A-30508	Sequence 30508, A
c 735	16	0.5	2526	6	US-10-084-839-459	Sequence 459, App	c 808	16	0.5	3001	5	US-09-539-333D-146	Sequence 146, App
c 736	16	0.5	2526	6	US-10-084-839-459	Sequence 459, App	c 809	16	0.5	3001	5	US-09-539-333D-146	Sequence 146, App
c 737	16	0.5	2526	6	US-10-084-839-2767	Sequence 2767, App	c 810	16	0.5	3012	5	US-09-724-676A-1434	Sequence 1434, App
c 738	16	0.5	2526	6	US-10-084-839-2767	Sequence 2767, App	c 811	16	0.5	3012	5	US-09-724-676A-1434	Sequence 1434, App
c 739	16	0.5	2529	5	US-09-620-312D-688	Sequence 688, App	c 812	16	0.5	3018	1	PCT-US02-40102-2	Sequence 2, Appl
c 740	16	0.5	2559	5	US-09-724-676-30515	Sequence 30515, A	c 813	16	0.5	3020	5	US-09-724-676-23878	Sequence 23878, A
c 741	16	0.5	2559	5	US-09-724-676A-30515	Sequence 30515, A	c 814	16	0.5	3020	5	US-09-724-676A-23878	Sequence 23878, A
c 742	16	0.5	2605	5	US-09-724-676-34196	Sequence 34196, A	c 815	16	0.5	3035	5	US-09-724-676-23886	Sequence 23886, A
c 743	16	0.5	2605	5	US-09-724-676A-34196	Sequence 34196, A	c 816	16	0.5	3035	5	US-09-724-676A-23886	Sequence 23886, A
c 744	16	0.5	2611	5	US-09-724-676-30539	Sequence 30539, A	c 817	16	0.5	3054	6	US-10-276-781-173	Sequence 173, App
c 745	16	0.5	2611	5	US-09-724-676A-30539	Sequence 30539, A	c 818	16	0.5	3064	1	PCT-US02-40717-19	Sequence 19, Appl
c 746	16	0.5	2615	5	US-09-724-676-30517	Sequence 30517, A	c 819	16	0.5	3074	5	US-09-724-676-23883	Sequence 23883, A
c 747	16	0.5	2615	5	US-09-724-676-30525	Sequence 30525, A	c 820	16	0.5	3074	5	US-09-724-676A-23883	Sequence 23883, A
c 748	16	0.5	2615	5	US-09-724-676A-30517	Sequence 30517, A	c 821	16	0.5	3079	5	US-09-724-676-23879	Sequence 23879, A
c 749	16	0.5	2667	5	US-09-724-676-30497	Sequence 30497, A	c 822	16	0.5	3079	5	US-09-724-676A-23879	Sequence 23879, A
c 750	16	0.5	2667	5	US-09-724-676-30497	Sequence 30497, A	c 823	16	0.5	3081	5	US-09-724-676-30499	Sequence 30499, A
c 751	16	0.5	2667	5	US-09-724-676A-30497	Sequence 30497, A	c 824	16	0.5	3081	5	US-09-724-676A-30499	Sequence 30499, A
c 752	16	0.5	2667	5	US-09-724-676A-30534	Sequence 30534, A	c 825	16	0.5	3082	5	US-09-724-676-33112	Sequence 33112, A
c 753	16	0.5	2671	5	US-09-724-676-30527	Sequence 30527, A	c 826	16	0.5	3082	5	US-09-724-676A-33112	Sequence 33112, A
c 754	16	0.5	2671	5	US-09-724-676A-30527	Sequence 30527, A	c 827	16	0.5	3085	5	US-09-724-676-1432	Sequence 1432, App
c 755	16	0.5	2671	5	US-09-724-676A-30527	Sequence 30527, A	c 828	16	0.5	3085	5	US-09-724-676A-1432	Sequence 1432, App
c 756	16	0.5	2677	5	US-09-724-676-20568	Sequence 20568, A	c 829	16	0.5	3133	5	US-09-724-676-23884	Sequence 23884, A

830	16	0.5	3133	5	US-09-724-676-30505	Sequence 30505, A	903	16	0.5	3567	6	US-10-131-823A-77	Sequence 77, Appl
c 831	16	0.5	3133	5	US-09-724-676A-23884	Sequence 23884, A	904	16	0.5	3567	6	US-10-131-824A-77	Sequence 77, Appl
832	16	0.5	3133	5	US-09-724-676A-30505	Sequence 30505, A	905	16	0.5	3567	6	US-10-131-826A-77	Sequence 77, Appl
833	16	0.5	3134	1	PCT-US02-33723-67	Sequence 67, Appl	906	16	0.5	3567	6	US-10-131-829A-77	Sequence 77, Appl
834	16	0.5	3134	5	US-09-724-676-48049	Sequence 48049, A	907	16	0.5	3567	6	US-10-125-926A-77	Sequence 77, Appl
835	16	0.5	3134	5	US-09-724-676A-48049	Sequence 48049, A	908	16	0.5	3567	6	US-10-127-829A-77	Sequence 77, Appl
836	16	0.5	3137	5	US-09-724-676-30500	Sequence 30500, A	909	16	0.5	3567	6	US-10-127-831A-77	Sequence 77, Appl
837	16	0.5	3137	5	US-09-724-676A-30500	Sequence 30500, A	910	16	0.5	3567	6	US-10-127-835A-77	Sequence 77, Appl
838	16	0.5	3147	6	US-10-301-997-84	Sequence 84, Appl	911	16	0.5	3567	6	US-10-127-837A-77	Sequence 77, Appl
839	16	0.5	3158	5	US-09-724-676-48050	Sequence 48050, A	912	16	0.5	3567	6	US-10-127-842A-77	Sequence 77, Appl
840	16	0.5	3158	5	US-09-724-676-48051	Sequence 48051, A	913	16	0.5	3567	6	US-10-127-850A-77	Sequence 77, Appl
841	16	0.5	3158	5	US-09-724-676A-48050	Sequence 48050, A	914	16	0.5	3567	6	US-10-127-901A-77	Sequence 77, Appl
842	16	0.5	3158	5	US-09-724-676A-48051	Sequence 48051, A	915	16	0.5	3567	6	US-10-128-689A-77	Sequence 77, Appl
843	16	0.5	3171	5	US-09-724-676-33110	Sequence 33110, A	916	16	0.5	3567	6	US-10-131-830A-77	Sequence 77, Appl
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847	16	0.5	3189	5	US-09-724-676-30506	Sequence 30506, A	920	16	0.5	3567	6	US-10-127-825A-77	Sequence 77, Appl
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857	16	0.5	3248	5	US-09-724-676-30516	Sequence 30516, A	930	16	0.5	3567	6	US-10-131-836A-77	Sequence 77, Appl
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876	16	0.5	3395	5	US-09-724-676-30510	Sequence 30510, A	949	16	0.5	3567	6	US-10-127-847A-77	Sequence 77, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application PC/TUS0221946A
; GENERAL INFORMATION:
; APPLICANT: Thomas Jefferson University
; APPLICANT: Alimenti, Emed S.
; TITLE OF INVENTION: PAF, AN ICE-PROTEASE ACTIVATING
; TITLE OF INVENTION: PAF, AN ICE-PROTEASE ACTIVATING
; FILE REFERENCE: 480140.477PC
; CURRENT APPLICATION NUMBER: PCT/US02/21946A
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
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; NAME/KEY: CDS
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Db 2701 AAACATTTGGAGAGGTCCCAACCTGCTCAAGCTTTGGGTTGAAAACTGGAGACTACA 2760
QY 2761 GATACAGAGATTAAGATTTTAGCTGCAATTTTGGGTTGAAAACTGGAGACTACA 2820
Db 2761 GATACAGAGATTAAGATTTTAGCTGCAATTTTGGGTTGAAAACTGGAGACTACA 2820
QY 2821 CAGTTGAATTTGGCGGAAATCGTGACGAGTGTGATGGCTTGCCTTCATGGGTGTA 2880
Db 2821 CAGTTGAATTTGGCGGAAATCGTGACGAGTGTGATGGCTTGCCTTCATGGGTGTA 2880
QY 2881 TTTGAGAACTTAAAGCAATTTAGTGTGTTTGGTGTAGTACTAAAGAAATTTTACCTGAT 2940
Db 2881 TTTGAGAACTTAAAGCAATTTAGTGTGTTTGGTGTAGTACTAAAGAAATTTTACCTGAT 2940
QY 2941 CCAGCATTTAGTCAAGAACTTACGAGTGTATCCAAAGTAACTTTTCTGCAAGAGCT 3000
Db 2941 CCAGCATTTAGTCAAGAACTTACGAGTGTATCCAAAGTAACTTTTCTGCAAGAGCT 3000
QY 3001 AGGCTTGTGGTGGCAATTTGATGATGATCTCAGTGTATTACAGTGTCTTTTAAA 3060
Db 3001 AGGCTTGTGGTGGCAATTTGATGATGATGATCTCAGTGTATTACAGTGTCTTTTAAA 3060
QY 3061 CTAGTAACTGCT 3072
Db 3061 CTAGTAACTGCT 3072

RESULT 2
PCT-US02-21946A-14
; Sequence 14, Application PC/TUS0221946A
; GENERAL INFORMATION:
; APPLICANT: Thomas Jefferson University
; APPLICANT: Alenuri, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; TITLE OF INVENTION: FACTOR
; FILE REFERENCE: 480140.477PC
; CURRENT APPLICATION NUMBER: PCT/US02/21946A
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-21946A-14

Query Match 95.0%; Score 2919; DB 1; Length 3219;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3069; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATCAATTTCAATGAAGCAATAGCCGAGCCCTTATTCAAAGATGGGAATGACTGTATATA 60
Db 145 ATGAATTTCAATGAAGCAATAGCCGAGCCCTTATTCAAAGATGGGAATGACTGTATATA 204

QY 61 AAGCAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAAGTAACATC 120
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Db 205 AAGCAATCACAGATGACCTATTGTTATGGAATGTTCTGAATCGCGAAGAAAGTAACATC 264
QY 121 ATTGCTCGAGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 180
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Db 265 ATTGCTCGAGAAGGTGGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGA 324
QY 181 AAGGTTACAGAGTCTGTAACTCTTTCTTAATCCCTTAAAGAGTGGAACTATCCTCTA 240
Db 325 AAGGTTACAGAGTCTGTAACTCTTTCTTAATCCCTTAAAGAGTGGAACTATCCTCTA 384
QY 241 TTTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAAGGAGCTTGGACGAT 300
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Db 385 TTTCAGGACTTGAATGGACAAAGTCTTTTTCATCAGACATCAGAAAGGAGCTTGGACGAT 444
QY 301 TTGGCTCAGGATTTAAAGACTTGTACCATACCCATCTTTCTGAACCTTTTATCCCTT 360
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Db 445 TTGGCTCAGGATTTAAAGACTTGTACCATACCCATCTTTCTGAACCTTTTATCCCTT 504
QY 361 GGTGAAGATATGACATTTATTTTAACTTGAAGAGCACTTCACAGAACCTGTCTGTGG 420
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Db 505 GGTGAAGATATGACATTTATTTTAACTTGAAGAGCACTTCACAGAACCTGTCTGTGG 564
QY 421 AGAAGGACCAACACATCACCCTGTGGAGCAGCTCAACCTGAATGGCTCTGTGAGGCT 480
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Db 565 AGAAGGACCAACACATCACCCTGTGGAGCAGCTCAACCTGAATGGCTCTGTGAGGCT 624
QY 481 CTTGAGAGCCCTGATCATTTGAAGGGGAATCTGGAAGCAAGTCCACTCTGTGCGAG 540
Db 625 CTTGAGAGCCCTGATCATTTGAAGGGGAATCTGGAAGCAAGTCCACTCTGTGCGAG 684
QY 541 CGCATTTGCCATGCTCTGGGGCTCCGAAAGTCAAGGCTCTGACCAAGTTCAAATTCGTC 600
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Db 685 CGAATTTGCCATGCTCTGGGGCTCCGAAAGTCAAGGCTCTGACCAAGTTCAAATTCGTC 744
QY 601 TTTCTTCTCCGCTCTCAGAGAGGCCACAGGCTGGACTTTTGAACCTCTGTGATCAACTC 660
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Db 745 TTTCTTCTCCGCTCTCAGAGAGGCCACAGGCTGGACTTTTGAACCTCTGTGATCAACTC 804
QY 661 CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGCGCCATGCTGTGAAGCTGGG 720
Db 805 CTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGCGCCATGCTGTGAAGCTGGG 864
QY 721 CAGAGGTTCTTTTCTTCTGATGCTACATGAATCAAGCCCGCAGAACTGCCCAGAA 924
Db 865 CAGAGGTTCTTTTCTTCTGATGCTACATGAATCAAGCCCGCAGAACTGCCCAGAA 984
QY 781 ATCGAAGCCCTGATAAGGAAGAAACCCGCTTCAGAACATGGTCTGTCACACTACC 840
Db 925 ATCGAAGCCCTGATAAGGAAGAAACCCGCTTCAGAACATGGTCTGTCACACTACC 984
QY 841 ACTGAGTGCCTGAGGCACATACGCGAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATG 900
Db 985 ACTGAGTGCCTGAGGCACATACGCGAGTTTGGTGGCCCTGACTGCTGAGGTGGGGATATG 1044
QY 901 ACAGAAGCAGCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGAGCTTGTCTGAAGGC 960
Db 1045 ACAGAAGCAGCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGAGCTTGTCTGAAGGC 1104
QY 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTT 1020
Db 1105 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTT 1164
QY 1021 GTGGTCTACATCTGTGCAATCCAGATGGGTGAAAGTGAAGTTCACCTCTCACACAAACA 1080
Db 1165 GTGGTCTACATCTGTGCAATCCAGATGGGTGAAAGTGAAGTTCACCTCTCACACAAACA 1224
QY 1081 ACGCTGTTCCATACCTTCTATGATCTGTGTATACAGAAAAACAAACAAACATAAAGGT 1140
Db 1225 ACGCTGTTCCATACCTTCTATGATCTGTGTATACAGAAAAACAAACAAACATAAAGGT 1284
QY 1141 GTGGCTGCAAGAGTCTTCATTCTGGAGCCTGGACCCTGTGGAGACCTAGCTCTGGAGGT 1200
|||||

Db 1285 GTGGCTGCAAGTGACTTCATTCCGAGCCTGGACCCTGTGGAGACCTAGCTCTGGAGGT 1344
QY 1201 GTGTTTTCOCACAAAGTTTGATTTTCGAACCTGCAGGATGTCTCCAGCGTGAATGAGGATGC 1260
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Db 1345 GTGTTTTCOCACAAAGTTTGATTTTCGAACCTGCAGGATGTCTCCAGCGTGAATGAGGATGC 1404
QY 1261 CTGCTTACAACTGGGCTCCTCTGTAAATATACAGCTCAAAAGTTTCAAGCCAAAGATATAA 1320
Db 1405 CTGCTTACAACTGGGCTCCTCTGTAAATATACAGCTCAAAAGTTTCAAGCCAAAGATATAA 1464
QY 1321 TTCTTTTCACACTGCATCCAGGATACACAGCAGACGAGAACTCAGCAGTTTATTGAGC 1380
Db 1465 TTCTTTTCACACTGCATCCAGGATACACAGCAGACGAGAACTCAGCAGTTTATTGAGC 1524
QY 1381 TCTCAAGAGGAGGTGACCAAGGGGAATGTTACTTTCAGANAATGTTTCCAT 1440
Db 1525 TCTCAAGAGGAGGTGACCAAGGGGAATGTTACTTTCAGANAATGTTTCCAT 1584
QY 1441 TCGGAATTTACATTCACCTTATAGCAGCCTGTCTCCGGTACACCTGTGGGTCTCTGTGGAA 1500
Db 1585 TCGGAATTTACATTCACCTTATAGCAGCCTGTCTCCGGTACACCTGTGGGTCTCTGTGGAA 1644
QY 1501 GCCACTAGGCTGTATGAAGCAGCTTCGACAGCTGTATCAACACGCTGCCTTCTCGGA 1560
Db 1645 GCCACTAGGCTGTATGAAGCAGCTTCGACAGCTGTATCAACACGCTGCCTTCTCGGA 1704
QY 1561 CTTTCTATCGCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1620
Db 1705 CTTTCTATCGCCAAGAGGCTCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACACC 1764
QY 1621 ACTGAACTCAAGAAATCTGAAAGCCATAACATCAATCTCTTTGTAGAGTGTGGCATCCAT 1680
Db 1765 ACTGAGCAAGAAATCTGAAAGCCATAACATCAATCTCTTTGTAGAGTGTGGCATCCAT 1824
QY 1681 TTATATTAAGAGATACATCCAAATCAGCCCTGAGCAGAAATTTGAAGCTTCTTTTCAA 1740
Db 1825 TTATATTAAGAGATACATCCAAATCAGCCCTGAGCAGAAATTTGAAGCTTCTTTTCAA 1884
QY 1741 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATCTACTTATTTGACTTCTTTGAA 1800
Db 1885 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATCTACTTATTTGACTTCTTTGAA 1944
QY 1801 CATTGTCCAAATTTGCAAGTCTCTGGACTTCATTAACTGAGCTTTTATGGGAGCT 1860
Db 1945 CATTGTCCAAATTTGCAAGTCTCTGGACTTCATTAACTGAGCTTTTATGGGAGCT 2004
QY 1861 ATGGCTTCATGGGAAAGGCTGCAGAAACAGACAGCTGGAATCCACATGGAAGAGCCCA 1920
Db 2005 ATGGCTTCATGGGAAAGGCTGCAGAAACAGACAGCTGGAATCCACATGGAAGAGCCCA 2064
QY 1921 GAAACCACATTCAGAGGCTGTATCTTTGTTCTTCACTGGAAGCAGAAATTCAG 1980
Db 2065 GAAACCACATTCAGAGGCTGTATCTTTGTTCTTCACTGGAAGCAGAAATTCAG 2124
QY 1981 ACTCTGTAAGTCACTCCGGATTTCAAGCAAGTTGAATAAGCAAGATATCATATCTG 2040
Db 2125 ACTCTGTAAGTCACTCCGGATTTCAAGCAAGTTGAATAAGCAAGATATCATATCTG 2184
QY 2041 GGGAAATATTTCAGCTCTGCCACAAAGCCTCAGGCTGCAAAATAAGAGATGTCTGTGTG 2100
Db 2185 GGGAAATATTTCAGCTCTGCCACAAAGCCTCAGGCTGCAAAATAAGAGATGTCTGTGTG 2244
QY 2101 GCTGGAAGCCTCAGTTTGTCTCTAGCAGCTTCAGGCTGCAAAATAAGAGATGTCTGTGTG 2160
Db 2245 GCTGGAAGCCTCAGTTTGTCTCTAGCAGCTTCAGGCTGCAAAATAAGAGATGTCTGTGTG 2304
QY 2161 GCCAGTCCCTCACCATAGAAGATGAGAGGACATCACATCTGTAACAACTGGAAC 2220
Db 2305 GCCAGTCCCTCACCATAGAAGATGAGAGGACATCACATCTGTAACAACTGGAAC 2364
QY 2221 TTGAGTATTCATGAGCTACAGAACTAACGCTGCGGCTGCTGACTGACAGCTTGGT 2280
|||||

Qy 961 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTGAGGAATCTCATGAAGACCCCTCTCTTT 1020
Db 1192 TTGTTGCTCCAAATTCAGAAATCCAGGTGCTGAGGAATCTCATGAAGACCCCTCTCTTT 1251
Qy 1021 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTTCACACACAACA 1080
Db 1252 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTTCACACACAACA 1311
Qy 1081 ACGCTGTTCCTACACTTCTATGATCTGTGATACAGAAAAACAACAACAATAAAGGT 1140
Db 1312 ACGCTGTTCCTACACTTCTATGATCTGTGATACAGAAAAACAACAACAATAAAGGT 1371
Qy 1141 GTGGTCGAAGTGAATTCATTCGGAGCCTGCACCACTGTGAGACCTAGCTCTGAGAGGT 1200
Db 1372 GTGGTCGAAGTGAATTCATTCGGAGCCTGCACCACTGTGATACCTAGCTCTGAGAGGT 1431
Qy 1201 GTGGTCGCCCAAGTTGATTTCCAACTGCAGATGTGTCAGGGGCAATGAGATGTC 1260
Db 1432 GTGGTCGCCCAAGTTGATTTCCAACTGCAGATGTGTCAGGGGCAATGAGATGTC 1491
Qy 1261 CTGCTGACAACTGGCTCCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAA 1320
Db 1492 CTGCTGACAACTGGCTCCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAA 1551
Qy 1321 TTCCTTCAAGTCAATTCAGGAGTACACACAGAGCAAGACTCAGCAGTTTATGAGC 1380
Db 1552 TTCCTTCAAGTCAATTCAGGAGTACACACAGAGCAAGACTCAGCAGTTTATGAGC 1611
Qy 1381 TCTCATGAGCAGAGGAGTGAACCAAGGGAATGGTTACTTGCAGAAAAATGGTTCCATT 1440
Db 1612 TCTCATGAGCAGAGGAGTGAACCAAGGGAATGGTTACTTGCAGAAAAATGGTTCCATT 1671
Qy 1441 TCGGACATTACATCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGTCACTGTGGAA 1500
Db 1672 TCGGACATTACATCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGTCACTGTGGAA 1731
Qy 1501 GCCACCAAGGCTGTATGAAGCACTCGCAGCAGTGTATCAACACGGCTGCTTCGGGA 1560
Db 1732 GCCACCAAGGCTGTATGAAGCACTCGCAGCAGTGTATCAACACGGCTGCTTCGGGA 1791
Qy 1561 CTTTCCATCGCAAGAGCCCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACCC 1620
Db 1792 CTTTCCATCGCAAGAGCCCTCTGGAGACAGGAATCTTTGCAAGTGTGAAAAACCC 1851
Qy 1621 ACTGAGCAAGAAATCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCCAT 1680
Db 1852 ACTGAGCAAGAAATCTGAAAGCCATAAACAATCAATTCCTTTGTAGAGTGTGGCATCCAT 1911
Qy 1681 TTATATCAAGAGTACATCAAAATCAGCCCTGAGCCAGAAATTTGAAGCTTCTTCAA 1740
Db 1912 TTATATCAAGAGTACATCAAAATCAGCCCTGAGCCAGAAATTTGAAGCTTCTTCAA 1971
Qy 1741 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATTACTTATTTGACTCTTTGAA 1800
Db 1972 GGTAAAGCTTATATCAACTCAGGGAACATCCCGATTACTTATTTGACTCTTTGAA 2031
Qy 1801 CATTTGCCCAATGTGCAAGTCTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCT 1860
Db 2032 CATTTGCCCAATGTGCAAGTCTCTGGACTTCATTAACCTGGACTTTTATGGGGAGCT 2091
Qy 1861 ATGGCTTCATGGAAAAAGGCTGCAGAGACACACAGGTGGAATCCACATGGAAGAGGCCCA 1920
Db 2092 ATGGCTTCATGGAAAAAGGCTGCAGAGACACACAGGTGGAATCCACATGGAAGAGGCCCA 2151
Qy 1921 GAAACCTACATTCACGACGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGG 1980
Db 2152 GAAACCTACATTCACGACGGCTGTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGG 2211
Qy 1981 ACTCTGGAGGTCACACTCCGGGATTTTCAGCAAGTTTGAATAAGCAAGATATCAGATNTCTG 2040
Db 2212 ACTCTGGAGGTCACACTCCGGGATTTTCAGCAAGTTTGAATAAGCAAGATATCAGATNTCTG 2271

Qy 2041 GGGAAJATATTTACGCTTGCCACAAGCCTCAGGCTGCAAAATAAAGAGATGCTGCTGGTGTG 2100
Db 2272 GGGAAJATATTTACGCTTGCCACAAGCCTCAGGCTGCAAAATAAAGAGATGCTGCTGGTGTG 2331
Qy 2101 GCTGGJAGCCTCAGTTTGGTCTCAGCACCTGTGAAGAACATTTATTTCTCTCATGCTGGAA 2160
Db 2332 GCTGGJAGCCTCAGTTTGGTCTCAGCACCTGTGAAGAACATTTATTTCTCTCATGCTGGAA 2391
Qy 2161 GCCAGJCCCTCCACATAGAAGATGAGAGGCACATCATCTGTAAACAAACCTGAAAAACC 2220
Db 2392 GCCAGJCCCTCCACATAGAAGATGAGAGGCACATCATCTGTAAACAAACCTGAAAAACC 2451
Qy 2221 TTGAGJATTCATGACCTTACAGAATCAACGGCTGCGGGTGTCTGACTGACAGCTTGGGT 2280
Db 2452 TTGAGJATTCATGACCTTACAGAATCAACGGCTGCGGGTGTCTGACTGACAGCTTGGGT 2511
Qy 2281 AACCTTGAGACCTTACAAAGCTCATATATGATACATTAAGATCAATGAAGAGAGTCT 2340
Db 2512 AACCTTGAGACCTTACAAAGCTCATATATGATACATTAAGATCAATGAAGAGAGTCT 2571
Qy 2341 ATAAAAJTAGCTGAAGGCTGAAAAACCTGAAGAAGATGTTTATTTTCATTTGACCCAC 2400
Db 2572 ATAAAAJTAGCTGAAGGCTGAAAAACCTGAAGAAGATGTTTATTTTCATTTGACCCAC 2631
Qy 2401 TTGTCTJACATTTGAGAGGGAATGGATTAACATAGTCAAGTCTCTGTCGAAGTGAACCTGT 2460
Db 2632 TTGTCTJACATTTGAGAGGGAATGGATTAACATAGTCAAGTCTCTGTCGAAGTGAACCTGT 2691
Qy 2461 GACCTTJAAAGAAATTCATTAATAGTCTCCTGCTGCTTGTCTGCAAAATGCAAGTGAAGAAATCCTA 2520
Db 2692 GACCTTJAAAGAAATTCATTAATAGTCTCCTGCTGCTTGTCTGCAAAATGCAAGTGAAGAAATCCTA 2751
Qy 2521 GCTCAGJATCTTCAAAATTTGGTCAAACTGAGCATCTTGTGATTTATCAGAAAAATACCTG 2580
Db 2752 GCTCAGJATCTTCAAAATTTGGTCAAACTGAGCATCTTGTGATTTATCAGAAAAATACCTG 2811
Qy 2581 GAAAAAJATGGAATGAAGCTCTTCATGAACATGACAGAGTGAAGTCTAGAACAG 2640
Db 2812 GAAAAAJATGGAATGAAGCTCTTCATGAACATGACAGAGTGAAGTCTAGAACAG 2871
Qy 2641 CTCACJCACTGATGCTGCCCTGGGCTGTGACCTGCAAGCAGCCCTGAGCAGCTGTTG 2700
Db 2872 CTCACJCACTGATGCTGCCCTGGGCTGTGACCTGCAAGCAGCCCTGAGCAGCTGTTG 2931
Qy 2701 AAACATJTGAGAGGTCACCAACTCTCAAGCTTGGTTGAAAACTGGAGACTCACA 2760
Db 2932 AAACATJTGAGAGGTCACCAACTCTCAAGCTTGGTTGAAAACTGGAGACTCACA 2991
Qy 2761 GATACAGATTAGAATTTTAGTGCATTTTGGAAAGAACCCCTCTGAAAACTTCAG 2820
Db 2992 GATACAGATTAGAATTTTAGTGCATTTTGGAAAGAACCCCTCTGAAAACTTCAG 3051
Qy 2821 CAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGAATGGCTTGCCCTTCATGGGTGA 2880
Db 3052 CAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGAATGGCTTGCCCTTCATGGGTGA 3111
Qy 2881 TTTGAGATCTTAAGCAATTAGTGTTTTGGACTTTTAGTACTAAGAAATTTCTACCTGAT 2940
Db 3112 TTTGAGATCTTAAGCAATTAGTGTTTTGGACTTTTAGTACTAAGAAATTTCTACCTGAT 3171
Qy 2941 CCAGCATTAGTCAGAAAACTTAGCCAAAGTGTATCCCAAGTTAACTTTTCTCAAGAGCT 3000
Db 3172 CCAGCATTAGTCAGAAAACTTAGCCAAAGTGTATCCCAAGTTAACTTTTCTCAAGAGCT 3231
Qy 3001 AGGCTTGCTGGTGGCAATTTGATGATGATGATCTCAGTGTATTACAGAGTGTAAAA 3060
Db 3232 AGGCTTGCTGGTGGCAATTTGATGATGATGATCTCAGTGTATTACAGAGTGTAAAA 3291
Qy 3061 CTAGTAATTCGT 3072
Db 3292 CTAGTAATTCGT 3303

RESULT 4

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US-10-203-138A-4307
; Sequence 4307, Application US/10203138A
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203,138A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 4307
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011232.3
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; US-10-203-138A-4307

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DEPT 5

RESULT 5
 US-10-203-138A-9429
 ; Sequence 9429, Application US/10203138A
 ; GENERAL INFORMATION:
 ; APPLICANT: Molecular Dynamics, Inc.
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ;
 ; TITLE OF INVENTION: RECEPTOR GENES ASSOCIATED WITH DISEASE, METHODS OF DETECTION
 ; FILE REFERENCE: CL000848
 ; CURRENT APPLICATION NUMBER: US/09/949,004
 ; CURRENT FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: 60/232,045
 ; PRIOR FILING DATE: 2000-09-13
 ; NUMBER OF SEQ ID NOS: 6961

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6715
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-004-6715

Query Match 0.7%; Score 20; DB 5; Length 601;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 693 ATTATGGCCATGCTGCTGA 712
|||||
Db 140 ATTATGGCCATGCTGCTGA 159

RESULT 7
; Sequence 693, Application US/09949004
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR GENES ASSOCIATED WITH DISEASE, METHODS OF DETECTION
; FILE REFERENCE: C1000848
; CURRENT APPLICATION NUMBER: US/09/949,004
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/232,045
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 6961
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 693
; LENGTH: 209798
; TYPE: DNA
; ORGANISM: Human
US-09-949-004-693

Query Match 0.7%; Score 20; DB 5; Length 209798;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 693 ATTATGGCCATGCTGCTGA 712
|||||
Db 102520 ATTATGGCCATGCTGCTGA 102539

RESULT 8
US-09-531-113-38966/c
; Sequence 38966, Application US/09531113
; GENERAL INFORMATION:
; APPLICANT: Byrum, Gregory R.
; APPLICANT: Heck, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15761)B
; CURRENT APPLICATION NUMBER: US/09/531,113
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 48629
; SEQ ID NO 38966
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700943742H1
US-09-531-113-38966

Query Match 0.6%; Score 19; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 988 TGGTTGAGGAATCTCATGA 1006
|||||
Db 23 TGGTTGAGGAATCTCATGA 5

RESULT 9
US-10-240-425-462
; Sequence 462, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Foland, Joseph F.
; APPLICANT: Ford, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 462
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AI082708
US-10-240-425-462

Query Match 0.6%; Score 19; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2193 CATCACCTCTCTAACAAAC 2211
|||||
Db 346 CATCACCTCTCTAACAAAC 364

RESULT 10
US-09-724-676-1613/c
; Sequence 16013, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16013
; LENGTH: 5513
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-16013

Query Match 0.6%; Score 19; DB 5; Length 5513;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1576 AGGCCTCCTGGAGACAGG 1594
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Db 1853 AGGCCTCCTGGAGACAGG 1835

RESULT 11
US-09-724-676A-16013/c
; Sequence 16013, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16013
; LENGTH: 5513
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-16013

Query Match 0.6%; Score 19; DB 5; Length 5513;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1576 AGGCCTCTGGAGACAGG 1594
|||||
DB 1853 AGGCCTCTGGAGACAGG 1835

RESULT 12
PCT-US02-32727-122/c
; Sequence 122, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Fanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514c1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 122
; LENGTH: 8632
; TYPE: DNA
; ORGANISM: Propioni acnes
PCT-US02-32727-122

Query Match 0.6%; Score 19; DB 1; Length 8632;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1612 AAAACACCACCTGAGCAAG 1630
|||||
DB 8118 AAAACACCACCTGAGCAAG 8100

RESULT 13
US-10-057-498-122/c
; Sequence 122, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 122
; LENGTH: 8632
; TYPE: DNA
; ORGANISM: Propioni acnes

US-10-057-498-122

Query Match 0.6%; Score 19; DB 6; Length 8632;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1612 AAAACACCACCTGAGCAAG 1630
|||||
DB 8118 AAAACACCACCTGAGCAAG 8100

RESULT 14
US-10-293-783-96/c
; Sequence 96, Application US/10293783
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST E
; FILE REFERENCE: ISPH-0544
; CURRENT APPLICATION NUMBER: US/10/293,783
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US/09/800,631
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US/09/657,346
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 96
; LENGTH: 30310
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19791)...(19802)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21160)...(21370)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (24168)...(24307)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25696)...(25908)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27235)...(27246)
US-10-293-783-96

Query Match 0.6%; Score 19; DB 6; Length 30310;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1265 TGACAACTGGGCTCCTCTG 1283
|||||
DB 13062 TGACAACTGGGCTCCTCTG 13044

RESULT 15
PCT-US02-32700-8
; Sequence 8, Application PC/TUS0232700
; GENERAL INFORMATION:
; APPLICANT: Keith, Tim
; APPLICANT: Little, Randall D.
; APPLICANT: Van Eerdewegh, Paul
; APPLICANT: Dupuis, Josee
; APPLICANT: Del Mastro, Richard G.
; APPLICANT: Allen, Kristina
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2976-4045
; CURRENT APPLICATION NUMBER: PCT/US02/32700
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/328,424
; PRIOR FILING DATE: 2001-10-11

; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 302603
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US02-32700-8

Query Match 0.6%; Score 19; DB 1; Length 302603;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2192 ACATCACATCTCTACAAA 2210
|||||
Db 156828 ACATCACATCTCTACAAA 156846

RESULT 16
US-10-271-416-8
; Sequence 8, Application US/10271416
; GENERAL INFORMATION:
; APPLICANT: Keith, Tim
; APPLICANT: Little, Randall D.
; APPLICANT: Van Eerdewegh, Paul
; APPLICANT: Dupuis, Josee
; APPLICANT: Del Mastro, Richard G.
; APPLICANT: Allen, Kristina
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE: 2976-4045
; CURRENT APPLICATION NUMBER: US/10/271,416
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/328,424
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 302603
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-271-416-8

Query Match 0.6%; Score 19; DB 6; Length 302603;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2192 ACATCACATCTCTACAAA 2210
|||||
Db 156828 ACATCACATCTCTACAAA 156846

RESULT 17
US-09-948-124-119/c
; Sequence 119, Application US/09948124
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON CH
; TITLE OF INVENTION: Y, METHODS OF DETECTION, AND USES THEREOF
; FILE REFERENCE: CL001301
; CURRENT APPLICATION NUMBER: US/09/948,124
; CURRENT FILING DATE: 2002-12-23
; NUMBER OF SEQ ID NOS: 183
; SEQ ID NO 119
; LENGTH: 428573
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(428573)
; OTHER INFORMATION: n = A,T,C or G
US-09-948-124-119

Query Match 0.6%; Score 19; DB 5; Length 428573;

Best Local Similarity 100.0%; Pred. No. 44;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1496 TGGAAACCCACAGGGCTGT 1514
|||||
Db 166944 TGGAAACCCACAGGGCTGT 166926

RESULT 18
US-10-303-778-1:466
; Sequence 1546, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: Rsettagenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1546
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-1:466

Query Match 0.6%; Score 18; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTCATTAAGGAC 18
|||||
Db 1 ATGAATTCATTAAGGAC 18

RESULT 19
US-10-310-188-29161
; Sequence 29161, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: Rsettagenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY G
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29161
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-29161

Query Match 0.6%; Score 18; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTCATTAAGGAC 18
|||||
Db 1 ATGAATTCATTAAGGAC 18

RESULT 20
US-60-427-836-33174/c
; Sequence 33474 Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xu; Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 33474
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-33474

Query Match 0.6%; Score 18; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1337 TCCAGGAGTACACAGCAG 1354
Db 24 TCCAGGAGTACACAGCAG 7

RESULT 21
US-09-513-999C-19061
; Sequence 19061, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 19061
; LENGTH: 116
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-19061

Query Match 0.6%; Score 18; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 AGCAATACACAGATGACC 79
Db 47 AGCAATACACAGATGACC 64

RESULT 22
US-10-286-136-502/c
; Sequence 502, Application US/10286136
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Murine Polynucleotide Tags
; FILE REFERENCE: LEX-0049-USA
; CURRENT APPLICATION NUMBER: US/10/286,136
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US/09/677,367
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US 60/157,364
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 1000
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 502
; LENGTH: 124
; TYPE: DNA
; ORGANISM: mus musculus
US-10-286-136-502

Query Match 0.6%; Score 18; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2378 TGTGTTTATTTCATTGA 2395
Db 99 TGTGTTTATTTCATTGA 82

RESULT 23
US-10-266-131-1575
; Sequence 1575, Application US/10266131
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Murine Polynucleotide Tags and
; TITLE OF INVENTION: Mutant Cells and Mutant Animals Defined Thereby
; FILE REFERENCE: LEX-0030-USA
; CURRENT APPLICATION NUMBER: US/10/266,131
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/09/617,675
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/143,878
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 2908
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1575
; LENGTH: 143
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-266-131-1575

Query Match 0.6%; Score 18; DB 6; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2411 TTGGAGAGGGAATGGATT 2428
Db 52 TTGGAGAGGGAATGGATT 69

RESULT 24
US-09-531-113-19390/c
; Sequence 19390, Application US/09531113
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15761)B
; CURRENT APPLICATION NUMBER: US/09/531,113
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 48629
; SEQ ID NO 19390
; LENGTH: 199
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700957045H1
US-09-531-113-19390

Query Match 0.6%; Score 18; DB 5; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2746 AACTGGAGACTCACAGAT 2763
Db 124 AACTGGAGACTCACAGAT 107

RESULT 25
US-09-531-113-22263/c
; Sequence 22263, Application US/09531113
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.

; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15761)B
; CURRENT APPLICATION NUMBER: US/09/531.113
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 48629
; SEQ ID NO 22263
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700952841H1
US-09-531-113-22263

Query Match 0.6%; Score 18; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3016 CAATTGTGATGATGAT 3033
|||||
Db 145 CAATTGTGATGATGAT 128

RESULT 26
US-09-531-113-25999/c
; Sequence 25999, Application US/09531113
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15761)B
; CURRENT APPLICATION NUMBER: US/09/531.113
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 48629
; SEQ ID NO 25999
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 700905370H1
US-09-531-113-25999

Query Match 0.6%; Score 18; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 915 CCAGGCTCTCATCCGAGA 932
|||||
Db 164 CCAGGCTCTCATCCGAGA 147

RESULT 27
US-09-531-113-37454
; Sequence 37454, Application US/09531113
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15761)B
; CURRENT APPLICATION NUMBER: US/09/531.113
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 48629
; SEQ ID NO 37454
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700945701H1
US-09-531-113-37454

Query Match 0.6%; Score 18; DB 5; Length 270;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 TGGAACTATCCTCTATTT 243
|||||
Db 215 TGGAACTATCCTCTATTT 232

RESULT 28
US-09-513-999C-13408/c
; Sequence 13408, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Luciert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 13408
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 123
; OTHER INFORMATION: y-c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 130
; OTHER INFORMATION: k-g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 423
; OTHER INFORMATION: w-a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 423
; OTHER INFORMATION: r-a or g
US-09-513-999C-13408

Query Match 0.6%; Score 18; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATATCATAAAGGAC 18
|||||
Db 106 ATGAATATCATAAAGGAC 89

RESULT 29
US-10-203-138A-4790/c
; Sequence 4790, Application US/10203138A
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Ruck, David R.
; APPLICANT: Huzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203.138A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456

```
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 4790
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL109823.11
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.2
US-10-203-138A-4790

Query Match          0.6%; Score 18; DB 6; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 GGGGAATCGGCAAGGC 522
DB 29 GGGGAATCGGCAAGGC 12

RESULT 30
US-09-513-999C-1807
; Sequence 1807, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1807
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 300..464
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 127
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 139
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 455
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 456
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 53
```

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; OTHER INFORMATION: Xaa=Ile or Leu
US-09-513-999C-1807

Query Match          0.6%; Score 18; DB 5; Length 466;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 731 TTTTCCTTCTTGATGGCT 748
DB 220 TTTTCCTTCTTGATGGCT 237

RESULT 31
US-10-203-138A-1760
; Sequence 1760, Application US/10203138A
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203,138A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 1760
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010087.2
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
US-10-203-138A-1760

Query Match          0.6%; Score 18; DB 6; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 AGAAGGTGGAGGAGGATG 148
DB 143 AGAAGGTGGAGGAGGATG 160

RESULT 32
US-09-747-358A-688/c
; Sequence 888, Application US/09747358A
; GENERAL INFORMATION:
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Polynucleotides and
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: LEX-0112-USA
; CURRENT APPLICATION NUMBER: US/09/747,358A
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 60/174,283
```

; PRIOR FILING DATE: 2000-01-03
; NUMBER OF SEQ ID NOS: 1008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 688
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(481)
; OTHER INFORMATION: n = A,T,C or G
US-09-747-358A-688

Query Match 0.6%; Score 18; DB 5; Length 481;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 379 ATTTTAACTGAAAGC 396
|||||
Db 253 ATTTTAACTGAAAGC 236

RESULT 33
US-09-949-002-8756/c
; Sequence 8756, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8756
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-8756

Query Match 0.6%; Score 18; DB 5; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3025 GATGATGATCTCAGTGT 3042
|||||
Db 256 GATGATGATCTCAGTGT 239

RESULT 34
US-09-949-002-8757/c
; Sequence 8757, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8757
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-8757

Query Match 0.6%; Score 18; DB 5; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3025 GATGATGATCTCAGTGT 3042
|||||
Db 350 GATGATGATCTCAGTGT 333

RESULT 35
US-09-134-000C-1076
; Sequence 1076, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1076

Query Match 0.6%; Score 18; DB 5; Length 885;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2492 GCTTGT.TGCAATGCAG 2509
|||||
Db 107 GCTTGT.TGCAATGCAG 124

RESULT 36
US-09-134-000C-1076
; Sequence 1076, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1076
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1076

Query Match 0.6%; Score 18; DB 5; Length 885;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2492 GCTTGT.TGCAATGCAG 2509
|||||
Db 107 GCTTGT.TGCAATGCAG 124

RESULT 37
US-09-724-676-3618/c
; Sequence 3688, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3688
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-3688

Query Match 0.6%; Score 18; DB 5; Length 986;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGAC 18
|||||

Db 630 ATGAATTTTCATAAAGGAC 613
|||||

RESULT 38
US-09-724-676-3693/c
; Sequence 3693, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3693
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-3693

Query Match 0.6%; Score 18; DB 5; Length 986;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGAC 18
|||||

Db 630 ATGAATTTTCATAAAGGAC 613
|||||

RESULT 39
US-09-724-676A-3688/c
; Sequence 3688, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3688
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-3688

Query Match 0.6%; Score 18; DB 5; Length 986;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGAC 18
|||||

Db 630 ATGAATTTTCATAAAGGAC 613
|||||

RESULT 40

US-09-724-676A-3693/c
; Sequence 3693, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3693
; LENGTH: 986
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-3693

Query Match 0.6%; Score 18; DB 5; Length 986;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGAC 18
|||||

Db 630 ATGAATTTTCATAAAGGAC 613
|||||

RESULT 41
US-09-724-676-3689/c
; Sequence 3689, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3689
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-3689

Query Match 0.6%; Score 18; DB 5; Length 998;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGAC 18
|||||

Db 630 ATGAATTTTCATAAAGGAC 613
|||||

RESULT 42
US-09-724-676-3694/c
; Sequence 3694, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3694
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-3694

Query Match 0.6%; Score 18; DB 5; Length 998;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATTTTCATAAAGGAC 18

Db 630 ATGAATTCATAAAGGAC 613
|||||

RESULT 43

US-09-724-676A-3689/c

; Sequence 3689, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724.676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3689

; LENGTH: 998

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676A-3689

Query Match 0.6%; Score 18; DB 5; Length 998;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATTCATAAAGGAC 18

|||||

Db 630 ATGAATTCATAAAGGAC 613

RESULT 44

US-09-724-676A-3694/c

; Sequence 3694, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724.676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3694

; LENGTH: 998

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676A-3694

Query Match 0.6%; Score 18; DB 5; Length 998;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATTCATAAAGGAC 18

|||||

Db 630 ATGAATTCATAAAGGAC 613

RESULT 45

US-10-264-237-181/c

; Sequence 181, Application US/10264237

; GENERAL INFORMATION:

; APPLICANT: Birse et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: P131P1

; CURRENT APPLICATION NUMBER: US/10/264.237

; CURRENT FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: PCT/US01/16450

; PRIOR FILING DATE: 2001-05-18

; PRIOR APPLICATION NUMBER: US 60/205,515

; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ ID NOS: 2876

; SOFTWARE: PatentIn Ver. 3.1

; SEQ ID NO 181

; LENGTH: 1243

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-264-237-181

Query Match

Best Local Similarity 100.0%; Score 18; DB 6; Length 1243;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 415 CTGTGKAGGAAGGACCA 432

|||||

Db 474 CTGTGKAGGAAGGACCA 457

RESULT 46

PCT-US02-38446-58

; Sequence 98, Application PC/TUS0238446

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: TANG, Y. Tom

; APPLICANT: CHAWLA, Narinder K.

; APPLICANT: IU, Dyung Aina M.

; APPLICANT: PHAN, Farrah A.

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: SWARNAKAR, Anita

; APPLICANT: ZIMZAI, Yalda

; APPLICANT: MARQUIS, Joseph P.

; APPLICANT: PRAGUE, William W.

; APPLICANT: EMERLING, Brooke M.

; APPLICANT: YUE, Henry

; APPLICANT: EROWSKY, Mark L.

; APPLICANT: ECHA, Shaoya D.

; APPLICANT: ISON, Craig H.

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: HAFALIA, April J.A.

; APPLICANT: KING, Huibin Z.

; APPLICANT: WARREN, Bridget A.

; APPLICANT: GIEZEN, Kimberly J.

; APPLICANT: IRAN, Oyen K.

; APPLICANT: LEE, Soo Yeun

; APPLICANT: ERNESTINE A.

; APPLICANT: RICHARDSON, Thomas W.

; APPLICANT: KABLE, Amy E.

; APPLICANT: BURFORD, Neil

; APPLICANT: LEHR-MASON, Patricia M.

; APPLICANT: GORVAD, Ann E.

; APPLICANT: LEE, Sally

; APPLICANT: BLAKE, Julie J.

; APPLICANT: HONCHELL, Cynthia D.

; APPLICANT: THANGAVELU, Kavitha

; APPLICANT: RAMKUMAR, Jayalaxmi

; APPLICANT: CHEN, David

; APPLICANT: JIN, Pei

; APPLICANT: CHANG, Hsin-Ru

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: NUYNEN, Dannie B.

; APPLICANT: KHARE, Reena

; APPLICANT: BHATIA, Umesh

; APPLICANT: BURRILL, John D.

; APPLICANT: HJ, Anne

; APPLICANT: ZIENG, Wenjin

; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT

; FILE REFERENCE: P1-1302 PCT

; CURRENT APPLICATION NUMBER: PCT/US02/38446

; CURRENT FILING DATE: 2002-11-25

; PRIOR APPLICATION NUMBER: US 60/334,182

; PRIOR FILING DATE: 2001-11-28

; PRIOR APPLICATION NUMBER: US 60/342,052

; PRIOR FILING DATE: 2001-12-18

; PRIOR APPLICATION NUMBER: US 60/350,410

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: US 60/353,284

; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: US 60/363,649

```

; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 98
; LENGTH: 1297

```

Query Match 0.6%; Score 18; DB 1; Length 1297;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0 Indels

